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(54) Title: BIALLELIC MARKERS

(57) Abstract

The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele–specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, Ann. Rev. Biochem. 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) Is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., Am. J. Hum. Genet. 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic
analyses (see WO 90/13668; WO90/11369; Donis-Keller, *Cell*
51, 319-337 (1987); Lander *et al.*, *Genetics* 121, 85-99
(1989)). When a heritable trait can be linked to a
5   particular RFLP, the presence of the RFLP in an individual
can be used to predict the likelihood that the animal will
also exhibit the trait.

Other polymorphisms take the form of short tandem
repeats (STRs) that include tandem di-, tri- and tetra-
10   nucleotide repeated motifs. These tandem repeats are also
referred to as variable number tandem repeat (VNTR)
polymorphisms. VNTRs have been used in identity and
paternity analysis (US 5,075,217; Armour *et al.*, *FEBS Lett.*
307, 113-115 (1992); Horn *et al.*, WO 91/14003; Jeffreys, EP
15   370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide
variations between individuals of the same species. Such
polymorphisms are far more frequent than RFLPs, STRs and
VNTRs. Some single nucleotide polymorphisms occur in
20   protein-coding sequences, in which case, one of the
polymorphic forms may give rise to the expression of a
defective or other variant protein and, potentially, a
genetic disease. Examples of genes, in which polymorphisms
within coding sequences give rise to genetic disease
25   include β-globin (sickle cell anemia) and CFTR (cystic
fibrosis). Other single nucleotide polymorphisms occur in
noncoding regions. Some of these polymorphisms may also
result in defective protein expression (e.g., as a result
of defective splicing). Other single nucleotide
30   polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same
manner as RFLPs and VNTRs, but offer several advantages.
Single nucleotide polymorphisms occur with greater

frequency and are spaced more uniformly throughout the
genome than other forms of polymorphism. The greater
frequency and uniformity of single nucleotide polymorphisms
means that there is a greater probability that such a
5   polymorphism will be found in close proximity to a genetic
locus of interest than would be the case for other
polymorphisms. The different forms of characterized single
nucleotide polymorphisms are often easier to distinguish
than other types of polymorphism (e.g., by use of assays
10   employing allele-specific hybridization probes or primers).
        Only a small percentage of the total repository of
polymorphisms in humans and other organisms has been
identified. The limited number of polymorphisms identified
to date is due to the large amount of work required for
15   their detection by conventional methods. For example, a
conventional approach to identifying polymorphisms might be
to sequence the same stretch of DNA in a population of
individuals by dideoxy sequencing. In this type of
approach, the amount of work increases in proportion to
20   both the length of sequence and the number of individuals
in a population and becomes impractical for large stretches
of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a
5   polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying
10 the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These
15 oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table,
20 column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a
25 set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases
30 present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION
DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or
double-stranded. Oligonucleotides can be naturally

5   occurring or synthetic, but are typically prepared by
synthetic means. The oligonucleotides of the present
invention can comprise all of an oligonucleotide sequence
presented in column 7 of the Table or a segment of such an
oligonucleotide which includes a polymorphic site.

10 Oligonucleotides can be all of a nucleic acid segment as
represented in column 7 of the Table; a nucleic acid
sequence which comprises a nucleic acid segment represented
in column 7 of the Table and additional nucleic acids
(present at either or both ends of a nucleic acid segment

15 of column 7); or a portion (fragment) of a nucleic acid
segment represented in column 7 of the Table which includes
a polymorphic site. Preferred oligonucleotides of the
invention include segments of DNA, or their complements,
which include any one of the polymorphic sites shown in the

20 Table. The segments can be between 5 and 250 bases, and,
in specific embodiments, are between 5-10, 5-20, 10-20, 10-
50, 20-50 or 10-100 bases. The polymorphic site can occur
within any position of the segment. The segments can be
from any of the allelic forms of DNA shown in the Table.

25   Hybridization probes are oligonucleotides which bind in
a base-specific manner to a complementary strand of nucleic
acid. Such probes include peptide nucleic acids, as
described in Nielsen et al., Science 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-

30 stranded oligonucleotide which acts as a point of
initiation of template-directed DNA synthesis under
appropriate conditions (e.g., in the presence of four
different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from
5   15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.
10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with
15 the complement of the 3' end of the sequence to be amplified.

     As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same
20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

     As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site
25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include
30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified
allelic form is arbitrarily designated as the reference
form and other allelic forms are designated as alternative
or variant alleles. The allelic form occurring most
5 frequently in a selected population is sometimes referred
to as the wildtype form. Diploid organisms may be
homozygous or heterozygous for allelic forms. A diallelic
or biallelic polymorphism has two forms. A triallelic
polymorphism has three forms.
10   A single nucleotide polymorphism occurs at a
polymorphic site occupied by a single nucleotide, which is
the site of variation between allelic sequences. ~The site
is usually preceded by and followed by highly conserved
sequences of the allele (e.g., sequences that vary in less
15 than 1/100 or 1/1000 members of the populations).
    A single nucleotide polymorphism usually arises due to
substitution of one nucleotide for another at the
polymorphic site. A transition is the replacement of one
purine by another purine or one pyrimidine by another
20 pyrimidine. A transversion is the replacement of a purine
by a pyrimidine or vice versa. Single nucleotide
polymorphisms can also arise from a deletion of a
nucleotide or an insertion of a nucleotide relative to a
reference allele. Typically the polymorphic site is
25 occupied by a base other than the reference base. For
example, where the reference allele contains the base "T"
at the polymorphic site, the altered allele can contain a
"C", "G" or "A" at the polymorphic site.
    Hybridizations are usually performed under stringent
30 conditions, for example, at a salt concentration of no more
than 1 M and a temperature of at least 25°C. For example,
conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM
EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe
hybridizations. Equivalent conditions can be determined by
varying one or more of the parameters given as an example,
as known in the art, while maintaining a similar degree of
5   identity or similarity between the target nucleotide
sequence and the primer or probe used.

    The term "isolated" is used herein to indicate that the
material in question exists in a physical milieu distinct
from that in which it occurs in nature. For example, an
10   isolated nucleic acid of the invention may be substantially
isolated with respect to the complex cellular milieu in
which it naturally occurs. In some instances, the isolated
material will form part of a composition (for example, a
crude extract containing other substances), buffer system
15   or reagent mix. In other circumstance, the material may be
purified to essential homogeneity, for example as
determined by PAGE or column chromatography such as HPLC.
Preferably, an isolated nucleic acid comprises at least
about 50, 80 or 90 percent (on a molar basis) of all
20   macromolecular species present.

    I. Novel Polymorphisms of the Invention
    The novel polymorphisms of the invention are listed in
the Table. The first column of the Table lists the names
assigned to the fragments in which the polymorphisms occur.
25   The fragments are all human genomic fragments. The
sequence of one allelic form of each of the fragments
(arbitrarily referred to as the prototypical or reference
form) has been previously published. These sequences are
listed at http://www-genome.wi.mit.edu/ (all STS's
30   (sequence tag sites)); http://shgc.stanford.edu (Stanford
STS's); and http://ww.tigr.org/ (TIGR STS's). The Web
sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are
expressed sequence tags, and some are random genomic
fragments. All information in the websites concerning the
fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.
       The second column lists the position in the fragment in
which a polymorphic site has been found. Positions are
numbered consecutively with the first base of the fragment
sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base
occupying the polymorphic site in the sequence in the data
base. This base is arbitrarily designated the reference or
prototypical form, but it is not necessarily the most
frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The
fifth column of the Table lists a 5' (upstream or forward)
primer that hybridizes with the 5' end of the DNA sequence
to be amplified. The sixth column of the Table lists a 3'
(downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified.
The seventh column of the Table lists a number of bases of
sequence on either side of the polymorphic site in each
fragment. The indicated sequences can be either DNA or
RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site
is indicated in EUPAC-IUB ambiguity code.

       II. Analysis of Polymorphisms
          A. Preparation of Samples
          Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic
DNA, virtually any biological sample (other than pure red
blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For

5   example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. *See generally PCR Technology:*

10 *Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucleic Acids Res.* 19, 4967 (1991); Eckert *et al.*, *PCR*

15 *Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren *et al.*, *Science* 241, 1077 (1988),

20 transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification

25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30   B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is
carried out to identify polymorphic sites not previously
characterized (i.e., to identify new polymorphisms). This
analysis compares target sequences in different individuals
5   to identify points of variation, i.e., polymorphic sites.
By analyzing groups of individuals representing the
greatest ethnic diversity among humans and greatest breed
and species variety in plants and animals, patterns
characteristic of the most common alleles/haplotypes of the
10 locus can be identified, and the frequencies of such
alleles/haplotypes in the population can be determined.
Additional allelic frequencies can be determined for
subpopulations characterized by criteria such as geography,
race, or gender. The de novo identification of
15 polymorphisms of the invention is described in the Examples
section. The second type of analysis determines which
form(s) of a characterized (known) polymorphism are present
in individuals under test. There are a variety of suitable
procedures, which are discussed in turn.

20   1. Allele-Specific Probes
        The design and use of allele-specific probes for
analyzing polymorphisms is described by e.g., Saiki et al.,
Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki,
WO 89/11548. Allele-specific probes can be designed that
25 hybridize to a segment of target DNA from one individual
but do not hybridize to the corresponding segment from
another individual due to the presence of different
polymorphic forms in the respective segments from the two
individuals. Hybridization conditions should be
30 sufficiently stringent that there is a significant
difference in hybridization intensity between alleles, and
preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are
designed to hybridize to a segment of target DNA such that
the polymorphic site aligns with a central position (e.g.,
in a 15-mer at the 7 position; in a 16-mer, at either the 8
or 9 position) of the probe. This design of probe achieves
good discrimination in hybridization between different
allelic forms.

    Allele-specific probes are often used in pairs, one
member of a pair showing a perfect match to a reference
form of a target sequence and the other member showing a
perfect match to a variant form. Several pairs of probes
can then be immobilized on the same support for
simultaneous analysis of multiple polymorphisms within the
same target sequence.

    2. Tiling Arrays

    The polymorphisms can also be identified by
hybridization to nucleic acid arrays, some examples of
which are described in WO 95/11995. One form of such
arrays is described in the Examples section in connection
with de novo identification of polymorphisms. The same
array or a different array can be used for analysis of
characterized polymorphisms. WO 95/11995 also describes
subarrays that are optimized for detection of a variant
form of a precharacterized polymorphism. Such a subarray
contains probes designed to be complementary to a second
reference sequence, which is an allelic variant of the
first reference sequence. The second group of probes is
designed by the same principles as described in the
Examples, except that the probes exhibit complementarity to
the second reference sequence. The inclusion of a second
group (or further groups) can be particularly useful for
analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur
within a short distance commensurate with the length of the
probes (e.g., two or more mutations within 9 to 21 bases).

3.   Allele-Specific Primers

5   An allele-specific primer hybridizes to a site on
target DNA overlapping a polymorphism and only primes
amplification of an allelic form to which the primer
exhibits perfect complementarity. See Gibbs, *Nucleic Acid
Res.* 17, 2427-2448 (1989). This primer is used in

10   conjunction with a second primer which hybridizes at a
distal site. Amplification proceeds from the two-primers,
resulting in a detectable product which indicates the
particular allelic form is present. A control is usually
performed with a second pair of primers, one of which shows

15   a single base mismatch at the polymorphic site and the
other of which exhibits perfect complementarity to a distal
site. The single-base mismatch prevents amplification and
no detectable product is formed. The method works best
when the mismatch is included in the 3'-most position of

20   the oligonucleotide aligned with the polymorphism because
this position is most destabilizing to elongation from the
primer (see, e.g., WO 93/22456).

4.   Direct-Sequencing

The direct analysis of the sequence of polymorphisms of

25   the present invention can be accomplished using either the
dideoxy chain termination method or the Maxam Gilbert
method (see Sambrook *et al., Molecular Cloning, A
Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind
et al., Recombinant DNA Laboratory Manual, (Acad. Press,

30   1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase
chain reaction can be analyzed by the use of denaturing
gradient gel electrophoresis. Different alleles can be
5   identified based on the different sequence-dependent
melting properties and electrophoretic migration of DNA in
solution. Erlich, ed., *PCR Technology, Principles and
Applications for DNA Amplification*, (W.H. Freeman and Co,
New York, 1992), Chapter 7.

10   6. Single-Strand Conformation Polymorphism Analysis
Alleles of target sequences can be differentiated using
single-strand conformation polymorphism analysis, which
identifies base differences by alteration in
electrophoretic migration of single stranded PCR products,
15 as described in Orita *et al.*, *Proc. Nat. Acad. Sci.* 86,
2766-2770 (1989). Amplified PCR products can be generated
as described above, and heated or otherwise denatured, to
form single stranded amplification products. Single-
stranded nucleic acids may refold or form secondary
20 structures which are partially dependent on the base
sequence. The different electrophoretic mobilities of
single-stranded amplification products can be related to
base-sequence differences between alleles of target
sequences.

25 III. Methods of Use
After determining polymorphic form(s) present in an
individual at one or more polymorphic sites, this
information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. *See*
5 *generally* National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard *et al.*, National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

p(ID) is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y, the probability of each genotype in a diploid organism is (see WO 95/12607):

Homozygote: $p(AA) = x^2$
Homozygote: $p(BB) = y^2 = (1-x)^2$
Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity p(ID) for a 3-allele system where the alleles have the frequencies in the population of x, y and z, respectively, is equal to the sum of the squares of the genotype frequencies:

$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate p(ID) and p(exc).

The cumulative probability of identity (cum p(ID)) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

$$\text{cum } p(ID) = p(ID1)p(ID2)p(ID3) \ldots p(IDn)$$

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The cumulative probability of non-identity for n loci
(i.e. the probability that two random individuals will be
different at 1 or more loci) is given by the equation:
cum p(nonID) = 1-cum p(ID).

5   If several polymorphic loci are tested, the cumulative
probability of non-identity for random individuals becomes
very high (e.g., one billion to one). Such probabilities
can be taken into account together with other evidence in
determining the guilt or innocence of the suspect.

10   B.   Paternity Testing
The object of paternity testing is usually to determine
whether a male is the father of a child. In most cases,
the mother of the child is known and thus, the mother's
contribution to the child's genotype can be traced.
15   Paternity testing investigates whether the part of the
child's genotype not attributable to the mother is
consistent with that of the putative father. Paternity
testing can be performed by analyzing sets of polymorphisms
in the putative father and the child.
20   If the set of polymorphisms in the child attributable
to the father does not match the set of polymorphisms of
the putative father, it can be concluded, barring
experimental error, that the putative father is not the
real father. If the set of polymorphisms in the child
25   attributable to the father does match the set of
polymorphisms of the putative father, a statistical
calculation can be performed to determine the probability
of coincidental match.
The probability of parentage exclusion (representing
30   the probability that a random male will have a polymorphic
form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

p(exc) = xy(1-xy)

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site p(exc) = xy(1-xy) + yz(1- yz) + xz(1-xz)+ 3xyz(1-xyz))), where x, y and z and the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

p(non-exc) = 1-p(exc)

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

cum p(non-exc) = p(non-exc1)p(non-exc2)p(non-exc3)....p(non-excn)

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

cum p(exc) = 1 - cum p(non-exc).

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell
mutation confers resistance to malaria, but a homozygous
sickle cell mutation is usually lethal. Other
polymorphisms occur in noncoding regions but may exert
5   phenotypic effects indirectly via influence on replication,
transcription, and translation. A single polymorphism may
affect more than one phenotypic trait. Likewise, a single
phenotypic trait may be affected by polymorphisms in
different genes. Further, some polymorphisms predispose an
10   individual to a distinct mutation that is causally related
to a certain phenotype.

        Phenotypic traits include diseases that have known but
hitherto unmapped genetic components (e.g.,
agammaglobulimenia, diabetes insipidus, Lesch-Nyhan
15   syndrome, muscular dystrophy, Wiskott-Aldrich syndrome,
Fabry's disease, familial hypercholesterolemia, polycystic
kidney disease, hereditary spherocytosis, von Willebrand's
disease, tuberous sclerosis, hereditary hemorrhagic
telangiectasia, familial colonic polyposis, Ehlers-Danlos
20   syndrome, osteogenesis imperfecta, and acute intermittent
porphyria). Phenotypic traits also include symptoms of, or
susceptibility to, multifactorial diseases of which a
component is or may be genetic, such as autoimmune
diseases, inflammation, cancer, diseases of the nervous
25   system, and infection by pathogenic microorganisms. Some
examples of autoimmune diseases include rheumatoid
arthritis, multiple sclerosis, diabetes (insulin-dependent
and non-independent), systemic lupus erythematosus and
Graves disease. Some examples of cancers include cancers
30   of the bladder, brain, breast, colon, esophagus, kidney,
leukemia, liver, lung, oral cavity, ovary, pancreas,
prostate, skin, stomach and uterus. Phenotypic traits also
include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5   individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the
10   individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be
15   performed by standard statistical methods such as a κ-squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with
20   heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In
25   the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular
30   monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the
possibility of transmitting such a polymorphism from her
husband to her offspring. In the case of a weaker, but
still statistically significant correlation between a
5   polymorphic set and human disease, immediate therapeutic
intervention or monitoring may not be justified.
Nevertheless, the patient can be motivated to begin simple
life-style changes (e.g., diet, exercise) that can be
accomplished at little cost to the patient but confer
10   potential benefits in reducing the risk of conditions to
which the patient may have increased susceptibility by
virtue of variant alleles. Identification of a polymorphic
set in a patient correlated with enhanced receptiveness to
one of several treatment regimes for a disease indicates
15   that this treatment regime should be followed.

For animals and plants, correlations between
characteristics and phenotype are useful for breeding for
desired characteristics. For example, Beitz et al., US
5,292,639 discuss use of bovine mitochondrial polymorphisms
20   in a breeding program to improve milk production in cows.
To evaluate the effect of mtDNA D-loop sequence
polymorphism on milk production, each cow was assigned a
value of 1 if variant or 0 if wildtype with respect to a
prototypical mitochondrial DNA sequence at each of 17
25   locations considered. Each production trait was analyzed
individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \ldots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijknp} is the milk, fat, fat percentage, SNF, SNF
percentage, energy concentration, or lactation energy
30   record; μ is an overall mean; YS_i is the effect common to
all cows calving in year-season; X_k is the effect common to
cows in either the high or average selection line; β_1 to β_{17}
are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent
environmental effect common to all records of cow n; a_n is
effect of animal n and is composed of the additive genetic
contribution of sire and dam breeding values and a
5   Mendelian sampling effect; and e_p is a random residual. It
was found that eleven of seventeen polymorphisms tested
influenced at least one production trait. Bovines having
the best polymorphic forms for milk production at these
eleven loci are used as parents for breeding the next
10 generation of the herd.

    D.   Genetic Mapping of Phenotypic Traits
    The previous section concerns identifying correlations
between phenotypic traits and polymorphisms that directly
or indirectly contribute to those traits. The present
15 section describes identification of a physical linkage
between a genetic locus associated with a trait of interest
and polymorphic markers that are not associated with the
trait, but are in physical proximity with the genetic locus
responsible for the trait and co-segregate with it. Such
20 analysis is useful for mapping a genetic locus associated
with a phenotypic trait to a chromosomal position, and
thereby cloning gene(s) responsible for the trait. *See*
Lander *et al.*, *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357
(1986); Lander *et al.*, *Proc. Natl. Acad. Sci. (USA)* 84,
25 2363-2367 (1987); Donis-Keller *et al.*, *Cell* 51, 319-337
(1987); Lander *et al.*, *Genetics* 121, 185-199 (1989)).
Genes localized by linkage can be cloned by a process known
as directional cloning. *See* Wainwright, *Med. J. Australia*
159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6
30 (1992).
    Linkage studies are typically performed on members of a
family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a
set of polymorphic markers. The distribution of
polymorphic markers in an informative meiosis is then
analyzed to determine which polymorphic markers co-
5   segregate with a phenotypic trait. *See, e.g.*, Kerem *et
al.*, *Science* 245, 1073-1080 (1989); Monaco *et al.*, *Nature*
316, 842 (1985); Yamoka *et al.*, *Neurology* 40, 222-226
(1990); Rossiter *et al.*, *FASEB Journal* 5, 21-27 (1991).

     Linkage is analyzed by calculation of LOD (log of the
10   odds) values. A lod value is the relative likelihood of
obtaining observed segregation data for a marker and a
genetic locus when the two are located at a recombination
fraction θ, versus the situation in which the two are not
linked, and thus segregating independently (Thompson &
15   Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders
Company, Philadelphia, 1991); Strachan, "Mapping the human
genome" in *The Human Genome* (BIOS Scientific Publishers
Ltd, Oxford), Chapter 4). A series of likelihood ratios
are calculated at various recombination fractions (θ),
20   ranging from θ = 0.0 (coincident loci) to θ = 0.50
(unlinked). Thus, the likelihood at a given value of θ is:
probability of data if loci linked at θ to probability of
data if loci unlinked. The computed likelihoods are
usually expressed as the $\log_{10}$ of this ratio (i.e., a lod
25   score). For example, a lod score of 3 indicates 1000:1
odds against an apparent observed linkage being a
coincidence. The use of logarithms allows data collected
from different families to be combined by simple addition.
Computer programs are available for the calculation of lod
30   scores for differing values of θ (e.g., LIPED, MLINK
(Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446
(1984)). For any particular lod score, a recombination
fraction may be determined from mathematical tables. *See*

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Smith *et al.*, *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5   of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV.   Modified Polypeptides and Gene Sequences
20   The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown
in the Table.

Variant genes can be expressed in an expression vector
in which a variant gene is operably linked to a native or
5   other promoter. Usually, the promoter is a eukaryotic
promoter for expression in a mammalian cell. The
transcription regulation sequences typically include a
heterologous promoter and optionally an enhancer which is
recognized by the host. The selection of an appropriate
10 promoter, for example trp, lac, phage promoters, glycolytic
enzyme promoters and tRNA promoters, depends on the host
selected. Commercially available expression vectors can be
used. Vectors can include host-recognized replication
systems, amplifiable genes, selectable markers, host
15 sequences useful for insertion into the host genome, and
the like.

The means of introducing the expression construct into
a host cell varies depending upon the particular
construction and the target host. Suitable means include
20 fusion, conjugation, transfection, transduction,
electroporation or injection, as described in Sambrook,
supra. A wide variety of host cells can be employed for
expression of the variant gene, both prokaryotic and
eukaryotic. Suitable host cells include bacteria such as
25 E. coli, yeast, filamentous fungi, insect cells, mammalian
cells, typically immortalized, e.g., mouse, CHO, human and
monkey cell lines and derivatives thereof. Preferred host
cells are able to process the variant gene product to
produce an appropriate mature polypeptide. Processing
30 includes glycosylation, ubiquitination, disulfide bond
formation, general post-translational modification, and the
like.

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The protein may be isolated by conventional means of
protein biochemistry and purification to obtain a
substantially pure product, *i.e.*, 80, 95 or 99% free of
cell component contaminants, as described in Jacoby,
5   *Methods in Enzymology* Volume 104, Academic Press, New York
(1984); Scopes, *Protein Purification, Principles and*
Practice, 2nd Edition, Springer-Verlag, New York (1987);
and Deutscher (ed), *Guide to Protein Purification, Methods*
in Enzymology, Vol. 182 (1990). If the protein is
10 secreted, it can be isolated from the supernatant in which
the host cell is grown. If not secreted, the protein can
be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman
animals capable of expressing an exogenous variant gene
15 and/or having one or both alleles of an endogenous variant
gene inactivated. Expression of an exogenous variant gene
is usually achieved by operably linking the gene to a
promoter and optionally an enhancer, and microinjecting the
construct into a zygote. *See* Hogan *et al.*, "Manipulating
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor
Laboratory. Inactivation of endogenous variant genes can
be achieved by forming a transgene in which a cloned
variant gene is inactivated by insertion of a positive
selection marker. *See* Capecchi, *Science* 244, 1288-1292
25 (1989). The transgene is then introduced into an embryonic
stem cell, where it undergoes homologous recombination with
an endogenous variant gene. Mice and other rodents are
preferred animals. Such animals provide useful drug
screening systems.
30 In addition to substantially full-length polypeptides
expressed by variant genes, the present invention includes
biologically active fragments of the polypeptides, or
analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active
fragments include any portion of the full-length
polypeptide which confers a biological function on the
variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by
nucleic acids, proteins or polypeptides, small biologically
active molecules, or large cellular structures.
        Polyclonal and/or monoclonal antibodies that
specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided.
Antibodies can be made by injecting mice or other animals
with the variant gene product or synthetic peptide
fragments thereof. Monoclonal antibodies are screened as
are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York
(1988); Goding, *Monoclonal antibodies, Principles and*
Practice (2d ed.) Academic Press, New York (1986).
Monoclonal antibodies are tested for specific
immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene
product. These antibodies are useful in diagnostic assays
for detection of the variant form, or as an active
ingredient in a pharmaceutical composition.

    V.   Kits
25   The invention further provides kits comprising at least
one allele-specific oligonucleotide as described above.
Often, the kits contain one or more pairs of allele-
specific oligonucleotides hybridizing to different forms of
a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate.
For example, the same substrate can comprise allele-
specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.
Optional additional components of the kit include, for
example, restriction enzymes, reverse-transcriptase or
polymerase, the substrate nucleoside triphosphates, means
5   used to label (for example, an avidin-enzyme conjugate and
enzyme substrate and chromogen if the label is biotin), and
the appropriate buffers for reverse transcription, PCR, or
hybridization reactions. Usually, the kit also contains
instructions for carrying out the methods.
10   The following Examples are offered for the purpose of
illustrating the present invention and are not to be
construed to limit the scope of this invention. The
teachings of all references cited herein are hereby
incorporated herein by reference.

15   EXAMPLES
The polymorphisms shown in the Table were identified by
resequencing of target sequences from three to ten
unrelated individuals of diverse ethnic and geographic
backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The
strategy and principles for design and use of such arrays
are generally described in WO 95/11995. The strategy
provides arrays of probes for analysis of target sequences
showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1.
The reference sequences were sequence-tagged sites (STSs)
developed in the course of the Human Genome Project (see,
e.g., Science 270, 1945-1954 (1995); Nature 380, 152-154
(1996)). Most STS's ranged from 100 bp to 300 bp in size.
30   A typical probe array used in this analysis has two
groups of four sets of probes that respectively tile both
strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect
complementarily with one of the reference sequences. Each
probe in the first probe set has an interrogation position
that corresponds to a nucleotide in the reference sequence.
5   That is, the interrogation position is aligned with the
corresponding nucleotide in the reference sequence, when
the probe and reference sequence are aligned to maximize
complementarily between the two. For each probe in the
first set, there are three corresponding probes from three
10 additional probe sets. Thus, there are four probes
corresponding to each nucleotide in the reference sequence.
The probes from the three additional probe sets are
identical to the corresponding probe from the first probe
set except at the interrogation position, which occurs in
15 the same position in each of the four corresponding probes
from the four probe sets, and is occupied by a different
nucleotide in the four probe sets. In the present
analysis, probes were 25 nucleotides long. Arrays tiled
for multiple different references sequences were included
20 on the same substrate.

     Multiple target sequences from an individual were
amplified from human genomic DNA using primers for the
fragments indicated in the listed Web sites. The amplified
target sequences were fluorescently labelled during or
25 after PCR. The labelled target sequences were hybridized
with a substrate bearing immobilized arrays of probes. The
amount of lable bound to probes was measured. Analysis of
the pattern of label revealed the nature and position of
differences between the target and reference sequence. For
30 example, comparison of the intensities of four
corresponding probes reveals the identity of a
corresponding nucleotide in the target sequences aligned
with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the
nucleotide occupying the interrogation position of the
probe showing the highest intensity (see WO 95/11995). The
existence of a polymorphism is also manifested by

5   differences in normalized hybridization intensities of
probes flanking the polymorphism when the probes hybridized
to corresponding targets from different individuals. For
example, relative loss of hybridization intensity in a
"footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a
polymorphism) (see EP 717,113). Additionally,
hybridization intensities for corresponding targets from
different individuals can be classified into groups or
clusters suggested by the data, not defined a priori, such

15 that isolates in a give cluster tend to be similar and
isolates in different clusters tend to be dissimilar.
Hybridizations to samples from different individuals were
performed separately. The Table summarizes the data
obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.
        From the foregoing, it is apparent that the invention
includes a number of general uses that can be expressed
concisely as follows. The invention provides for the use
of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer,
inflammation, heart disease, diseases of the CNS, and
susceptibility to infection by microorganisms. The
invention further provides for the use of any of the
nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The
invention further provides for the use of any of the DNA
segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and

5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
WI-7070	226	C	T		---	TGTGAAACTCCCACTTGAAGCCAAAGAAAGAAAGAAAACTCACACTTAAAACACATGCCAGTTGGGAAGGTCT GAAAACTCAGTGCATAATAGGAACACTTGAGACTGAAAGACATTGAAGAGAGAGGTGAGACCAATCTTTATTT GTACTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTGGAAAAAGCTTTGAGGATAATGT TACTAGACTTTATGCCATGGTGCTTT[C/T]AGTTTAATGCTGTGTCTGTCTCAG
WI-10744	61	G	C		---	AAGCCATTGACGTAACATCTCAGAGGTTATTGTTGCATGGATTGACTCCTGGGACAAAAGGAC[G/C]AA AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTT GATAATACATAAGCCCTAGGATTTAGATACAATCTTGAAAGAAACTGAGACAGATAATTCTGAATT AAATGAGGTAAAGTTTCAGGCACTCA
WI-9975	126	C	T		---	GGGCAAATTACCAGCACAAAAAAGTCAAATTACCAGCATCAAAGTCAGGTGCAAAGGAGGTAGAACAA TTACAGTAACTATGTCAATCTTTTGTATATTAGTATTATCTGCCCAATGCCTAGAATA[C/T]AGTTG GGTCCCTAATAGTTATTAGTTCCTTTTCTCCTCTTCTCATTCTCTGAATTTATTTTTATACTTAA GGGATTAGTTACCACCAAAAATGTATTCAATTGTATCAATTGATTCTTACTGAA
WI-8010	247	G	T		---	GCTAGGTTTGTTTGTTGGCTGTCTTCACTAGACTTGAGATGACTTGATTTACAGTAATCCCTATGT GATGTAACTAGTGTGAGACCTTCCCTCTCCGCCAATTCCCAGGTTTCAGAAAGTATGCCACAC TCAACCCTTCTCTCCAGTTCATCCATCGTGTATTAATTTCTTCCCATATTAATTCAAAGGGAGTGGGACAGGT CCCTGGCTGAAAAGAAAATAAAGAGATCCCAAAGTGGTGGGG[G/T]CTT
WI-5222b	85	G	C		---	GCCCGGCCTATCTTTAATTTAACTTGTATCTTTGGTGTTTCTCCATCCTAGGATTCTGCCTTATAAT CTTTGTCCTGTCTGTA[G/C]ATTACCTGATTCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAATTCTTCAGGTCTCTTGAATTTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTCGACTCTATAACAACTCCAACAGAA
WI-5222	52	G	C		---	GCCCGGCCTATCTTTAATTTAACTTGTATCTTTGGTGTTTCTCCATCCTA[G/C]GATTCTGCCTTAT AATCTTTGTCCTGTCTGTGTAGATTACCTGATTCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAATTCTTCAGGTCTCTTGAATTTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTCGACTCTATAAACTCCAACAGAA
WI-8007	242	C	A		---	TATGCACTTCCACAAAAGGATATAACTTTATTACTAACTAGTCCTTCTTGGAAGGAACACCCAAACCAATACTT ATATGTTATTATAGGCATTTATTACTAACTAGTCCTTCTTGGAAGGAACACCCAAACCAATACTT ATAAAGTACATGTAATTTATAGTAACATATTTACTATATACAATCATATGGAAAAATCATATTCTCACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTTGGAC[C/A]AGCTGCTG
WI-9823	97	C	T		---	TCAGTTGCAAAAATTGCTGCCATAAAACATGCTTTGCTTATCTCTGCATAAACATGTTTATGTGTGTTTTGTTAG TCTATATTCACACATATGGTGAAATTTC[C/T]GGGGCATGGAAATACATCTTTATGAGACATTGA ACTGCTCACCACTATCATCATATGTACTCATTTAAACAGACCAACAATGTATAAGAATTCCCTTTGTTTTAC ATGCTTTCCAATCTGATTTGTATGACTATTGTATGCACAGTTGGATCACC

ID	Pos	Alleles	Sequence
WI-9651b	105	A / T	TCTCTACATTCTATGGACAACCTCCATGCCTTTGCACATGCTGTGATCCTCCTCCTCCTGGAATTCCTTTCCT ACTTGTCCTCCATGTACACAATTTTCTGCTCGTCCTTCA[A/T]GGGGCAGCTTGCAAGCCTCCCTTAGAC ACCCTCACAGGTACAGCCGACCATGCCCTACCTCCCATGGCCACTGCCAGGGGACCCTTATAGGCCTCTG TCTTTAAACCTGTAATGGTATATTAATCCTTGGTGTTTGAATGTCTCTC
WI-9651	139	T / C	TCTCTACATTCTATGGACAACCTCCATGCCTTTGCACATGCTGTGATCCTCCTCCTCCTGGAATTCCTTTCCT ACTTGTCCTCCATGTACACAATTTTCTGCTCGTCCTTCAAGGGGCAGCTTGCAAGCCTCCCTTAGACACCT C[T/C]ACAGGTACAGCCGACCATGCCCTACCTCCCATGGCCACTGCCAGGGGACCCTTATAGGCCTCTGT CTTTAAACCTGTAATGGTATATTAATCCTTGGTGTTTGAATGTCTCTC
WI-7676b	309	A / C	GTGACCTTCCTGCAGCGTGGGAGATGGCACATCCTTGCTGCGTGGGGACTTGGCCCCTGCTATTATTTTTG TATTTATGTCTTAATCTCTTCCACTGATGCATCCTCCAAGGGTAGATGGGGAGGGTCTGTGTGAGGG GCCGGCCTTCTCTTGGTGCCTGCCTGGGTTGCAGGGTGCAGGGAAGCGTGTGGACTTGTGCTGGTGC TCCCCCGGTCCTCCTCTGGAGGCAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139	C / T	GTGACCTTCCTGCAGCGTGGGAGATGGCACATCCTTGCTGCGTGGGGACTTGGCCCCTGCTATTATTTTTG TATTTATGTCTTAATCTCTTCCACTGATGCATCCTCCAAGGGTAGATGGGGAGGGTCTGTGTGAGGG GC[C/T]TGGCCTTCTCTTGGTGCCTGCCTGGGTTGCAGGGGCCAGGAAGCGTGTGGACTTGTGCTGGTGC GTGCTCCCCCGGTCCTCCTCTGGAGGCAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105	G / A	CATTATCTGTCCTGTCTGTTCATTCACTTTCCTCTCTCCAATGAAGAGGATATTTAAGCATCATT CATCTGGCCCTTTTTTGAGTTTGAATCATTTTTGT[G/A]TGACTCCTATGCACATGATAAAATTTGTTA TGCTTGTCTTCTTATCTTTTGTTATAGGAGTTTGGCCATGACCCTTATGAGGAGAAAAGGGA TCACCCCCTTTTGCCTCTACAACCTTATAGATATTTAAAATATCTTT
WI-9986	42	T / C (A)	TTGGTGTGAACTCAGAACATAGGGAAAAATAAGACAAATTTGAA[T/A,C]GTACCCCAGGAAACAAGAG CCCTGCACTTGACTCCAAAAGGAGTTCTATTATTCTGGCTGTTTCCAGACTTTATTGTATCTTGAGAA GAGAACTGTTTTCCCTCTAAATCAGTTTCATCATCGTATCCTAAACTTATTGCAATT ATATCAATAGCATGCATATGGGGTGTTGGATTCTTAGAACTTATTGCAATT
WI-7041	174	C / A	GTCTATTGCAGGAGGAAACGTCCCTTGCCACTCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGGA GGGGCCTGCACATGCACAACTCCAGTCCCTGCCCTCTGCCCCTGCCCTCTC[C/A]CCACCTTCTTTGGGAGCAAGGGTCCCTCGGTCTTTATT CAGGGCTTGCATGCATGCGCTCTATTCCCCCCTCTGCCCCTCTC[C/A]CCACCTTCTTTGGGAGCAAGGAGATGC AGCTGTATTGTGTAACAAGCTCATTTGTACAGTGTCTGTTCATGTAATAA
WI-7224	134	T / C	ATAAACCCTTGTGTATGTATCACCCAACTCACTAATTATCAACTTATGTGCTATCAGATATCCTCTCT ACCCTCACGTTATTTTGAAGAAAATCCTAAACATCAAATACTTTCATCCATAAAAATGTCAGCATT[T /C]ATTAAAAACAATAACTTTTAAAGAACAATAAGGACACATTTTCAAATTAATAAAAATAAAG GCATTTAAGGATGGCCTGTTATTCTGGGAAGCCAGAGAGTCAGGAGAGTTCATGCATGCTAG

ID	Pos			Sequence
WI-10826	132	A	C	TCTTATTTGCATTTCACAGTAGCCCATGAAGTAGGTATAACCAGCCTCTATTTTAACATGAGAAGAT GGAGGCCTTTCCAAAATGGACTAGTAGTAATGTGTCTCAGGTTTCCTAATAAGCAAAGACCTGCA[A/C] CCCTGGCTTCCTGACTCCAAAGCTTATCCCTTGCTGTCGTCGACCCCATGCGCA GAAAGCCCAGCCTCTCCATCCCCCAC
TIGR-A004S25	145	G	A	AGATCTGCCATTAGTATTTATTCCTTTGAAGATACTTTGGAGATTCATTTCTTGAGTGGCACTGCAT GCTCATTCAGTGAAGAAACTTGTGGGGTATAGAAAATGGAATGGAGAGTTCAAACAGCTTTGCTGAAAC TGTACTTTGG[G/A]CTCCAGACTTCACTGTCCTAGGCATTGAAACCATCACCTGGTTGCATTCTTC ATGACTGAGGTTAACTTAAAATGACTGAGGTTAACTTAAAAC
WI-1021	24	A	T	AAACACACAGAATCATCAAAGCAC[A/T]ATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACTCTGAAATAGTAGGATAGTAGTATTCATTCCTGTAATAGATTCACCTCTCAGCAAT TGGTCTGTTTCATTCTATGGAAACTCTCCGTACTGTAATTTCATTCTATGGAAACTCCCCATACTGT AATTGGACAGTTTTGGTTTCCAC
WI-4687	121	G	T	TAGTATGTCACTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTTGAATGGTCTTGTCC TTTCAATAAAAGAGTGACACATGATGATTGAACATGTGTTTAGATAAAGGCACTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGATTAAGGAAGATCAGGAGAAGAAAGTAGCAATGGGAATGAAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAAACCAAGAGAAGAAAGAAACTTGAT
WI-4719b	107	T	G	TTCATTTCCCTTCCAAAATCCTTAGGAAATTTACATTATGGGCTAGTGCTTTGGGTGTGAGCGGATT ATGTCTGACGCGCCATGGTGTTCATAAGTGACT[T/G]ACTGTGAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAACAATTCGTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCCCACTTGTCAACTTATCCTTAAGACATTTTCACAGGA
WI-4719	70	G	A	TTCATTTCCCTTCCAAAATCCTTAGGAAATTTACATTATGGGCTAGTGCTTTGGGTGTGAGCGGATT AT[G/A]TCTGACGCGCCATGGTGTTCATAAGTGACTTGAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAACAATTCGTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCCCACTTGTCAACTTATCCTTAAGACATTTTCACAGGA
WI-9484b	216	G	C	TCAACACGCTTTATTGCCACTTCTGGCTCCCCTGCGTCCCAGCAAGATTCCTACCTCTTACCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGGTGGGGGTGTTACCCACTCTCCTCTGCACACTGCCAAGT TAAAGAAAACCCTGCTTCTT[G/C]ACTGCACAGAGTATAGGGACCAGGGTTCCAAACTTT AGTCCCACTTCTT[G/C]ACTGCACAGAGTATAGGGACCAGGGTTCCAAACTTT
WI-9484	178	G	A	TCAACACGCTTTATTGCCACTTCTGGCTCCCCTGCGTCCCAGCAAGATTCCTACCTCTTACCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGGTGGGGGTGTTACCCACTCTCCTCTGCACACTGCCAAGT TAAAGAAAACCCTGCTTCTTGCTGGAGAGGGAGGGCCAGACAGG[G/A]AGGAATTCAAGGGCATGTATG GCTCAGTCCCACTTCTTGCTGCACAGAGTATAGGGACCAGGGTTCCAAACTTT

Marker	Pos			Sequence
WI-7330	207	C	T	AGGATGGAAGGAGACACGGGGCAGGGGAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTTCTTTAATTGTGGCATATAGGTTT GTGACACAAGAAGTCATACTTTGGTGGCTAAGTTTTACTAAGGAAAATAACTGAAAAGATTAAAAG TGAGAG[C/T]TGAAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGTCACAG
WI-9443	211	G	A	TTAAAAACAGTTCAGGTTGGTGAAGCAGAAAAGGGATGTGATTACAATTTAAATGAATCAGTCACTT GCACAACTTAATCCTCTTGGCATCATACAAACTGGGTTTAATGGCAAATGACATCATAGCATGA CCAACACTCATGGAAGGCAGTCTAGAGTCCATCACGCTCACACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGACCTTGGACTGACTACACAGATGACACCACCATGCCCACTT
WI-7166	59	C	T	TCTCTCAAAAGAGAAAAACAAAACCCCTAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAAGATTCCTTGTGCAAAATATTGACTATTCTGTATCTTCATCCTTGACTAAATTCGTG ATTTTCAAGCAGCATCTTCTGGTTAAACTGTTGCTGTGAACAATTGTCGAAAAGAGTCTTCCAAT TAATGTCTTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCCGAG
WI-7259b	189	T	C	GCTTCTTCCCCAGGAAGCGGGGGTCTTGGCCTGGAACCTTCCAGAGGAGGAGGCGGGGAGCAATTTAGCC CCACCCTGCTCCCATCTGCCCCCCTGCAACAGCTGCAGGCTGCTCCTCTCTCGAGTTCCTCTCTGGGCT GCGCAGGCTCCCCTGGGAATAGAGCAAGAGCGTGAGTCCTAACCTGGCCACAG[T/C]TGGGGGAGCAG AGCCAGCAGGTGGACACAGGTGTTTGCAGGGGCCCAACTTCCCCTGGAGCTC
WI-7259	188	G	T (C)	GCTTCTTCCCCAGGAAGCGGGGGTCTTGGCCTGGAACCTTCCAGAGGAGGAGGCGGGGAGCAATTTAGCC CCACCCTGCTCCCCTGCCCCCCTGCAACAGCTGCAGGCTGCTCCTCTCTCGAGTTCCTCTGGGCT GCGCAGGCTCCCCTGGGAATAGAGCAAGAGCGTGAGTCCTAACCTGGCCACA[G/C,T]TTGGGGGAGCA GAGCCAGCAGGTGGACACAGGTGTTTGCAGGGGCCCAACTTCCCCTGGAGC
WI-7322	275	A	G	GTACTTTAGGCCTGTGTGGAGGGTGGGCCATTAGTGTGACCCTTGCACCCAGGGTTTTCTAACAGATGAC CCTGTGAATCATAATTTAAACCTGCATATTTATAGCCAGTCACATTGCCCTCCTCACCCTATATG GCCATAAACTGCCTAAGCACTCAGGCCTCCCACTCATCAACCCCTTTGACCAGAGAAAGAAGCACTC TGGTTCTCTATCCCCTTGTCACATAGAGAGTTTGTCATGGGGCCTCTGGCTG
WI-7685	46	T	C	TCAGTTCTAGTCTCTCTGGGGCCACACAGAAACTCTTTTGGGCTC[T/C]TTTTCTCCCCTCTGGATCA AAGTAGGCAGGACCATGGACCAGGTCTTGGAGCCTGAGCCTCTCACCTGTACTCTTCCGAAAAATCCT CTTCCTCTGAGGCTGGATCCTAGCCTTATCCTCCATGGCTTCCTCCTCCCTCTCGCCGACTC CTGGGTTGAGCTGTTGCCTCAGTCCCCAACAGATGCTTTCTGTCTC
WI-563	87	G	A	TGTGACCAATTGTTATTTTAGAGGGTTTAACAATGGCCTGACTATCACCTGATGGTCGCCGAGAATTC CTGGGGGAGGGCCTCCCCT[G/A]CCCTGACTCATGTCGATCATGTCGATCATGTCTAACAATACTACTCC TGTGGTATGGGGATCCTAAGCCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCCTCAGTAAAGGCAAATTTAAATCTCTTTGGGATAACCCAGGGCACAT

ID	Pos	Alleles	Sequence
WI-931c	191	C A	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTTTCTCTCCCCTCCCTATCCCCTCACCAACCACCTTCCAGTGCTGCTTATTCTGCTGTGTCAAAATGATCCTTCTGTTGCTGCACTGTCATTACTGTGTATGGGGAAAGGCATGGGGGAAAGATGTGTCAGATACAGAAAAGGCATGGGGGAAAGATGTGTCAGA
WI-931b	81	A G	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTTTCTCTCCCCTCCCTT[A/G]TCCCCTCACCAACCACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCTTCTCTGTTGCTGCACTGTCATTACTGTTGTATGGATTTATAATTATTGTCAAAAAGCCCCGAGCCTGGTACAGAAAAGGCATGGGGGAAAGATGTGTCAGA
WI-931	31	A G	GACCAGGGCACCAGAAAGCCACGGAAGCCACGGCAC[A/G]GCCACTAGCCCTGAACCTTGCACACCCCTGGAGTTTCTCTCCCCTCCCTATCCCCTCACCAACCACCTTCCAGTGCTCTTATTCTGCTGTGTCAAAATGATCCTTCTCTGTTGCTGCACTGTCATTACTGTTGTATGGATTTATAATTATTGTCAAAAAGCCCCGAGCCTGGTACAGAAAAGGCATGGGGGAAAGATGTGTCAGA
WI-10870b	91	C T	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACACACCCTGACTGGGATGGCAGAGACATCCACCTTAGCAAAGTGGGG[C/T]ACCTACTTAGGGACCTGTACTCCTGATACAAAATAAGGACATGGGTCAGCCTGAGCCACTCTCTTAAACCATCACCATTTAAATAACGTTGCCCCCC
WI-10870	103	G A	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACACACCCTGACTGGGATGGCAGAGACATCCACCTTAGCAAAGTGGGGCACCTACTTAGA[G/A]CAGTGGAGTACCCTGAGTACGACCCCCTTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACATGGGTCAGCCTGAGCCACTCTCTTAAACCATCACCATTTAAATAACGTTGCCCCCC
WI-7719b	281	T C	AGTTTATTCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAGTCTTGGGAAATATTTGGGCATTGGTCTGGCCAAGTCTACAGTTATCCATTCAAGATCAAGACTACACGGTCTATGAGCAATAATGTGATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163	A G	AGTTTATTCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAGTCTTGGGAAATATTTGGGCATTGGTCTGGCCAAGTCTACAGTTATCCATTC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAATGTTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAATGTGATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAA
WI-10396	72	C A	GCCTTGGGAGTATATCTAAACTGTGGCCTCCACTTTCATTTTTCTTGAAACATTGCTATCAACTGGGAAGAGT[C/A]TGTGACTTTATGCCCAGTTTCCCCTCTCAGATTTTATGACGGTTGTTTTCTTTTGTTATGCCATTTGAGGGGATTGATGTTTCTTAAACTACTTGGCTGTCTCTCCATTGCTGTTGTTCAGGTTAACAGCCACCATTTGTAAACACTTTGT

				Sequence
WI-10673	94	C	G	TCCCTTTATGCACCCAAGAGATATTATTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACCCACCCCCGTGGCACTCATGGAGGGG[C/G]TGCAGGTTGGAACTATGCAGTGTGCTCCGGCCACACATCCTGCTGGGCCCCCTGCCCCAATTCAATCTGCCAATAAATCCTGTCTTATTTGTTCATCCTGGAGAATTGAAGGGAGGTCAAGTTGTTTGTCAATGATTGTCAGAGAACCT
WI-7842	57	T	C	CACAGCCATGCCCTTGAGGAGCCGGCCACCAGATGCTGAATCCCTATCCCATTCTGT[T/C]GTATGAGTCCCATTTGCCTTGCAATTAGCATTCTGTCTCCCCAAAAAGAATGCTATGAAGCTTTCTTTCCTACACACTCTGAGTCTCTGAATGAAGCTCTTAGTACCAGAGCTAGTTTTCAGCTGCTCAGAATTCATCTGAAGAGAGACTTAAGATGAAAGCAAATGATTCAGCTCCCTTATA
WI-7721	145	A	C	CTGCCTCATCACGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGGAGGAGCAAGGGGGCCACATCCCCACCCCCAGCGTGTTACCCAGCCCGGGCAGGTGCAGCCCTTCCTCCCTGTCTCTGC[A/C]TCTGACCTCTCTTTGAGGTCCCTGTATGTCACCTCTGACTTCTGTGGTCCCTCTGTGTCTGCTCTCATCCATTCCTCTTACTGGGGCTCTAGCCCAA
WI-4767b	173	C	A	TTTCCAGTCTGTTTTATCCTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCTCAGGTCTGGGTAATCCTAGATCTTCCTATATCCATTGAGTGTGATGGAGTTGGAGAGAGGGTATGTTCTTGCCTTGAGAAATCCTAGAAAGCACAGGGATGACA[C/A]AAATCACTCAAGGAATTCCACTAAGACTCTCCTCAACCCAGAGATTTTAACCT
WI-4767	50	A	G	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGATTACAGAAACTGATGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAGATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAAGCTGTGTTGAAACAGAAAAATAAGTCAAAGGAACAAAAATTACAAAGAGA[C/T]CATGCGAGGAAGGAAAACTATGTATTAAT
WI-7718f	222	C	T	ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT[T/C]GCAAGGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAGATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAAGCTGTGTTGAAACAGAAAAATAAGTCATTAAT
WI-7718e	60	T	C	ATTGCACTGAAGTTTTGAAATACCTTTGTA[G/A]TTACTCAAGCAGTTACTCCCTACACTGATGCAAGGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAGATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAAGCTGTGTTGAAACAGAAAAATAAGTCAAAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATTAAT
WI-7718d	31	G	A	ATTGCACTGAAGTTTTGAAATACCTTTGTA[G/A]TTACTCAAGCAGTTACTCCCTACACTGATGCAAGGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGGCCCGGAGATAGATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAAGCTGTGTTGAAACAGAAAAATAAGTCAAAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATTAAT

Label	Pos	A1	A2	Sequence
WI-7718c	91	C	G	ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGATTACAGAAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACACATGTTCTGGGGGCCCGGAGATAGATGACTTTGCAGATGGAAAAGAGTGAAAATGAAGAAGGAAGCTGTTGAAACAGAAAAATAAGTCAAAAGGAACAAAAAATTACAAAGAACCATGTCAGGAAGGAAAACTATGTATTAAT
WI-7718b	248	A	G	ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACACATGTTCTGGGGGCCCGGAGATGATGACTTTGCAGATGGAAAAGAGTGAAAATGAAGAAGGAAGCTGTTGAAACAGAAAAATAAGTCAAAACTTTGCAGATGGAACAAAAATTACAAAGAACCATGTCAGGAAGGAAAACTATGTATT[A/G]AT
WI-7718a	42	A	T	ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGC[A/C,T]GTTACTCCCTACACTGATGCAAGGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACACATGTTCTGGGGGCCCGGAGATAGATGACTTTGCAGATGGAAAAGAGTGAAAATGAAGAAGGAAGCTGTTGAAACAGAAAAATAAGTCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTA
WI-7227d	99	G	C	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTCCGTGGACCAATTCATCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGCTTTTTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGACGGACTAATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291	G	A	AGGGAATTGTGTTGCTCCTGGAGGAAGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTCCGTGGACCAATTCATCTTTCAGACAA[G/T]CTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTTAGCCCCAGAAGGGACTGAGCTAAACAGTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGACGGACTAATGCAAT
WI-7227b	93	G	T	AGGGAATTGTGTTGCTCCTGGAGG[A/G]AGCCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTCCGTGGACCAATTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTAAACAGTGTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGACGGACTAATGGTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24	A	G	CCACAATGCCTCTCCCACGATGTCAAGGACTCCTGCTGTCGTCTCCTGGAGGTGGGAGACAAGGAACCTCCGAAGAGGAAGCAAGAAAGCCGTACTGTTCTATGTTGTGATCCTTCATCGAACAAACTGATGCGAAAACTTGAATCTGTTACTGAAGTGAAATGAGGAGGAGGACATGTCTATTGAACTGCTATTGAACTGAGCCAAACACACTGTAAAT
WI-7310b	234	A	C	ATCCACAGACTCCCTCCCCTGCCCCCCATCCCA[A/C]ATGATCTTGAGATTTC

ID	Pos	Alleles	Sequence
WI-7310a	64	T/A	CCACAATGCCTCCTCCCACGATGTCAAGGACTCCTGTCTGTCCTGGAGGTGGGAGACAAGGAACC[T/A]CCGAAGAGGAAGCAAGAAAGCCGTACTGTTCTGTATGTTGTGATCCTTCATCGAACAAAACTGATGCGAAAACTTGAATCTGTTACTGAAATGAGGAGGAGAAGGACATGTGCTATTGAACTGAGCCAAACACACTGTAAATATCCACAGACTCCCTCCCCTGCCCCCATCCCAAATGATCTTGAGATTTC
WI-7878b	162	A/G	CCAGCAACACCTACACCCTTGTCACCTGCCTGGGACTCCTATGGCCTGCTGGTTGATAATAATCAGATCATGCCCAAGACGGGCCCTCCTGATAATCGTCTTGGGCATGAATGGAGGGCAAATGCGTCCCTGAGGAGAAAATCTGGGAGGAGCTG[A/G]GTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTGTGGGGAGCCCAGGAGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAACTA
WI-7878a	51	C/G	CCAGCAACACCTACACCCTTGTCACCTGCCTGGGACTCCTATGATGGCCTG[C/G]TGGTTGATAATAATCAGATCATGCCCAAGACGGGCCCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGGCAAATGCGTCCCTGAGGAGAAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTGTGGGGAGCCCAGGAGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAACTA
WI-7381c	213	C/T	CTCCACATTCCCACAGGCCTTGAGCAGAATTTCTGAGACTGAAGGGAAATCCCCCTTTCTTTCTTCTAGCCCTGCAAGTTTCCTCATGGACGCTCGCGAGGACAGGTTCCTGCCTATGGTGAGATCAGATGTGGCCAAGGAGAAGGAGCTCTGGTTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAGACAAAACGGGCCTC[C/G]TGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54	C/G	CTCCACATTCCCACAGGCCTTGAGCAGAATTTCTGAGACTGAAGGGAAATCC[C/G]CCTTTCTTTCTACCAGCCCTGCAAGTTTCCTCATGGACGCTCGCGAGGACAGGTTCCTGCCTATGGTGAGATCAGATGTGGCCAAGGAGAAGGAGCTCTGGTTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAGACAAAACGGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53	C/G	CTCCACATTCCCACAGGCCTTGAGCAGAATTTCTGAGACTGAAGGGAAATCC[C/G]CCTTTCTTTCTACCAGCCCTGCAAGTTTCCTCATGGACGCTCGCGAGGACAGGTTCCTGCCTATGGTGAGATCAGATGTGGCCAAGGAGAAGGAGCTCTGGTTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAGACAAAACGGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93	G/A	AAATTGCTCTATTCGGACCCTCATATTAAATAAGAGCAATGAGAGCGAGGGAAAATTGAACTCTCTCAGGTACTGACTGTGGGACCAGACAAG[G/A]GATGTAGATTGTCACATTCAATCCTGAAACAAACCTGCCAGGCAAGTCTTCTTCCCATTTTACAAATAAGGAGACAAAAATTAAATAACTCATCACTGTTTCAAAATAAGGAGTGTGTGAGGTTTTGTCCC
WI-1017a	92	G/A	AAATTGCTCTATTCGGACCCTCATATTAAATAAGAGCAATGAGAGCGAGGGAAAATTGAACTCTCTCAGGTACTGACTGTGGGACCAGACAA[G/A]GGATGTAGATTGTCACATTCAATCCTGAAACAAACCTGCCAGGCAAGTCTTCTTCCCATTTTACAAATAAGGAGACAAAAATTAAATAACTCATCACTGTTTCAAAATAAGGAGTGTGTGAGGTTTTGTCCC

ID	Pos			Sequence
WI-1795b	130	T	C	GAAGCAACCAGAAAGTATCTTATCCCCATCTAGATTAATTGTATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGCTTTGCAGAAAGAAAAGT[T/C]CGTCTACCATTTCACCAAATTTCGTACAAATTTAAGTATCTCTTGTTATCTCCCTAGGAGTCTAAAGTGAGCTGGGGAAGGCAGGGATTT
WI-1795a	47	T	C	GAAGCAACCAGAAAGTATCTTATCCCCATCTAGATTAATTGTATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGCTTTGCAGAAAGAAAAGTC[T/C]TTCCAGACTCCTACGATTAAATTGTATGCATGTGAACAACTGATGAGGTACTTAGATCTCAGTGCTTTGCAGAAAGAAAAGTCGTCTACCATTTCACCAAATTTCGTACAAATTAAGTATCTCTTGTTATCTCCCTAGGAGTCTAAAGTGAGCTGGGGAAGGCAGGGATTT
WI-10616d	136	G	A	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGTCCCACATAGAGAACGCTTTACTTCCCTTCCCCTTCCCCCTTACAGGCCCTCTTCAGGCGCCCTCTTCAGGGCCCCAGTCCCCCCTGAGACTCCCC[G/A]TAGCCCTCCTCCTTCCCCTTCCCCCCTTCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-10616c	136	G	A	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGTCCCACATAGAGAACGCTTTACTTCCCCTTCCCCCTTACAGGCCCTCTTCAGGCGCCCTCTTCAGGGCCCCAGTCCCCCCTGAGACTCCC[G/A]TAGCCCTCCTCCTTCCCCTTCCCCCCTTCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-10616b	141	C	T	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGTCCCACATAGAGAACGCTTTACTTCCCTTCCCCGTCTCCATACGTAGGTCCTGGTCTCCTATCACATTGCCACGTAGC[C/T]TCCCTCCCTTCCCCTTCCCCCCTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-10616a	116	G	C	CACACAATTTGCAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGTCCCACATAGAGAACGCTTTACTTCCCTTCCCCTTCCCCGTCTCTCCATACGTAGGTCCTG[G/C]TCTCCTATCACATTGCCACGTAGCCCTCCTCCTTCCCCTTCCCCCCTTCTGTATCAGGCAGTGATTTAACTCCTTTTTGT
WI-1126c	52	G	A	CTCTTATTTCTCTGGGCACTGCTTTCTTGGGGGCAAACTTCCAGTATCATCACT[G/A]ATACTAATATAAAACCCTGTAAGTCTGCTTGCATTTCAAGATTCAATATATCCAGCAAGAAAATTTATTTCTCAAGATATAAAAAATAAATATTTAATTCAGTTTCCTCAAAAGGAATATGAAATTTGTTAAAATGCAAATCCAGCTGTAACTTTTTGTCTTTATTTCTT
WI-1126b	230	T	C	CTCTTATTTCTCTGGGCACTGCTTTCTTGGGGGCAAACTTCCAGTATCATCACTGATACTGATACTAATATAAAACCCTGTAAGTCTGCTTGCATTTCAAGATTCAATATATCCAGCAAGAAAATTTATTTCTCAAGATATAAAAAATAAATATTTAATTCAGTTTCCTCAAAAGGAATATGAAATTTGTTAAAATGCAAATCCAGCTGTAACTTTTT[T/C]GGACTTGTCTTTATTTCTT

ID	Pos.			Sequence
WI-1126a	97	T	C	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTTCCAGTATCACTGATACTAATAATAAAAA CCCTGTAAGTCTGCTTGCATTTCAAGAT[T/C]CAATATATATCCAGATTGTTTTCCCAGCAAAGAAA AITTTATTTCTCAAGATATAAAAAATAAATATTAATTCAGTTCCTCAAAAGGAATATGAAATTT GTTAAAATGCAAATCCAGCTGTAACTTTTTATTCTT
WI-11183c	124	C	T	TAGTGCTAATTTTTGGAAAAGTTTGCTGATTTTTAAAAATCTTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTGCCCTTGT[C/T]ACTAACA TTTATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192	T	C	TAGTGCTAATTTTTGGAAAAGTTTGCTGATTTTTAAAAATCTTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTGCCCTTGTCACTAACATTT ATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAA[T/C]ATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118	C	T	TAGTGCTAATTTTTGGAAAAGTTTGCTGATTTTTAAAAATCTTTTTAAACTTGAAAATTTAGAGTAC ATATAAATAAAATAAAGACCAGATAGGTATTAATTCAGATGTATTTTGC[C/T]CTTGTCACTAACA TTTATGACATACAAATGACCAAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174	G	A	GCTTGGTTGCTTAGTCTTATTGTCTCAGTCTTGAGTTCTCCCTTCTGCCTGGCCCTTTGTATTCA CCCATACCTCTGATGCCTGCTCTCAGACCATTCCTCTATCTGGAGCGGCTCTTCCTTGTACTTCTCCTG TTCACCAACCTCTTTTATTCTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCCTTTCCC
WI-10770a	49	G	T	GCTTGGTTGCTTAGTCTTATTGTCTCAGTCTTGAGTTCTCCCTTCTG[G/T]CCTGGCCCTTTGTATT TCACCCATACCTCTGATGCCTGCTCTCAGACCATTCCTCTATCTGGAGCGGCTCTTCCTTGTACTTTCTC CTGTTCACCAACCTCTTTTATTCTTCAGGACACTCAGTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCCTTTCCC
WI-9667b	82	C	T	GATGACAACTTCTGCTGTGACCCTTAGTCCTTGCTCATGACACTTTCAATCTCTGCCTTGTATCATGG TTATCACTGGACA[C/T]AGCCACCTCCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCTGTCTA ATGTGCCGTTCTCCTTATGTGTATTACACACAGTCATGGCATGGTCAACTAATGGATCTTGGCT GTTAAACCTTTTCTGTGTCTACCCAGTACCTAAGTCCAAACTTGCATTCT
WI-9667a	68	G	C	GATGACAACTTCTGCTGTGACCCTTAGTCCTTGCTCATGACACTTTCAATCTCTGCCTTGTATCATG[G/C]TTATCACTGGACACAGCCACCTCCCCAGCAGGCTTAGAACTCCATGAGTAAGGGACCCTGTCTA ATGTGCCGTTCTCCTTATGTGTATTACACACAGTCATGGCATGGTCAACTAATGGATCTTGGCT GTTAAACCTTTTCTGTGTCTACCCAGTACCTAAGTCCAAACTTGCATTCT

Clone	Position	Allele 1	Allele 2	Sequence
WI-10400d	189	A	G	ACATTTTATTAGCAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTCAGACACATCTGCTGGTTAAC[G]TTATAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTATTCTAATTTTTCTTTCCCTTACCTTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATGTTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400c	166	A	C	ACATTTTATTAGCAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTCAGACACATCTGCTGGTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTATTCTAATTTTTCTTTCCCTTACCTTTACTTGCCCCACCCA[A/C]AAATAACGTAAGTACCTATGTCATGCCATGTAGTTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400b	165	A	G	ACATTTTATTAGCAAACAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTCAGACACATCTGCTGGTTAACTGTTATAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTATTCTAATTTTTCTTTCCCTTACCTTTACTTGCCCCACCC[A/G]AAAATAACGTAAGTACCTATGTCATGCCATGTAGTTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10400a	46	T	C	ACATTTTATTAGCAAACAAATCAGCAAAATAATAAATAGAAAGTAA[T/C]TGCATTTCAGACACATCTGCTGGTTAACTGTTATAAGATGGTTTAGCACTTACTAACACAATATTTATTCTAATTTTTCTTTCCCTTACCTTTACTTGCAAATTATTCAAAGGCCGTTAATGCATTATGAGTTTTTGGTTCATTTACTTGCAAATTATTCAAAGGCGTTAATGCATTATG
WI-10809b	78	C	T	AAAGGGCTACAAACTAGGCCAAAAACCATGAACGGTATAAGGAGGGGTAAATGCAAGGGGAGACCCACCTCTCCACCA[C/T]TTAGAAAAAGGGCATTTCAAGCACACATTCAATGAGGCTTCATATACTGGTTAGCAAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCCAGTGATGAGGCCACAGTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACACATAGGCTTAA
WI-10809a	33	C	T	AAAGGGCTACAAACTAGGCCAAAAACCATGAA[C/T]GGTATAAGGAGGGGTAAATGCAAGGGGAGACCCCACCTCTCCACCACTTAGAAAAAGGGCATTTCAAGCACACATTCAATGAGGCTTCATATACTGGTTAGCAAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCCAGTGATGAGGCCACAGTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACACATAGGCTTAA
WI-7038c	266	T	C	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTTCCCTGCCCACATCCAGCTTGTTGTCCCAATGAAATACTGAGATGCTGCTGGGCGTGGGCCCCCAGCCCTGGCCCAGACAAGAAGACTGTCAGGAAGGGTCGGAGTTCTGTAAAACCAGCATACAGTTTGGCTTTTTCACATTGATCATTTTATATGAAATAAAAAGATCCTGCATTTATGGTGTAGTTCTGA
WI-7038b	140	A	C	CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTTCCCTGCCCACATCCAGCTTGTTGTCCCAATGAAATACTGAGATGCTGGGCGTGGGCCCCAGCCCTGGCCCAGACAAGA[A/C]GACTGTCAGGAAGGGTCGGAGTTCGTAAAACCAGCATACAGTTTGGCTTTTTCACATTGATCATTTTATATGAAATAAAAAGATCCTGCATTTATGGTGTAGTTCTGA

			Sequence
WI-7038a	31	G A	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTTG TCCCAATGAAATACTGAGATGCTGGGCTGTCTCCTCCCTTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAAACCAGCACATACAGTTTGGCTTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGA
WI-3429b	64	G T	ATACGCTTTCTGTCTGTCCCACAGTGGAACCAGCACCCAGGTGGCCAGGGTCGGGCTCCACACA[G/T] CCCTCAGCCCCTTCAGCTTTGCATGTGTCATCGGTGACTCAGCACAGAGTTTTCCAACCTCATGTGA CAAAAATACAGATTCCCAGTCTCCTCCTGGATTGGATCTAGCAAGACCAGAGACGGGTCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	ATACGCTTTCTGTCTGTCCCACAGTGGAACCAGCACCCAGGTGGCCAGGGTCGGGCTCCACA[C/T]AG CCCTCAGCCCCTTCAGCTTTGCATGTGTCATCGGTGACTCAGCACAGAGTTTTCCAACCTCATGTGA CAAAAATACAGATTCCCAGTCTCCTCCTGGATTGGATCTAGCAAGACCAGAGACGGGTCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	ATTTTAGGACAGTGAAAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGATAAAGAAGTGAGTGACGGTGACCT GTGAGCCCCATTCTTCT[G/A]TGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111	A T	ATTTTAGGACAGTGAAAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAGGAT[A/T]AAGAAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106	A T	ATTTTAGGACAGTGAAAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCTTTGGCGAAAG[A/T]GGATAAAGAAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226	G T	GGCTATTTGTAAATGCTTGGTTATTTGACTCCAAAATGAATAAGTAGTATTGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTAAACCTTCAGTTCCAATCACTCTGAAT TTCATATACCTCCATTATTAAATTCAATACATCATTGCAGAAAGACAACGGTGCCAACTGGGGTT TGGGTTGGTGCCTGCACACCCACAGTGGCAACTAAGTGTAATCTCTAAA[G/T]
WI-6711a	36	T C	GGCTATTTGTAAATGCTTGGTTATTTGACTCCAAAA[T/C]GAATAAGTAGTATTGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTAAACCTTCAGTTCCAATCACTCT GAATTTCATATACCTCCATTATTAAATTCAATACATCATTGCAGAAAGACAACGGTGCCAACTG GGTTTGGGTTGGTGCCTGCACACCCACAGTGGCAACTAAGTGTAATCTCTAAA

				Sequence
WI-10613b	172	A	C	ATTGTATGCCAAAATCATAATACCCTGCATTCTAGAAACATACAGTGTAATAGAATTTTGAGCCATATGGTGAAAAAATTTAGAAGTATTATTCTCTATATGTATATACTACGTTAACATCAATGAATGTGATTTTTTGTCAACTTTTGACAAGGCCAGGCAATTTATTTG[A/C]GCCCTAGGAGGGTTACTATAATTTAGAAAGGCTCTTACCTTCCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44	G	A	ATTGTATGCCAAAATCATAATACCCTGCATTCTAGAAACATACA[G/A]TGTAATAGAATTTGAGCCATATGGTGAAAAATTTAGAGAGTATTATTCTCTATATGTATATACTACGTTAACATCAATGAATGTGATTTTTTGTCAACTTTTGACAAGGCCAGGCAATTTATTTGAGCCCTAGGAGGGTTACTATAATTTAGAAAGGCTCTTACCTTCCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133	A	T	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTCCAACAAGTGACTACCCTTGAAGCACATCCCCTTCTGGATCTGAAAAGAGCCCTTGGCTCAGGGGCGTCTTTTCCAGCCCCTGAGGAAA[A/T]GGAATGAACCACTCCCTGCCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCCTCTTTCCCACATGCCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-7587b	81	G	A	GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTCCAACAAGTGACTACCCTTGAAGCACATCCCCTTCTG[G/A]ATCTGAAAAGAGCCCTTGGCTCAGGGGCGTCTTTTCCAGCCCCTGAGGAAAAGGAATGAACCACTCCCTGCCCATTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCCTCTTTCCCACATGCCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-7587a	28	C	T	GCTCTAGTGGGAAACCTCAGGTAGCTCC[C/T]GAAGATCTGTGCTTCCAACAAGTGACTACCCTTGAAGCACATCCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGGCGTCTTTTCCAGCCCCTGAGGAAAAGGAATGAACCACTCCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCCTCTTTCCCACATGCCCCCATATGTCTGAGCCAAACTGCACTGGGGGCTGCCCTC
WI-10681b	103	T	A	ATGACTCAGGTGACAAAAGAAGCATTGCCTAGACCCATTGACTTACGCAAACTCAATCAGCCAACCACAGAAAAGCTAAAGACACATCCTTTTTAAAAAGCC[T/A]AAAGACAGCCATTTAATCCTAATTCGTAGTTTATGATTTTCTCAAAATTCCCACCACAGAAGAAACTTCAAGGTTCTAAGTTCTAATGTTACCATTGCTAACACTATTGTCTTTGGAGAAGGAGGAGTGACGCTCTGTTAAAAG
WI-10681a	41	A	T	ATGACTCAGGTGACAAAAGAAGCTAAAGACATCCTTTTTAAAAAGCTAAAGACAGCCATTTAATCCTAATTCGTAGTTTATGATTTTCTCAAAATTGTCCCCACCACAGAAGAAACTTCAAGGTTCTAAGTTCTAATGTTACCATTGCTAACACTATTGTCTTTGGAGAAGGAGGAGTGACGCTCTGTTAAAAG
WI-7222c	126	G	T	GCCTCTCCTCAACTGTCCTGGACCCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTTAGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCTGTTCTCAAGTTGGGGGATGGG[G/T]AATAAAGGAGGGGGAATTCCCTTGAACAAGAAGAAACTGGGGTAGTTATATTTCCACCTGCCCTTGAAGCTTTAAGACAGTGATTTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTT

WI-7222b	255	G	A	GCCTCTCCTCAACTGTCCTGGACCCAAGGCTAGGAAAGGGCTAGGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCTCAGGTGAGCTCAGGTGTCCCTGTTCTCAAGTTGGGGATGGGGAATAAAGG AGGGGGAATTCCCTTGAAACAAGAAGAACTGGGGATAGTAGTTATATTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTTCTCA
WI-7222a	126	G	T	GCCTCTCCTCAACTGTCCTGGACCCAAGGCTAGGAAAGGGCTAGGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCTGTTCTCAAGTTGGGGGATGGG[G/T]AATAA AGGAGGGGGAATTCCCTTGAACAAGAAGAACTGGGGATAGTAGTTATATTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTTTGTGTAAGGTTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	C	A	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTT[C/A]TTATCTCCTCCCAGTTCAAAATG CTTGCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAAGCGCACTCAAGCCTTAGCA CAATCTTCTTTGTAGTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-8054c	237	G	T	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTTGTAGTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TGTCATAACGCCGCTTTCCCTGGGCGTACAGA[G/T]AATCCTTGCCCTT
WI-8054b	148	T	C	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTCTTCTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTTCTTTGTAGT[T/C]TTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-8054a	131	C	G	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTCTTCTTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAG[C/G]A CAATCTTCTTTGTAGTTTAGCCTTTTCCGGAAAATCGGCTTAGTTTGCCCACCATAGCCACTCTGCT TCCTGTCATAACGCCGCTTTCCCTGGGCGTACAGAGAATCCTTGCCCTT
WI-10854b	152	G	T	TTCCACAAAAACTTCCCTGGGCCGGGGTGACTAAGAGTGGGAGAACTGGGAGTAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACACGGGGATACGGTGGTTAATGAGACGATAGTTAACGTCTGGTAAGTT ACGGGTGTGCGAGGCAACA[G/T]GGAGAGGTACGGGAATAGTAGTTCTACTTCCTTGTTTTTATTCTTGTGTG TTTTAGACACAGGGTCTGCTGTGTTG
WI-10854a	102	C	T	TTCCACAAAAACTTCCCTGGGCCGGGGTGACTAAGAGTGGGAGAACTGGGATAGTTTAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACA[C/T]GAAGACGATAGTTAACGTCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTAGTTCTACTTCCTTGTTTTTATTCTTGTGTG TTTTAGACACAGGGTCTGCTGTGTTG

ID	Pos					Sequence
WI-9826b	127	G	A	---		AATTTTATATGTGAAGGGTTAGCAAAACTATGGCCCACAGGCCCATTCTAGCCATGCCTATTTTTTGTG TGCCTGATGGCTGTTTGGTGTTTGCACGGCAGTTGAGCCATTGTGACAGAGGCTGTTAT[G/A]GCCT CAAAGCCAAAAAAAAAATTACTCTCTGGCCTGACGGGAAAGTTTGCTGATTCTAGATATTTAAA GGCAGAGAAGATCAGAAGTGTTGAA
WI-9826	125	A	T	---		AATTTTATATGTGAAGGGTTAGCAAAACTATGGCCCACAGGCCCATTCTAGCCATGCCTATTTTTTGTG TGCCTGATGGCTGTTTGGTGTTTGCACGGCAGTTGAGCCATTGTGACAGAGGCTGTT[A/T]TGGCCTTC AAAGCCAAAAAAAAAATTACTCTCTGGCCTGACGGGAAAGTTTGCTGATTCTAGATATTTAAAG GCAGAGAAGATCAGAAGTGTTGAA
WI-15986	60	T	G	TTTGTTTGTGT GTGGGTTTTT	TGACATTATAT AAACGTAAAA GAAAATGT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTTGTTTGTTGTGTGTGGGTTTTTTTTT[T/G]TTAC ATTTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A	G	AACTGCAAAT AGGAAACCAG AG	CCACCTGGGGC TCCC	TTCAAGTAACTGCAAATAGGAAACCAGAG[A/G]GGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCACAGAACAGGGGGAGGGAGGGTGGCCCCTACACCCTTTAT
WI-8170b	259	G	A	---		GCACTTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACCACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAGTACTCTACCAGATGCTGTGGTAAGGTTAG CATTTGGTGGAGAGATTTACAAAGGTTAAGATCATGTTGTCCATCAAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAAGGGGCCCTCAAATGAAATCTACGGAAAAACATAACAGA
WI-8170a	204	T	A	---		GCACTTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACCACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAGTACTCTACCAGATGCTGTGGTAAGGTTAG CATTTGGTGGAGAGATTTACAAAGGTTAAGATCATGTTGTCCATCAAAGTGCAATCCTATCAATCAGAA A[T/A]AAAGGTAAAAGGGGCCCTCAAATGAAATCTACGGAAAAACATAACAC
WI-8172	136	C	G	CCTTTATTAAA ATTGTTTTCTT GACA	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAGTCATCTTCCAATACTCCAGGTCACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAAACAAGCTTTAAAATCCTTCGGTAACTCCCTTTATTAAAATTGTTTTCTTGACAT A[C/G]AGTACCTTTACAGGTATTACATTTCTCTTCACCGTTACA
WI-8183	56	G	A	TGAAATAAAA ACAATTTCTGT TGC	TGTGTTGAAAT CAAACCTGC	AGCAGGGGTTTGAAATTGATCCCTTATTTACATGAAATAAAAACAATTTCTGTTGC[G/A]GCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGCTCGTTTCTGATGCGAGGACAAATATCCACAAT ATTTAAAACTGCAAGCACCATGC
WI-14149	83	C	T	---		GCTTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAACCCAAGCATGGGATTTTGCCGGAAAT ATTAGCGTTAAAGGAG[C/T]TGAGTTGAGTCAAACACGGG
WI-8712	44	G	G	CACAGGGAAG AGGTAGTGGA G	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAACAGCACAGGGAAGAGGTAGTGGAG[G/A]GAGATGGTCAGGCTTCCTG TTCCTTAACCAGCAGAGCCCCAGCAACCTAGAAGCGCCTCACCTAGCCTCTTAAT

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WI-8827	22	C	T	TCCCCTGGGAG ACTATGG	GCGATTAGGAT TTTAGTGTTCA C	GGTGTCCCCTGGGAGACTATGG[C/T]AGTGAACACTAAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTTCTTAGTTCCTTCTTATCCCAGTCTCT
WI-8833	51	A	T	TCTTCCATGCC ATTCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCCTCTTAAAGCTCTCTGTAGACGTCGTCTCTCCATGCCATTCTCTG[A/T]TGCCCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCTTGTCATAAAGGTCAGCTATGT
WI-8377	63	A	G	---	...	ATTTTTAGCCATGTTGGTAAAAGTTCATTTCAGTACATGGGTAACACCCAGGCCCTTTCCC[A/G]T TATATCCAGGTATGCTACAAGTTCTCTTTAACTCTATCGACGAAGTTATTATTACTGTTCCTTAGAGAG GCTACCAGGCTAAAATTCACTTAGTTTGGTTGTCTAATGTCCTCATTATTTATCCTGAAGCTCGTG
WI-8850	21	A	G	GGGACTTAAC CTTTGGCCT	CAAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A/G]CCTGCCTGCTGTTGGCTCTGGCGTGTTTGGTTTTGGTTTCTT TCTCTTCTACTGGTCTTCCTTGTCTTGTTTGGCAGCCACCTATGCTGTGT
WI-8853	79	C	T	CCCGGGGCATTG AGGATA	AGTCTTCCTGA GCCTTCCAT	ACTTTCTTGAGCTGAGCAACCTCATCATCCTTTAGCTCTGGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA[C/T]ATGGAAGGCTCAGGAAGACTTCATTCTCAA
WI-8865b	52	A	G	---	...	AGGGTGACTGGAATCACACAGGCACAGACTGAGGAAGACAGTCATGGTCGAACA[A/G]ACAAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCCATATAAA
WI-8865a	42	T	C	CACAGACTGA GGAAGACAGT CCA	GGTAAGTCCGA AGCATGTTG	AGGGTGACTGGAATCACACAGGCACAGACTGAGGAAGACAGTCA[T/C]GGTCGAACAAACACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCCATATAAA
WI-8895	32	A	C	---	...	GTGCCCACAAACCTGGACACCACCAACCAACAGAAT[A/C]CTCCCGTCCTTTGAAATTCCATTAAGAGCA CAATGGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
WI-8456	93	G	C	---	...	CCTTTTAAAGTCACAGTCAACTCGACTGTGGACTGATGATATTGTGAAATATAATAAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G/C]TTATGTCAAGTTAATAAACATTCTAAGTGCTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCCAAACTCCCGTCTCGCGTCTCAGTCACCCAC TGGCATAGACGAGGGCTTCTCAAACTCCCGTCTCGCGTCTCAGTCACCCAC
WI-8496b	157	A	G	---	...	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAAGAATGGTAATG[A/G]TTGTATCAGTGCATATTCTATGGAAA ATTCATATATCTCAAGTAACTAGCCTAGAAATCAGAGACGAACGACTATGTCAAGCTAGTATACAAGGTCA AAGACACAAATGCTGCCAATGCA[A/G]TTAGTATATGAAATAATAACGCAGCTGTTAGAAAAGTCT GTGGCCAAGTGGGGATAAAAACAGTAGCAGTGCAC
WI-8496	41	G	A	---	...	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAATGGTAAT[G/A]TTGTATCAGTGCATATTCTATGG AAAATTCATATCTCAAGTAACTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTAGTACAAG GTCAAAGACACAAATGCTGCCAATGCAAATGGGGATAAAAACAGTAGCAGTGCAC TGTGGCCAAGTGGGGATAAAAACAGTAGCAGTGCAC
WI-14153	28	A	G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC[A/G]TCCCCTCCTGCCGTTGTCACCCATCCACAGAGCA GCCCTAGTGCCAGGTGCGCAGCCCACCGCCCACCCAGGCCACGGGAACAGGACCCCATGCTGC

ID	Pos	A1	A2	Seq 1	Seq 2	Sequence
WI-12108	40	C	T	TGGAAAAGGG TTAAACTCAA ATA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAAGGGTTAAACTCAAATATC[C/T]GAAAATACTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTAA
WI-5989	29	G	A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAAACGTCCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCTGTTATACCCCATATATTAC CCCTTCATGTCCTAAAGAAGACATTTCTCTTAGAGATTTCATTTAGTGTATCTTTAAAAAAAAT CTTGTGTTAACTTGCCTCCATCTTTTCTTGGGTGAGGACACC
WI-12201	61	C	T	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGTCTTTAGCCTTTTTCCTGGAGTGTTTATGTCCCAAGCCCACTGATCACCTGCATG[C/T]GCCA GGTATGTGGTCGGGGTGTGATGGACGTGGGGTTTGCAGCCCCTCCACTGCTCGATAAAGGC
WI-12018	31	A	T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAGGCAGCCAGCTCTGACTT[A/T]CTCTCTGTTCTGTCATCTCTCCCCACATACCA ACTTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A	G	TGGCCTCGCTG CCTC	AGGGATCAAA GAGAAAGGC	TTTTTCGTTTGTTTAATGATCCGAATGCTTGAGAAGAAAACCCTGGCCTCGCTGCCCTC[A/G]GCCTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAAGATGAGGTCCCAAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	A	G	CATGCCCTTA AGGATTAAGT TT	TCTTTTCTCTT TGGTAGTGTGG	AGCATGTAAGGAGGAGCAGTTTATTGATTGGTATATTCAGGTTTCTAACCAGCTGAAAAATTCAAATA CATGCCCCTTAAGGATTAAGTTTAA[A/G]CCACACTACCAAAAGAGAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T	C	GTTGAGTATTT GTTCTGCTCAT AATT	GGGAAGGTCTG GTACATATGG	TCTGATGTCATTATTGGCACAAAAATTATTCTGATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTTGTTCTGCTCATAATT[T/C]CCAATATGTACCAGACCTTCCC GTACATATGG
WI-12326	25	G	A	GACAGACTTC AAAAGCAATT CA	AGGTTTGAAAA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAAGCAATTCAC[G/A]CTTCCAGAATACAAAGTACTTAATACATATTTCAAAC CTGTTTGCATTCAAACAACAAGTTAGCGTTTTGTAAATCAAATTTGATAACCGACTAAAAT
WI-12361	63	C	T	---	---	TTAAATTCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTCAGCATATGTATTAT[C/T] TGAACTAAATTTACAAAAGTGAAGTTGGAAAGGTAGTTATAGGTGAACCTGAGGGTCGTTACC
WI-11305	87	C	T	CAGACACAGC ATCACACCA	GACCCTCCCGT GGGC	ATACTGGTTTAATCCATGTCAAATGTAGTTACAAAGGGAAAGGACAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCCCACGGGAGGGTCGGGGAGGACGACACTTTTCCCTGGG AAAGG
WI-11321	67	A	G	GGGGAGGAAAA TCCAATAAAT TTTT	CATTGGGGGAAT AGCTAAACCTT	ATTTTTATGAAGGTTTTCTGGTGAAATCTTTAAGCAGGAGGAGGAAAATCCAATAAATTTTTTAA[A/G]AAGGTTAGCTATTCCCCAATGCTATTTAATACAATTGAGGTTAGGACGTTAAGTCTTATCAGA CTGTGTACTGGAGCCCCG
WI-11324	40	C	G	GGATAAATCA TGTGCCCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCCA[C/G]AGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTATCTGTCC

ID	Pos			Seq 1	Seq 2	Seq 3
WI-11352a	69	T	C	AGCACAGCAC ATAGTGGAAA G	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTTCTGTTTTCCAGAAGGAGAGGAGAAGTCATCTCACATAAGCACAGCACATAGTGGAA AG[T/C]GCTAAGTGTCCTACGAGAGGTCAGATCATATCCATAGAAAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T	G	CAGCTTGGAG ATTCTGATTCA GCAC	GCCCCGCCTGA G	TTAGCCCATGCTGTCATTTGCAATCACCTGTGAAACCTATACCTGCCCAGGCTCAGCTT GGAGAATTCTGATTCAG[C/T]GTGTGCTCAGCGCGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTTCGATGCGTATAT
WI-11385	75	T C		ACAGAAGACT TTCATATTCTT GTTTTT	GATTCTATTCT AGTCATGGTCA TATTTT	CTTAAAGCATTATAGTTTGGCCTGATGGTGGACACAGAAGACTTTCATATTCTTGTTTTTAAAAGTC TCTTCAGT[C/I]AGGAAAAAAGCTACAGATTTAAAAAAATATGACCATGACTAGAATAGAATCAGC
WI-11388	88	C A		TGTTTGAAATT ACACGTAACT AAGTTC	TGCCTTGTATC CAAGTTAAAAT T	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAAGAATGAATGTTTG AAATTACACGTAACTAAGTTC[C/A]TATAATTTAACTTGGATACAAGGCATTGTTATGCTAAT
WI-11392	55	T	G	GGTTATGTGTT CTTGAACTTTA TGTTTTGTAAA AG	GTACATTCACG TGTTTTGTAAA ATAAAATAC	TTCTATCATTCCATTAAAATGGGCAGGTTATGTGTTTATGTGTTCTTGAACTTTAATAAATAC[T/G]CTTTTTACA AAACACGTGAATGTACTTTCTTCTTGTCAGAAGGGGAACACTGAGTCTCCGCCTCGAGATCCATTAACTGT CATACTCCTTCCCCAGA
WI-11396	52	A	T	TTTTGTTTTTG AAATGGTGTTT T	AGCTTATTTTC ATATTCACCCA TC	AAAGAATAAGATGGCATTTGTTCAGTTAATTTTGTTTTTGAAATGGTGTTTT[A/T]GATGGGTGAATA TGAAAATAAGCTTACCTCATCCCACTCTAAAAGGTAGTTGGTGATTTTGAACCGTTGTCAAT
WI-11441	100	C A		TCCCCCACCAAC CAGC	TGCCAGGGCCT TATTTG	CTGTCAGTCTTCCCAACTAAACCGTGAGTCCCAGTATGTGCGCAGCACGTCTGTCTTGTTCTTGGTG TATTCCCATTACTGAATCCCCAACCACCAGC[C/A]CAAATAAGGCCCTGGCACAAGTAAGCTCTCC ATTTTTGTAGAATGAAT
WI-11466	26	C T		TGAGAAGCCA TTTATTTTGCA	GTTTATTGTTA TAAAAATGAC CTACAACTT	ACTTTGAGAAGCCATTTATTTTGCAG[C/T]CTTCAGTCCAAAAAAAGTCAACATTTTCAGAATTTTT TATATAAGTTGTAGGTCATTTTTATAACAATAAACTTCTATTATCTATTTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A	G	...	...	TTTTTCTTTGTGTCTCTTTTTTTTTAGTAGAAGC[A/G]GAACAGTTGTCAATACTACCTTCTGTGTTGG TCCCCTGTTAGACAACATACCTTTCTTTGAAATGTAAAATGTCA
WI-11276	41	A	G	GGCAGCGCAGG AGCAGAC	TGTACTGAGGA GCGGGTG	AGGCAACACTGCTTTATTAGGCCGGGGCAGCGCAGGAGCAGAC[A/G]CACCGGCTCCTCCAGTACACATT CCCCCACCCCTGCTCGGTGTCCCCACTCAGGGCTGGGCATGGGAGGGGCCAGCCGTAGGTCTGGAA
WI-12210	76	A	G	ACTGGGAAAA CAACTATTGC A	TGCTAGTTTGC ATATGTTTTCC	ATTGGAAACAACTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAACAA CTATTGCCAT[A/G]TGCCATA[A/G]GGAAAAACATATGCAAACTAGCATCATTGTCTCTAGA
WI-14186b	88	A	G	...	...	AATGGTCTGGTTTATTGATGAGAAGCTGTTGGTCATTTGATGGAAAGACACATACGGTACAAAATTACA GGTGGTTTAGTTCATTACACATG[A/G]TACAAATCATTTACAAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT

ID	No.			Seq A	Seq B	Sequence
WI-14186a	52	C	T	GGTCATTTGAT GGAAAGACAC A	AACTAAAACCA CCTGTAATTT GTACC	AATGGTCTCGGTTTATTGAGAAGCTGTTGGTCATTGATGGAAAGACACATA[C/T]GGTACAAAATTACAGGTGGTTAGTTCATTACATGATGAAATCATTACAAGTCTTACAAGTCATTAGAGTCTTTGGATTTT
WI-12234	66	A	G	GAGAACACTT GTGGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTGGCTATAGGTCAGTGGTTCTAAAACTTGAGCTTGCAAGAGAACACTTGTGGGGCTT[A/ GTTCAAACATGGACTGATAGGTCCCACCCCAGATTTCTAACTGGGTAGGTCTGGGGTG
WI-12345	37	C	A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAAAGAGGAA[C/A]CCTGAACCCCTGCAAGTATTCTCTTCCTGACCAGCTGGGCTTGCGCACTTTGTGAGATTGCAAAA
WI-13416	71	C	A	AAATTTTTGG AAGTTTTTCAG AAA	AGTGTTTATAG TTCAATGAATA ATTTCAA	GAAAAGGCTGTAATTTATTTCAAATTTTGGAAGTTTTTCAGAAAAAAATAAAATGACAAGAACACATA[C/A]AAATTATTGAAATTATTCATTGAAACTATAAACACTTAGCAGAGGAAGGGACTTTGAT
WI-12310	46	G	A	TTATTCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTGGGTCCT AAA	TTTGAAAAGATGCTGAATTTATTCCCAAGTATAATTTTAAAAAGCT[G/A]TTAGGACCCAAACATATTTAAACATCTCTTACACATACAGAATTTCAGTTTACAAATATTCCAGAAGGCATTTCTTAAGCAGT
WI-12086	72	C	T	CCGGGAAAAC TTGGATTT	GGAGTCTTCGG GTCTTGG	GAACCGAGCTTATTGGAGCAAAGAGTGTGGACACTGTTCTCTCCAAGTGTCTTACAACAAAACGTTTCGGGAAAACTTGGATTT[C/T]CCAAGACCCGAAGACTCCTCCACTGTTAGTAAGGTCAATTGGGGGCAGAACAGGAACATGCCTTAGCT
WI-11549	102	T	G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGTCTTCACAGGTTGTATTTGTATCTCTAAATTTCATATTTATTGGCATAAAGTTGTCTATCTAAATTTCATATTTATTGGCATAAAGTTCATAATATTCTTTTATGATCTTTAAAATATCTGT[T/G]GGGGATTTGTACAGACTTTCCTC
WI-11585	79	T	C	TGGGGTTGCAA AAACAAAA	CCATGCTTCAC TGATACTTCC	TTAGAAGGAAAGAAATAAAACACGGTAATGGGAAAATCAGTTCAGAGGTAGGAAGAAGCTGGGTTTGCAAAAACAAAAT[T/C]GGGAAGTATCAGTGAAGCATGGCCTAGAAGTCCAAGAGCAGGGGTAGAGTTT
WI-11604	68	G	C	...	...	TTAGTTGGTTCCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATT[G/C]AGAACTAGGGACTTTCCATGAAAATAATTAAGAGCTAAGGAATTCTGACGCGCTCACCATTTTTCTTTGTTACTCTGCAGTT
WI-11614c	108	C	A	...	...	CAAAATCAAAAATTGAGGAGGCAAAGAACAGAAGTAAAATCCAGAAGACTCAGCTGCTTGAGGCATGTTCCCACCCTGGACTTGCCAACTTTCACTGTGAAACTGCAA[C/A]ATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60	A	G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAAGAACAGAAGTAAAATCCAGAAGACTCAGCTG[A/G]GGCATGTTCCCACCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83	T	C	...	...	TTGATTTTACTAAGGTCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAGATATTTTTAAAATAAA[T/C]TACTTAATAATAAGAAATAAGCCATTGCCATTCCATTGTGCCAT AAGAACAAATTGGCAATGA

WI-11626a	39	G	A	G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTACTAAGGTCTTCCACTGGAACATGAAGGTAG[G/A]GATAAGTAGTGTACAGGATAATATACT CAGATATTTTAAAATAACTTAATAATAAGAAATAGCCATACCACATTGTTCCATTGCTAC AAGAACAAATTGGCAATGA
WI-11627	23	T	C	CCTTCCTTCC ATTGTCCTC	CATTTGCAACC CATCTCAAG	ACCCCTTCCTTCCATTGTCCTC[T/C]CTTGAGATGGGTTGCAAATGGGAAGTAAAAGCAAAAGGG AGATGAGAAATACTGATGCCTTTTGTCTGGCTTACTTCCATTCGCATGTCAAGTCATCCATG
WI-11636	61	A	G	GGACTTAAAA AGATCTGCTTA TCCT	AGAAACTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAATACTATTTGTAAAGGTGGACTTAAAAAGATCTGCTTA[A/G]TA TATCCACATAACTCTAGTGTTACATAAAATATTTAGCAACAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTGGTA
WI-11537	119	C	G	ATTGCTCATCT GACCCAGCAA TACTCTGACCA T	GACCCAGCAA AAAGAAATGAT T	GTACCATTTCTTATGGTGGCAAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAATATTATGTTGCAATTGCTCATCT ACTCTGACCAT[C/G]ATAATCATTCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G	C	GCCAAAAGAC TATTCAGCAA CTG	GGCTCTCCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTCAGCAACTG[G/C]AAACTGTCCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATACTCTACTCAGAGTTCACACTCATATTTCATATTTTT ATTTTTGGGTGTTGGGT
WI-11656	28	G	A	ATTGATTTTAG AAGGAACTGC AA	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAACTGCAA[G/A]CTTTACTTGAGGACAAAGCCTTGCCTGCAGTTGTTT AAAATGTCCTGAAACAATCAGATTCCCAGCCTGGAT
WI-11680	55	T	C	...	...	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCCTTTT[T/C]TTGCATAAA GGCTGGGAAGGTGGTTGGCCAGACCGTACATCTTTT
WI-11696	47	T	C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACCTT	GTCCAAGAACAAAGATACTTTGACATCTTTATCACAGCAGGGGACAG[T/C]AAGGTTGGCTTCTCTA ATGCCCACCATCTGTGTTTCAGAATCTTTCCACTCTGCC
WI-11702	69	C	T	GAATAATACT GAAATAACCA CAGCAG	AGAACAACTT AAGCAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACTTTCAATAATTAAAAATCGAATAATACTGAAATAACCACAGC AG[C/T]TTTCAGTATAATTGCTTAAGTTGTTCTAGAAAACACTGCTAATTTTTGTTTCTGCAGA
WI-11706	60	C	T	TGGCTGGAATT TTCTCTCTT	ATCACCAAAG AACAAATTCCA	TGCTGATTCATCGCCTTCTACCATCTGGCTGGAATTTTCTCTCTTGTACAATTTATTTGC[C/T]GGCTG GAATTGTTCTTGGTGATTTGTCCCCTTGCTGCT
WI-11709	105	T	A	AGAAGCTTGC TTCAGTTTGC	TCATTTCTTCT AATTTTACGGG A	AATATCATCACTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCCTTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAAGCTTGCTTCAGTTTGC[T/A]GTCCCGTAAAATTAGAAGAAATGAAT GGCCAGATGGATGGAAAA
WI-11710	103	C	A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTTCCAGCACACAACAGCCAGCCCACACTCTAGACACGCCTTCAC TCCAGTCCATTCTGGCACCTAGCCTCAGTCTTCAC[C/A]CTCCTCCTCCCACACTCCTTC

Marker	Pos	A1	A2			Sequence
WI-11715b	123	C	T	AGGCTGGCTGC AGCTT	TCCCCATCCTG TGGCT	AGAATGGAGCTGTTGGGGAGGGGACATGCACACAATGTAAAACAGACAAAATGCATTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGAGGAAAGAGGCTGGCTGCGCAGCTT[C/T]AGCCAC AGGATGGGGACTGGGGAAGA
WI-11715a	49	A	C	GCACACAATG TAAAACAGAC AAA	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGGAGGGGACATGCACACAATGTAAAACAGACAAA[A/C]TGCATTACAACTG TGGTGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTTCAGCCAC AGGATGGGGACTGGGGAAGA
WI-11727	43	G	C	AACAATCCTT AAAACAACTA TCAACA	CCTGTGGTTG TGTTGCAG	CTGGGATTTCCTATACCTAACAATCCTTAAAACAACTATCAACA[G/C]CTGCAACAAACCACAGGC AAAATGAAAAACAGATGCCCAGACAGCACCCACCACATGGCACAC
WI-11728	16	C	G	---	---	TTTTATTTATCAAACT[C/G]CAATTCCATTCACAAATGTAAGTTATCATCAGCTCCCCATCCACTTT CTCCCCATCTCTTCTATCTCTTCCCACCCTACACTTTCTCTCCCCTACACCGGGTTCCAAA
WI-11758	61	A	G	ATCTGTGGTTT TCGCCTG	TGATTGGCCCT GTGGTCTA	TTTTTCTCTTTTTATTAAGTCCGGTATACTAACTAGAAGGAGAATCTGTGGTTTTCGCCTG[A/G]TAG ACCACAGGGCCAATCACCACCACAGCTTCTTGTAGAGAACATGGAGAGTGCCAAGATCACCATCA
WI-11295	37	A	T	GCCTCACAAA GTATTTCTAA AATATAA	AAAAGTGCTCA TCTGTGAACTC T	CCGGGCCTCACAAAGTATTTCTAAAATATAATTTGCT[A/G]TAGAGTTCACAGATGAGCACTTTTCA CATTAGGTGATATGCAAACAAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93	T	C	---	---	AGCACATGATATTCTGCCTGGAGTTTCTGTGAGCTCAGCAAACAGCAGAGTCAGAGATTAAGAATT ATTTATTGCCTCCTTTTTTCCCCC[T/C]GTGATTGTTAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42	C	G	GGCTCAGAGA GGCAAGGGAA GTGTG	AAAACTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTATTTAATGGGCTCAGAGAGAGCAAGGGAA[C/G]CACACAAAATTTACAGTCTGA GTTTGCGGCGCAGAGACCCCTCCCACCTTTTCATGCCTGTGTGTACACACACAGTGTCCAAGCCTC AGA
WI-11790	28	A	G	CCCAACTTACC AAACCTCTG	CGGTAGGCGAG GCTAAGC	TAATTCACCCAACTTACCAAACCTCTGT[A/G]GCTTAGCCTCGCCCTACACATGCTCAGAGCAC TTACATTAACCTACAATGGGCAAAATCATCTAACACAAGC
WI-11879	61	C	A	TCATCTAATCT GTGAGGTATTT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAAA	TTTTAATTCCCAAAGCTTACAACCATCTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C/A]AGT GATTTTCTCTTTCCTTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91	C	T	GTTTTAATGT GGTATTAGAA AAGTTTAAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTACTAATTTTCCATTTCCTCCCCTTTTATAGTTTTAATGTGGTATTAGAAAGTTTAAATTACAT ATGTGGCTTATATTCTATTTCTA[C/T]TTGACAGCACAGTTCTTCAAAGTTGCTATAGACAATCTGA AAATTGGGTTCTGAACT
WI-11906	52	A	G	TGTTATAACAT CAAAGAAAGA ATCTGAA	TTAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAAGAAAGAATCTGAAT[A/G]TGAGGGAACTG CAGAAATTAAACTTTCAGTCTAATTCTCAGAGTAAGATGAACCCTTTACAG

ID						Sequence
WI-11909	78	A	G	TTTGTGTTGGG TGGTCAAG	CCTCCTCTGAG ATTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGTGGAGCATACTGAAGACTATTCCTAAATGGCTATTTGTTG GGTGGTCAAG[A/G]CTATTCAGAAATCTCAGAGGAGGACAAATGATAGTGCACTGCAGCCAGCTCG GACTGGCTGCAAGAGTC
WI-11806	60	T	G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTAGCATCAATTGCCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]GTT TTATTAGTATATAAAATTGGCTTTACAGGAAGCATTATGG
WI-11946	31	C	A	...	...	CCCTAGTGAATACAACCTTTGTCCTGGAGAC[C/A]CCAGCTAGTCTAAGAAAACTTCCTAGGCTGAG CTCTCCTTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAAGGGAA
WI-11965	65	T	G	TGAAGATCAG ATCTCTGGTTT GATTT	CAGCTGTGGTG AATGTTGAT	ACAAAAATTCACAGTACAAACACTGCTTATTTCTGCTTGAAGATCAGATCTCTGGTTTATTTAAT[T/ G]ATCAACATTCACCACAGCTGAAGGAAATTAAACTGAACCT
WI-11027	90	T	A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAAACTGCAGAAAGGGCAGGACAAAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAA[T/A]AATAAAAATACTGTAACACATTCCTCATTTCTCTTACGA ATACTTCTTTTGATATTGCAAATTCTATGGCATACACAGAGGCACCTCCTCAATGCCCTG
WI-11049	95	C	T	...	...	TTCTGCTGAAGATCACAAAACAATTCAACCTCTGTGGTTCAAAAATAATTAAGGATCTTGTACCTTT GTGTTTATTTCTGTTTCAACTAAGGA[C/T]TAGACTTCAGAAGGCATAGCTTCCCTTGTAACGTTTT AAACATCTTTCATTTGTAGGAAGGAACATTCAAAAGCCCAA
WI-15488	69	C	T	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTGTG TAAC	CAACATTTATCAAACATGTAGGGAAAAAGTTCTCACTCTGCACTATAAAAGGACAGCCAGATATCA AC[C/T]GTTACAGAAATGAAATAAGATGGAAAATTTTAACAAATTG
WI-13654	49	A	G	AACAGTTAAT GAAAACACATC CGT	GGCTGGTGAAA TGATGTGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAAAACACATCCGTA[A/G]GTATGACATCATTT CACCAGCCAGCTACTTCATGTGCAGAAAAGGTAACCTTTCCCATTTACAGACAAAACCAGT
WI-11070b	135	C	T	...		ATGAGACCCTGCTTTGAACGTTTAAACGTTTTGGAATAATGGAAAAGGAGCTAGGACAATTCTTGCTT TCAAGTAAAATTGTGACTGAGCAGAAATCAGCCAGCTAGGAGAGGTACTCCAAGTA C[C/T]GTGGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAGGGAA
WI-11070a	110	G	T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCTGCTTTGAACGTTTAAACGTTTTGGAATAATGGAAAAGGAGCTAGGACAATTCTTGCTT TCAAGTAAAATTGTGACTGAGCAGAAATCAGCCAGCTATCTT[G/T]GGTGCAGAGAGGTACTCCAA GTACCGTGGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAGGGAA
WI-12020	121	T	C	...		AATCTTTATATTCCAGCTGTTGAGACAGTATTTTGAGGGCTGATGTTACCTCTCTAGCGGCGAAACC AGAGCCAGCTATTAAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCATT[T/C]CTCTTTTAGC ACGTTCTTGTTCTCCTC

Clone	No.			Flanking	Sequence
WI-11076b	142	G	A	...	CATGGTTCTGCCAGCTTACAGGAAGCATGGTCGTGCTGGCATCGGCTTATCTTCTTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAAGGGGGGAGCCATGTCACATACCCAGAGCAGGAGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACTCACTGTCAT G
WI-11076a	106	T	C	AGGGGGGAGC AGGCA / GTATGTGAC / TCCTGCTCTGG	CATGGTTCTGCCAGCTTACAGGAAGCATGGTCGTGCTGGCATCGGCTTATCTTCTTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAAGGGGGGAGCCAGGCAGT[T/C]GTCACATACCCAGAGCAGGAGAGA GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACTCACTGTCAT G
WI-14263	49	T	C	CGCAGAAAAA GGCATATTCA / GACA	ACCTTTAAAGTTTCTCCCCACCTACTCCCGCAGAAAAAGGCATATTCAA[T/C]TGTCCCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTCAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-14267	28	T	C	...	AATTATTGCTGAAATTAGGAAGGGAGCA[T/C]TGAAATGGGAAGGGGGAGGTTAGAGAAGACAGAG ATTTAAAAGAAGCAAGTACCATTTCCAAGTATAAAAACTCGTA
WI-13892	50	G	A	CTTTTCATTTT TGCTTTTAAA TAGAAC / TGATGATGTCA TATACTAAAA ATCAAG	GATTTGTTTATTCATTCTCGCTTTCATTTTTGCTTTTAAATAGAACA[G/A]CTTTGATTTTTAGTA TATGACATCATCATCATGAATTTTTTCTCTTACTTTGTATTTAGGCTCCACCTCAGTAGTTGACAA AGGTAGAATGAGTTCA
WI-15288	108	C	G	CATGAGAGGA TTCCCCTCTC / AAAAGCTTCTT TCCCCTTGGA	ACCTCTTTCTGATGACACTTGTACCTGTAAGGGGTCTAGAGAGAAAAGAGTAGTAGACTCCTACTTTGC TACAATTCAGGATGCAGGGCATGAGGATCCCTCTC[C/G]TCCAAGGGAAGAAGAGCTTTTGGC
WI-13951b	88	G	C	...	AATAAATGGAAGAAGGAGGTGAACAAAGTAATGAACAAAACAGACCCCAGATCAGAGGAAGATG GCTTTCTTGTTAATTCTGGAGCA[G/C]ATTCAAGCAGCAAATATTACTGAACACTTGCTATGTGCTG G
WI-13951a	39	C	T	GGAGTGAACA AGTAATGAA CAAAA / TTCCTCTGATC TGGGGTCT	AATAAATGGAAGAAGGAGGTGAACAAAGTAATGAACAAAA[C/T]AGACCCCAGATCAGAGGAAGAG ATGGCTTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAAATATTACTGAACACTTGTCTATGTGCTG G
WI-13264	25	G	A	AAAAAGGCTC TTGCCCAT / GGAGGGAGAG ACGGGAATA	GAGACCAAAAAAAGGCTCTTGCCCAT[G/A]TATTCCGTCTCTCCCTCCTGACTGACCCCAGTGTCTT ACAATGAAACATCCCTCCAGCCCCATGGCATGGTCATCCCCTTCTTGGGATCTGTGAATATAACCA ACTGTCTGTCAATGGC
WI-13960	39	A	C	AGCAAAAGGA AGTTAAATAC CTGATAGA / CATGAAAGGA CAAATTTGCAT C	TTATTTGTCATTAGCAAAAGGAAGTTAAATACTGATAGA[A/C]GATGCAAATTTGTCCTTTCATGCA TTTGTGGAGCAAGTACTAACTTGTTCCCTCACAAGGAGTTGAGCCCCTAGATGAC
WI-15843	62	C	T	ATCTTATAACC AAGAAGCCTT CAG / CTCTGGCTCAG ACTTGCTCT	AACTCTTTATTGTTTAGCTAGCCCCAGTGACTTTATGCATCTTATAACCAAGAAGCCTTCAG[C/T]TAG AGCAAGTCTGAGCCAGGAGGTTTATCACACTTTGTCCTCCACCAGGAACCAGGTCTTGGCT

ID	Pos			5' fragment	fragment	Sequence
WI-13983	52	G	A	TCTCTCCCACT CCTTAAACCT	CAATACTCTCT TAGCCCAGTGG	TTGTGTATCTGATTCGAAAACATAGAAATCTCTCTCCCACTCCTTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAAGAATATGCACTGACTTAACAGAATTAGAACATCCAGGCACTCACTGAGA
WI-13850	51	A	G	AATCTCAGGG TCACAGCTTTA TT	TGTTCCCTGAC AATGTTTGTAA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTTTAACAGCAGCCAT[A/G]TTACAAACATTGT CAGGGAACATTACAAGAATAAATAAGATGGACTTGCAGGTGTAAAAAGATTACACTTCA
WI-15295	27	G	C	A / TGTCAGTTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGAT[G/C]TTTCCTTTGCCAACTATTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAAAGGCCCCGAAAATATGAGTGAGACTCA
WI-14284	55	C	T	---	---	ATTTCAAACAAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA[C/T]TATGCCAT GCGGGAAATAAAATGCTTATCCAGTGGAGCGCTCCCCTGATGCATTGA
WI-14288	85	G	C	CCGCTGCTATT CCCAGAT	GGTCTCCTTCC ACCAAATCTT	ATGACCAGACCAGAGCCCCTGTTCTATATGAAGACAAACAGGTGGCCATACTTGGGTGGAGGGATA CCGCTGCTATTCCCAGAT[G/C]AAGATTTGGTGGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C	T	TGATGTAGTTA CCCCACTAAT ACAAC	CATAATATTTG AAGTCAGTGGT TCTC	TTTATTTGATGTAGTTACCCCACTAATACAAC[C/T]GAGAACCACTGACTTCAAATATTATGAGAG AAAATTACTCCAGGGAATTTTTGCAGAAGAGATAATA
WI-13529	42	T	C	CACAAACATT TATTGAAACAG TTACCA	TCTATACACTT CTCACTCTCTT GCTT	AAATATGATTCCATTCCACAAACATTTATTGAAACAGTTACCAT[T/C]AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGTCCCTGAGGGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84	G	A	---	---	TTATTTGTCAGAATTTCCAGAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTCAGGAAGAAAGGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T	C	---	---	TGAAAGGGATACAGAAAAAAACTCAGCGAAG[T/C]GAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTTCCAGTTGTCCTCCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G	A	---	---	TTTTATTGTTGGTAGAAAAACAGGCTCTTAACACTGAATAAACATCTCAC[G/A]AACTGTCGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCTTTGACGCCGGCCCCTGAATCTGACATTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61	A	G	---	---	TTGGTTTTTAATACCTCTTGTTGGATAAAAAGGACATTGTTTTTCATTAGCTTGTCTTCAAA[A/G]GAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAAATAGAAAATTAAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A	G	AAGG / TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA CAATG	TTGGTTTTAATACCTCTTGTTGGATAAAAAGG[A/G]CATTGTTTTTCATTAGCTTGTCTTCAAAGAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAAATAGAAAATTAAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

Marker	No.	Allele 1	Allele 2	Fragment 1	Fragment 2	Sequence
WI-14297	86	A	T	AATGTTGGGT ACTTTTTCCAA G	TGTGCACATTC AGAAACATTTT	CTGACTTTATTTAGCAGCATGCAATGCAATTTATTCTGGCAATAAATTAATAATGTGCAGTTATAAAAAT GTTGGGTACTTTTTCCAAG[A/T]AAAATGTTTCTGAATGTGCACACTAGAATATGCAGAATCCTTT AAACAGTCGACT
WI-12229	89	T	G	CATGTGCACA AAAAGAGTAA GAAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAAATT[T/G]ACCAAAAAATTAAAGATTTTTGGGACAATTCACATGTTC AAAAT
WI-13582	43	C	A	TGCAATCTAG AGACTGGGGA	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCCTTACTGGACCAATGCAATCTAGAGACTGGGGA[C/A]TGGAATCTAACTGCGCAGAG AATCAAAGACCGATGGTGTGAAATCTGGGCAGCTTCAAATTCTGCCTCCTAAAAACATTTCAC CCAATTTTCATTATTGCC
WI-13857	28	A	G	...	...	TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTAGGTATCTGGCACAATTAACCAAATGT CTGCCCATTTTGTGTAGCTTCATACAGTACAGATTTCATTGATGTCGCTCCCACATCTG
WI-15809	77	T	G	TGGTTTTCTGT TGTAAATGCC GTAAA	TAAGGTAGCTA ATTCAATGTTT GTAAA	GTTTAAGTTGCAGAGATGTGAATGGTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTTCTGTT GTAAATGCC[T/G]TTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123	A	T	...	...	TTAATCAGTCTGTGTCAAGAAGAAACAGGACTTGATCAAGCTTCCAGCCCTCCACCACTCTATCAGCA TAGCAATTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAAACCAAGAGAAGGAA[A/T]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81	T		CATACTCCACT CTAGCTGCAGT GAA	AGAAGAGTGG ATGGGATGC	TCTTTATTCCAAGAATGGGAAGCGCATTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACTCTA GCTGCAGTAATACT[T/G]GCATCCCATCCCACTCTTCTCTCTTTTTGACTGAAAACTCTTCAAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24	G	A	TTTATTCCAAG AATGGGAAGC GA	TCATTCAAGCC AATGAAAATG	TCTTTTATTCCAAGAATGGGAAGC[G/A]CATTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAATACTGCTACCCATCCATCCCACTCTTCTCTCTTTTTGACTGAAACTCTTCAAAGAACT GCTGAATGTCCTCTCTC
WI-13763	59	T	C	GGCTGGACACT GCAGTGAT CCCC	CCCACACCTGC CCCT	GCTCGTAATGAACAGCGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGATT[C/T]CAGGG GCAGGTGTGGGGCAGGGTGGGGCGCCTCTGAGCCGGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48	T	A	TCAATAAAGA GCAGAAAGAA AACC	CAGTGTGTAAG AACATCTTTT GTC	TTTTTTTGGTGAGTGTTTGTCTTCAATAAAGAGACAGAAAACC[T/A]AGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTGCACCCAAACATGATATTTGCTTTTCCCGAGGGCAAAAAGA GAGTCTTCCCAGAAACCTC
WI-13789	62	G	A	TTGGATGGCTG AGGGAG	CAGTGCGCTTC CTCTGTTC	TCCAAGGAAAAAGAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAATTGGATGGCTGAGGGGTT GAACAGAGGAAGCCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTGTAGGGTCCTCACTCTT GAGGTCCCT
WI-13594	66	G	A	TTTTTAACACA GATCACAAAA AGC	CCTTTGCGCCA GTACTTTTT	AATAACAAGTTAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTAACACAGATCACAAAAAGC[G/A]TGCACAAAAAGTACTGGCGCAAAGGACAAAATAATGCTAAGAATTAGGCCAAACAGCTGC

ID	No.				Sequence
WI-15625	40	C	T	...	GTTCTCCCCACCTACTCCCGCAGAAAAAAGGCATATTCAA[C/T]TGTCCCATACTAATTTTTGAATAACCTAACTCTCCCTTGTTTCTTACTAAGAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84	C	G	CCACACTGAA GACTCACCAG A / TCCCCACCCCA CCCT	GTCTCACTTTCTTGTCTAGGCTGTAAATTTCAGTTAACAGTTCTTATGTGATTGTTGGCCACACTGAAGACTCACCAGAA[C/G]AGGGTGGGGAATACTTAATCAATATTGTGGAATTTACCCGATGAAATCCAGTTATTCCT
WI-13600	26	G	T	TTAATGAGCC AAGCATCCAT	CATATTGAAAACTCACTTAATGAGCCAAGCATCATCTAGTAACAATTTCAATATGCACATTATATATACTGAAACAAAGAATACGGATTGTGTAGGGAAGAGCATAGAGAGGACCACCATCAGCAACCCTCTTTGTTACTAGATGATTCCCTTCTCTACCC
WI-13602	89	G	T	TCCATTCTGGA GACAACACA / GCATACCTCAT GACAATATTTA ATATTAAT	GATAGGAAAAGAAGAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCCTCCATTCTGGAGACAACACA[G/T]AAATCTATTAAATATTAAATATTGTCATGAGGTATGCACCT
WI-13650	76	A	T	AAAGATTCAC AATATTTCACT TTTAAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAACATTTAAAAATTCTGAGGGATATTGATGAGAACTATGATGAAAGATTCACAATATTCACTTTTAAAAC[A/T]TAAAAAACTACTCTTCATATCCTGATGACTTAAAAGTTACGG
WI-14319	83	C	T	CAATTCAAGG CACAAAGCTA A	CCAAATCATCT ATATTGTTGCA TG	TGTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAGGAAATAGCAATTCAAGGCACAAAGCTAAG[C/T]TACATGCAACAATATAGATATTGGGGGTACAGTACAGAATT
WI-13528	80	A	G	CAATACATT GCATTTTCCTA AAAA	CATGATACCAC AGTTTTCTCTG AA	ATTGGATACATGCTTTAAAAATGGTAGCTTTAAACTGTAATCAATACATTGCATTTTCCTAAAAAAGAAGAGACATTTA[A/G]TTCAGAGAAAACTGGTATCATGCAGGAAAAGCAGAAAAAATT
WI-13909c	93	A	T	...	...	ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTCCCAGTGAAGTTCATCTTCCTCACACTCTCTTCAAACTGCAATATCTTTTC[A/T]GAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80	G	A	TTCCTCACACT CTCTTCAAACT C	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTCCCAGTGAAGTTCATCTTCCTCACACTCTCTTCAAACTC[G/A]AATATCTTTTCAGAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86	C	A	...	...	TTTTTATTGAATTCCAAATGTAGCAAATCATTAAAACAAATTATAAAAGGGACAGAAAAATTAAGAATCAAACATCATTCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGGAGACCAGTAACTA
WI-14323a	78	T	C	ACAGAAAAAT TAAGAATCAA ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAATCATTAAAACAAATCATTAAAAGGGACAGAAAAATTAAGAATCAAACATCAT[T/C]CTGGACCATGGGAACCTTGAAAAGGCATGGCGCTGGAGACCAGTAACTA
WI-15389b	104	G	A	AGATAATGAA ACATCTGCGA AAA	GATGAGGTGAT TCCCACACTT	AAAATTGACAAATCAACTAGCTTGCTTTTGTCGTTTGGAAGACTACCATTATTCAAATTTATTATGTAATACACTCATCCAGATAATGAAACATCTGCGAAAA[G/A]AAGTGTGGGAATCACCTCATCGTGTGC

WI-153389a	33	G	A	AATCAACTAG CTTGCTTTTTG TC	TTTGAATAATG GTAGTCTTCCA AA	AAAATTGACAAATCAACTAGCTTGCTTTTTGTC[G/A]TTTGGAAGAGACTACCATTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAAACATCTGCGAAAGAAGAGTGTGGGAATCACCTCATCTGTGC
WI-15747	88	T	C	TGCTTCATTTT AAACTAATTT AGTGTTT	CATAATTCACC AAAAGTTCATA TAATTT	TGTAATCTGCTTACAGTCCTTGCAAAGACAGACATATGTTTTTGCATAAAGATATAAAATTGCTTCAT TTTAAACTAATTTAGTGTTT[T/C]TTTAAATTATTATGAACTTTGGTGAATTATGAACTGTACCAAAC C
WI-13752b	117	C	T	...	...	AAGAAAAGCACATACATTTCCAGAATTTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTGCTGGGATATACTTGGCTTGCAC[C/T]GGACACCTTTTACG GAGGGATTCCGGACAACT
WI-13752a	106	T	C	CCTTCTCGTTA AGTGCTGGA	CCCTCCGTAAA AGGTGTCC	AAGAAAAGCACATACATTTCCAGAATTTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTTAAGTGCTGGGATATAC[T/C]TGGCTTGCACCGGACACCTTTTACG GAGGGATTCCGGACAACT
WI-14339	102	T	G	CCCAATCAAA CAGTACATGA TTTAC	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCTTCACTGGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCACCCAATCAAACAGTACATTACT[T/G]CGGTTCCAGAAATCTGGATAC
WI-13744	115	C	T	TGGTGCTGAAC AAAACTGAA	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACGTAATGGAACTTCATGCAGCTTTAGAT TTCCTTTGCCCAGCTAGGAGCTTGTGTATGGTGCTGAACAAAACTGAA[C/T]GCTGTGTGCTTATCTTTC CTGATTCT
WI-14061	68	C	T	...	...	CCTTTGACTATATTGTTTTTCCAAAAATAGGACTATGTGTAGAAGAGAGCCCCGTACATACCTTAT [C/T]AACCATTTCATCCACCATTGTAAAAATCTCATCTTCTGGGTCTGGATACTCAAAAACAGAT
WI-15719	69	A	C	ACCCTTTCATC CATTCAGC	TGATACTTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAACACTACCACACTGAATATACTGAATTAACTATTCAACCCTTTCATCCATTCAG C[A/C]AATTAAAACTCTTGCCAAGTATCATGAACTTACGAAGAGAGATAAGAGATCTGATC
WI-13810	106	T	C	CTCTAAATCG ATACATCCAA AACTT	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAAATCACACTACTAGATCAAACAGAAGTACCACAGTATGCTTTATTTTGCA GGTATTAATTGGTTCTCTAAATGCATCCAAAAACTTT[T/C]GAGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27	G	T	ATTTTATTCAC ATTAAAACTTG CACA	GTTCTTTGATA TGTGGCTTAGT TTT	GGATTTTATTCACATTAAAACTTGCACA[G/T]TAGCAAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAAGAACAATATACAATAGAGATTTGAATTTCTCAATAGCATTGGAAGGTATTTCCATAAATA
WI-137785d	72	G	A	...	...	TCAAAACTGCACACTATAAAAGTGCTTTAAAATGCAGCAGCAGGAGATGTGAAGACACAAAATGAAC AAGTGC[G/A]TAGTGACACTATAGTGCTTGTCACAACACAGTG
WI-137785c	56	A	C	...	...	TCAAAACTGCACACTATAAAAGTGCTTTAAAATGCAGCAGCAGGAGATGTGAAGAC[A/C]AAATG AACAAGTGCGTAGTGACACTATAAAAGTGCTGTCACAACACAGTG

ID	Pos					Sequence
WI-13785b	40	C	G		---	TCAAAACTGCACACTATAAAAGTGCTTTAAAATGCAGCAG[C/G]AGGGAGATGTGAAGACACAAATG AACAAGTGCGTAGTGACACATAGCTGTCACAACACAGTG
WI-13785a	27	T	C	AAAACTGCAC ACTATAAAAG C TGCTT	TGTTGTGACAG CTATGTGTCAC T	TCAAAACTGCACACTATAAAAGTGCTT[T/C]AAAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAGTGCGTAGTGACACATAGCTGTCACAACACAGTG
WI-13793	88	C	G	GGATTTTACAT TCAGCCTAGAT ATAGG	GGGCAGGAGGA TTTGTTACT	AGAAACCAAGTATATCATAGGCAAATAAAAATAGTTTTACCCCCATTGATACAACATAAGGGATTT TACATTCAGCCTAGATAGG[C/G]AGTAACAAATCCTCTGCCATAAATCTATGACTTG
WI-13794	52	A	G	TTCCTCACCCT TTCTTTCTC	AGAATGGGCTC TTAACCTTGTA	TAGTCTCTACAATTCCTTCAATCCATTTCTTCCTCACCCTTTCTTCTC[A/G]TACAAGGTTAAGA GCCCATTCTTCAAACAAAAAACAAACACATAGAGCAAT
WI-15729	35	A	G	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACTTTGAACCATGTGTAGACGTGC[A/G]GGCACTTTAGAAAGAAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAGGAAGGGTAAGTCCCTGTTTGCAGCCCGGGCCTCGCTCATTGTTA
WI-13424	66	G	A	TGAGGTTTTTC ACCCTATTCTT AC	TTTTTCTCCCC AGGGTCTA	GTCCTTTGCACAAGTCTCCCAACTGGTTTGGAGTTTTCCCTTCTGAGGTTTTTCACCCTATTCTTC[G/A] TAGACCCTGGGGAGAAAAAACACATGTGTAAGTGGCTCAGGACATGAGGCAGCCGTTCACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29	T	C	TCTTATAAAA GGTCAGAGGC AATT	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTCAGAGGCAATTT[T/C]GAGATCCCAGATTCAGCTTGTCTCATAAAAGAT TCAACTTCAAGTAGCACAATTTCTTGTCTGCTTTAATCCTGAACATTCTTGAAGCACGAA
WI-13446	22	G	C	GCCATGTTCTT CTCACTCATCA	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTCACTCATCATCGA[G/C]CCCTTCTGTGTTTGATTTGATTTCCCTTCTGCTGTCGTAATTTTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTGTTTGAAGAAATTCTGGTTTTTGGAGTAGTGAGCCCTTTTACTTTTTTT CTGACTGCCTAATT
WI-13725	56	A	C	TGAGCACATA TGGGTGCC	CCTGCTGTCTC GGCC	TCACACAAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[A/C]GCCCGAG ACAGCAGGATAAGTTTCACAAAACTTGACCAGGCAGGTTAGAAGCAAGGCATGGTTCAGGATG
WI-15702d	107	T	C	---		CAAATGTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTGAGG AAAGCATGTGAGAGAAACTGTAACCCTGTAAACAATACTAA[T/C]GGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101	T	C	---		CAAATGTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGGTGAGG AAAGCATGTGAGAGAAACTGTAACCCTGTAAACAA[T/C]ACTAATGGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90	C	T	---		CAAATGTTTATGAAGAGACTCCGAACAAAATAAAGGGGGGTAAAGGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAC[C/T]CTGTAAACAATACTAATGGGGTTCTTTGAACAAATAGTTT TGA

Clone	Pos					Sequence
WI-15702a	48	G	C	AACAAAATAA AGGCTTTCAA AAAG	CCTCACCCCTT TACCCC	CAAATGTTTATGAAGAGACTCCGAACAAATAAAGGCTTTCAAAAAG[G/C]GGGGTAAAGGGGTG AGGAAAGCATGTGAGAGAAACTGTAACCCTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-13831b	113	T	C	---	---	TTTTTTTTATGGATGCACTGTACATGTGTTATTTAGCGAAGGTGACTTGGAAAAGGAGATTCACAT ACTTCCACTGTATCCTCCGGGTAAGTTTCCTTCTTCTTGTAGA[T/C]GTCTCCCATGTTACAGTCAAC TATAAAACATGGCTCA
WI-13831a	56	G	C	---	---	TTTTTTTTATGGATGCACTGTTACATGTTTATTTAGCGAAGGTGACTTGGAAAA[G/C]GAGATTCA CATACTTCCACTGTATCCTCCGGGTAAGTTTCCTTCTTCTTGTAGATGTCTCCATGTTACAGTCAAC TATAAAACATGGCTCA
WI-13806	62	G	A	---	---	TGATTGAGCTTAGAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAAACTAGGCCTCAGGT[G/A]C CCATTAAGCATGCTGTGAATGCAAAGGAAAAGCTTAAAAAATTTTTAAGGGTGACTCCAGTAAA CAT
WI-14372	86	A	G	---	---	CACATTTCAGCAAACAAATCGAGGTGCAAACAGGGTTTATTTCACCATTAATATATTAACTGGATTT TTTGTCAAATAAATAGGGA[A/G]TTCTCTTTAAATAACCATCTCCTCACTTCATGGCCAGT
WI-14373	95	A	G	---	---	AGGCTGTGTTTTTGAGGGCCTGAGGACCCCAACATGACAACGTAACCATGGTCATGTGAGTT ATGAGCTAGGAACCCTGGACGAAACCA[A/G]CACATATACAATCATCTCCCACCTCCCAACGCCTTT ACTTTCACAGCCTCTGCA
WI-14078	61	C	T	AAAGAAGTAA ATTAGGAAGA GCAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAAGAACCACATGGTGTATCCAAAGAAGTAAATTAGGAAGAGCAAGA[C/T]G CAGTAAGAGACACATGCACACAAATCGAAACAAGGCATGGAAGGACTTTAGATGGTCACG
WI-14083	47	C	T	AGACTTGAGA GCTTAAAACA ACACT	GCCTACTGGAC CTCTAAACTAC TGA	TTGCTACATAACACATTACTCCAGACTTGAGAGCTTAAAACAACACT[C/T]ATTGTTATTTCACAG CTCAGTAGTTAGAGGTCCAGTAGGCTTGGCTGAGTTGTTTGCTTAAGGTCTTACAAGGCCAA
WI-14085	31	A	G	CATTTATTTTC ATGTGTAAGA AGAAAAA	CAGTCATGTTC ACGTGCTAGTT	TGCATTTATTTCATGTGTAAGAAGAAAAAC[A/G]TAACTAGCACGTGAACATGACTGCATGGATAC ACGGGCTCAGCAGCGAGGCTAAAGTCAGAAGTGAGTGAAAACAAAATAGCATGTTGATTTAAGTGAAA TAACAGAACAGGAGGCCTTT
WI-12169	121	G	C	AATAAAACTT CCTATTTTTCTT TTGCTT	GGGTTCTGAGG TGAAAGAAAA A	GTCAAAGGTTGGCAAATTTATTTCCCACTTATCAAGAACTTACAAAATATTTTTGTTTCATTTCTAAA TTTTCACCTTTATTGCTAAGTTATAAAATAAAACTTCCTATTTTTCTT[G/C]TTTTTCTTCA CCTCAGAACCCCTTA
WI-15705	50	A	G	GGAGGGAGAT TTTAGACTGA ATC	AGCTGTAGTCG TCAAATACTCT AGAA	TTGTTTTATTTGGGGAGAATGAAGGAGGAGGGAGATTTTAGACTGAATC[A/G]TTCTAGAGTATTT GACGACTACAGCTCTCTTGTCTTGTACTACGGAGACCCTGCTATAGCCGCTATAGCCGCTATAGCCTCA TCTGCGGTTGCCAGACAG

ID	No.					Sequence
WI-14379	102	C	T	TCTATTAACA GGGTTATGTCA CACC	ATCATCTGTTT TGAGGTTGACA	TTTATGCTGTTGTTGTTTCTACTGGTGGTCGTCGCTCACTAATATCCAGTATGATTTCTTT TACTTGTGTCTATTAACAGGGTTATGTCACACC[C/T]TGTCAACCTCAAAACAGATACT TAAATAAAACAAAGCAGAAAA[C/A]CCCACCATTAACAAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCCCGGAGGCTGGCGCAGGACTGCCCACTCACTCCAAATTTCTTTGGAGCAGAG
WI-14102	22	C	A	---	---	
WI-15937	24	A	G	CGCAGAGCTG CTGTATTTAAA A	GCAGAGATCCA GACGCTTGT	ACCCGCAGAGCTGCTGTATTTAAA[A/G]ACAAGCGTCTGGATCCTCTGCAGGGGCTGGGACCAGCTGC AGTGGGGGCTCCGGCACTGCTCCTGCTCTCCAGGACTCTTCCCACCACCCC
WI-15944	24	A	C	AAACTGAAAC GTATTTCCTCC A	GGCCTTTAAGT TTCTACGGTG	TGAAACTGAAACGTATTTCCTCCA[A/C]ACACCGTAGAAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGCGGCGAAAAAGGAAGTTTCAGGTGATACAAGATGTCCTGCCATCACACCTGAGGAT GGTT
WI-14124	92	A	G	---	---	ATGTTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAAAATCAT ATTTAAGTCCCCGTTAACACTAAGCC[A/G]TTATTATTCAAAAATGTGTTTCAAAATACTTCAGCCAGAT CACCCAAAGCTCAGTCACTAC
WI-14125	88	C	T	GGTTTGACCTG CATAGATTTTT	GGAATGGCATG GCCAC	GACAAAGAGGCAGTTTCTGTAGTTCCAGCAGGGCCAGAGCAGTTATCAGAAACGGGTTGGTTTGACCT GCATAGATTTTTGACGACTA[C/T]GTGGCCATGCCATTCCTGTAAGTGAAATTAATGAACA
WI-14136	120	G	A	GCTTCTCACC ATGTCTTCACA A	CTTGTTCTGTC TCTTTGGGC	GTTTATTTTCTCACAGTTCTGGAGGTTAGAAGTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTTCTCACCATGTCTTCACCATG[G/A]GCCCAAAGAGAC AGAACAAGCTCTCTGGT
WI-14138	23	C	T	CAGTATGTACA GTGACATAACA TGTTGGCACCA GAAAAGCT	TAGAACA	TTGTTGTTGGGCACCAGAAAAGCT[C/T]ATGTTCTATGTTTATGTCACTGTACATACTGTAAACAAGACT GCATTAAATATTGTTTCTTTATGATTTGTTCAATG
WI-13551	74	G	A	TCCTTCAGTAG TAGTATATTCA GACAATC	GCTCATTTCTT TAGTGCTAAG TAATATT	GGCAGGTTATTCATAATTTCAAAACTTGGAAGCAACCAAGATGTCCTTCAGTAGTAGTATTCA GACAATC[G/A]AATATTACTTAGCACTAAAAGAAATGAGCTATCAAGTCATGAAAGACATGCAGG AACCTAAATGGATATTACT
WI-15953b	59	C	T	---	---	TTTTTAAGAGTGTCCTTCACATCATTTATATTGTATTGCACACAAACTTTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCAGTGCTTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC
WI-15953a	26	T	G·A	TTTTAAGAGTG TCCTTCACATC TGTTGTTTTTG A	TCATCTGTTCT TGTTGTTTTTG A	TTTTTTAAGAGTGTCCTTCACATCAT[T/G]TATATTGTATTGCACACAAACTTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCAGTGCTTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC

ID	No.	Allele	Flank 1	Flank 2	Sequence
WI-14631	82	G A	---		TGAATTCAAATGGACAGTTTTGCCTCTCTGTTTAGTGAAACCCTCACAAGCACTCTGCATAGTGTCGCTTTCTGTCTTCTTTAAC[G/A]TGCCTGGTTCCCTCGCCCAAACTTTAGGATTGGGCCTCCTCAGGGCCTTGTCCTGA
WI-6053	24	A G	---		ATCACCACCGGTGTCTGTCTAAGAACAAC[A/G]TCTTCATGTCCAACTCATATCCCGGGACTTTGTCAACTGCAGTAGCACTTCCTGCATTGAACCTGGCTTCCTGGAGGGAAGCCTCCTAGAGGCCAGGTAAGGGGGTGCAGCCAGTGAGGGGTATATCTGGGCTGGCCAGTTGGAACCACGGAG
WI-15964	99	T A	GCTCTCTGTCC CTGGAGGTA	GACTTCTCCAC CCTCTTGC	CAGAAACCTCTTCTGTTGTATTAAGCTGATGCTAAAGTCAGAGCAGTCAAAGGCAGGAGGCTGCCTTGGGAGGTAGTAAGCTCTCTGTCCCTGGAGGTA[T/A]GCAAGAGGGTGGAGAAGTCTTGGCAAG
WI-12075	103	G A	AGCAGCTGGG GGCAC	CCCCTTCTTTC TCTTCCTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAAGCCAGGCAAATACCCATCAGAGACAGTGACAAGCAGCTGGGCACGCTGGGGGGCACGGGGGGGAGGC[G/A]GAAGGAAGAGAAGAGGGGAGGAGCCT
WI-12179	96	G A	GGAGGTACGG TGGAGGTCA	TCGAATGACCC TGTAGATGC	TAATTTAAAAACACGCCCTTCCCACATAGTGCGTGAGGCATCTGCACATTTCCTAGAAGGACATGAATAGTGATGTGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCATTCGGAGGAACAG
WI-14651	49	C G	CAAGAATCAT TCTCATTTAAA ATTGT	GGAGATATTGA TCTTTTTCTGA CTTATTT	CACAAATAGTGAAATTATCTGAGCAAGAATCATTCTCATTTAAAATTGT[C/G]AAATAAGTCAGAAAAAGATCAATATCTCCCCTGCTTCAAAAATGACACTCCAATTTTCACAGGTAACCACTGTTA
WI-14666	105	T A	---		AATGTGGACTTTCAAACAACAGGGTTTAAAACTAATCTAATACAACTTCTACAACACATTCCAGAGCATTATAACAAGAATTATTTACAGGCAGCTAATGTATTAAA[T/A]AACCATGAAAAGAAAAACTTG
WI-13473	31	C T	---		ATCCTAGATGTCAGCAAATGGGCTGAGACTGT[C/T]TGTCTGGTAGATGCAGTGTTTGTGTGTTTCTACTCTATTACAAAAATTAACAGAAATATGGCTTCGCTTTGTGCAAATGTTTATATCACAGTC
WI-13967	103	A C	AAAAGACTAC AGATACAAGG AAATAAAAA	TTGTGTTTTCA TCTCCTAAAAG TG	AATTTAATAGCAGCTCTGTGTTGTGATTTTAAAGAACAAGATAAAAATATGTCATTCAGCAGTCATTAAAAAATAAAAAGACTACAGATACAAGGAAATAAAAA[A/C]CACTTTTAGGAGATGAAAACACAAA
WI-14408	60	T A	GCAGACACAC TATTACAGGCT G	TTAATTGTGTA AAACTCATTTG TTACTTT	TTAATATTCAGCAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTG[T/A]AAAGTAACAAATGAGTTTTACACAATTAAAATATTAACACATACTTATGGGATTTGTTGAATGA
WI-13683	47	C G	---		TTTTGTGTTAAGAACACAGCATTTTGAAAATAAAAACCTATCTGCCCATG[C/G]TTTACAGCCTTTTAAATTTGTAATATTTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63	C T	CACCATGGCA CGTCCT	CATTGAGATAA AGCACACTTAT CAC	TTAGAAAACTGATAAAGCAACACAACTTTGGGGAAAGCACCATGGCACGTCCTTGTGCTA[C/T]GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A	---		ACATGGCAGATACAGAGCTGTGTC[G/A]TCTTGAAGACCACCACTGACCAGGAAATGCCACTTTACAAAATCATCCCCCTTTCATGATTGGAACAGTTTTTCCTGACCGTCTGCGGAGGGTTGAAGGGTGACCAGCACATTTGCACATGCAAAA

ID	Pos					Sequence
WI-16002	59	T	C	GATAACATAAAATGATCATGCAGAATTTC	GCCATCTCCTCTTTGACTTT	CCAACATTTTAAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAATTTCA[T/C]GTTAAAAGTCAAAGAGGAGATGGCTAATGCATGCTGGGCT
WI-15361b	101	A	G	CCCACTTGAACTCAAGTCATCA	AAACTAAAACCTTTGTGCCTAAAA	GTGGAATTTTATTAAGCCATCAAATTTCCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAACTCAAGTCATCA[A/G]TTTAGGCACAAGGTTTAGTTTTCTCGG GAAATCAAGTTTAACCA
WI-14759	73	T	C	GCGTTTGACTTGTGCGG	TCCCACACTGCCCCC	TGAGTTACAACAAATGAGCAACAAGTTAGAAAAAATTGGTTTATTCAAACTTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAAATGGGGGGCAGTGTGGGACGGGGATTGCAACCAGAGTTCATACTG CAA
WI-12535	50	A	T	CTAGGAGGGTTGAGGTGTAGATAT	GCTCCACGAGAAGAGAGGAA	TCCCTAACATTTATTTCAGGTGGTGACTAGGAGGGTTGAGGTGTAGATAT[A/T]CTTCCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGGTTCTGTGTTTATCAGCTGAGAAGGGCAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112	G	A	AAAGGCACACGGGGAA	CTCAGCCTGCCTTGACC	TTCCATTCATTATGCTTGGCTTTACCCAATTTTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGGTCAGAAAAAGGCACACGGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18	T	C	---	---	ACACAATATAATTCCATT[T/C]CGAGTGATTAAAACCTATTTGTTGTTTAGAACCAAACAAAAACTAC AAGAAAACATTTCAAAACCTTTTTTTCAGGCTGA
WI-14808	52	T	A	ACCCACCACACTACCCTGT	GAGGCATCACAATGTTAAGATTTT	CTTTGAAACACTTAAGCAAACAGTTAAAAAGTACCCACCACCACTACCCTGTT[T/A]AAAATCTTAAC ATTGTGATGCCTCTGCATCAATTTTTAGAAAAACAAGAAAACACAACTGAAGGCCCCATGTA
WI-14816	29	A	T	---	---	AGTTAAAAAAAAATCGAGTCAGCATTTATT[A/T]AAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCCTGAAACATGAAACATGAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTTC
WI-12542c	71	G	T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70	G	T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]GTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45	C	T	GCTATTAGGCAAACTGAACATTTAAA	TCTAGAGCCCTCACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTAAATGTC[C/T]ATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57	C	T	GGATACAGCAGTAAAGAATAATCAAAAA	CCACCTCTAGAATGTATGCTCTATAA	CACCTAAATCATTCTAGAAACTGGGATACAGCAGTAAAGAATACAAAAAATCCTGC[C/T]CTTATA GAGCATACATTCTAGAGGTGGGAAAGAGGCAATAAATA

ID	Pos	A1	A2	Fragment 1	Fragment 2	Sequence
WI-14836	28	T	C	...		TCTTTGGGAGGGGATAGAGAGGACAGAGAGTGT[T/C]GTTGATTTTCGGTTCGGTTGGTTGTCATT GGTTTTGTTTTTGCTAATTTTGCCCCACCCTATAAAAAGCAGTGCCACCCAGAGGCAG
WI-14856	60	A	T	TGGTGACACG GAAAATACTT AA		ACATTCCTTATGATGACAACAACTAAATATGATGGTGACACGGAAAATACTTAAT[A/T]TAA AGTTGTAAAAGTAGCAACAAAATTGAGTATATACTATAAGTGATAGAGGATGTATATGAAAAA GGCTATAAAAGCTCCAAA
WI-14863	61	G	A	...		ATGGCAATTTACTTATAGCAATGAACAAATATTTGTCAAAGGGCAAATATTTTTGTCTG[G/A]AG TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACTATTATTGATTGCCACT ACCTGGC
WI-14867	46	T	C	GACATTCCAA GGCTCTCTAAC A	TGGGGCTGCAG ACACTC	TTTTAATTAAAACGTAAAAAGGCAGGACATTCCAAGGCTCTCTAACA[T/C]GAGTGTCTGCAGCCCCA TTCGCTTGAGATGTGAATGTGTTAACCCAGGGTGGA
WI-14733	98	G	A	CCAAATTGAC AGATATTCTGC A	GATGAGGTCAG GCCATTTATT	ACGGAGTCGTCTCTGATGTATTCTTGTCAAAAAATGTTTGCCTGATTCTAATCATGAAAGAACAATT AGAAAAAATCCAAATTGACAGATATTCTGCA[G/A]AATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAAACACAAAA
WI-148898b	79	A	C	...		TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGAGTTGTCTCATAAGGTGCCACTAAGGAAA ACTTCTCCCAT[A/C]AGCTGCGTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGCTGCATCT GCCTGTGTTCTGTCTT
WI-148898a	50	A	C	CATGTACAGG AAGAGTTGTCT CA	AAGTTTTCCTT AGTGGCACCT	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGAGTTGTCTCAT[A/C]AGGTGCCACTAAGG AAAACTTCTCCATAAAGCTGCTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGCTGCATC TGCCTGTGTTCTGTCTT
WI-14907	48	G	A	GGCACACATT GGGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTTATTTCCGACATTACTGTGAGGCACACATTGGGACTCTGAC[G/A]ATTCCCCTTGCAGCAG ACATTGTGAAGCTGCTGGTCGGCGGCCACCATCAATCAGTGACTCCTGCTGACTCCTGCGAGAGGGGCCACATG CACGATGCTCACGTGTG
WI-14911	52	G	A	CCAATACATT CAGTTCCTGGT C	CAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAGGTCCAAGCTCAGTGCACCAATACATTCAGTTCCTGGTC[G/A]AAGGTCCTTTTC CTGGTTTGCAGACAGATACCTTGCTGTATCCTCACATGGCAGAGAAAGAGGAAGTAATCT
WI-14913	88	C	A	...		CTGATGCTTTGACATCTGGGGCATTGCTGCTGTCTCTAGAGAGGACTACTTCTCCTGGGACCAGCCAATTC TAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTCATATACAGATCAACCAATCCAAAAC CTACACCTCCAACCACCT
WI-14914	66	G	C	CTGGACACAG TTTTTCTCTAGC A	CAAGCCCAGGA CAATAAATTC	ATTTCCTTGATTGGCTGTCGTCGTAAAGCCTGTGAAGTCATCATGCACATCTGGACACAGTTTTTCTCTAGCA[G/ C]GAATTTATTGTCCTGGGCTTGATGGCTTTCACAGC
WI-14926	49	T	C	...		GTTTATTTTCAAAATGACACATCCCAGATTGAAATGGGCACTTAGCGAA[T/C]ACTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAAGACAGTTTTCAAATAAAAATTTTCCTTAATCAGGTCCA

ID	Pos			Col A	Col B	Sequence
WI-16083	89	C	T	ATGTTTAACA CAAACATATC AAGGAT	TGGAAAAGATT CCAGCCC CATTAAAGCAC	GCATCTTTATTACCACAGAAACTCATTATGTGTCCTTAATCATTGTTTAATATAATATATAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTTCCATTCTATAGAAAAGCACTAACCATC
WI-14930	55	C	T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTTGGTTGGTGGTGATTTGGGGAGCACGAGGAGAGCAA
WI-14946	47	T	C	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTGCCCCCAGACATAACAT[T/C]CTCTAAATCATCCTCTA GATCAGGGAGGAGTCATAAGGACCATTAAGGCTCATTACACAGTACTTTATGGAAAGGATT
WI-15987b	80	A	G	---	---	ACATTAAAACAGCACAATTAAAGGGGTCCCAA[C/T]GAGGTTGGTAGTGCCTTCCACTATGTGGAGGA TAAGAAGATGGTC[A/G]TCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32	C	T	CACAATTAAA GGGGTCCCAA	GGAAGGCACTA CCAACCTC	ACATTAAAACAGCACAATTAAAGGGGTCCCAA[C/T]GAGGTTGGTAGTGCCTTCCACTATGTGAGGA CACTAAGAAGATGGTCATCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56	T	C	AGGGAAACTG CTAACTGTGTCA G	GATGATCTTAC ATCAGTTGTTG GA	GAATAAGTTCTATTGCCGTTCCTTCAGGGAACAGGGAAACTGCTAACTTGTCAG[T/C]TCCAACA ACTGATGTAAGATCATCTTCTGACCATAGCGAACCTGCTGTAAGGCTTGCTGTTCCCTCCAGCTGA
WI-16100	52	A	G	CAAAAAGCTA TTTCCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCCTACACTTGAC[A/G]GTAATATACTG TTTTCTGACATTCCTGTTATCAACTCCTGAAAATC
WI-14958	83	A	G	AATAATTTAT CTCTTTCTTT CAAGGG	AATGCATTCAT TTGGGTTTTT	GTGATTGATCTGTAATTATTGGGATTATTATTCAACTCTAAAATTCAAGATGAAAATAATTTATCT CTTTCTTTCAAGGG[A/G]AAAAAACCCAAATGAATGCATTTCAGTTCTCCAGGCCTTTGAACTGC AGCAGAAATTCAAGGA
WI-14976	35	C	T	GTTGATTGCT TCGTTCAAAG	TCAAACTAAAT CTTCCATTCTA AGC	TATTTTTTAATTGGTTGATTGCTTCGTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTAGTTTGAGGAG GGGCAGGTTTGGGGTTAGGCTCAGCGGGCATAGTGCCACAAGAAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31	G	T	TCAGTGGTGTT TATTGGATTTT T	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTTTATTGGATTTT[G/T]TTTATGCTAAGTATTATGTCAGAGGTGGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTCACAGGAAGTTTTGA GAGCTCACAAA
WI-14992	80	C	T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCCT	TGATTACATTTTTAAAATCATGCTACCAGCCAATTCAAACACCACTCTGCATTA AATGAAGCTGCAG[C/T]AGGAAAGCTCAGCACAACTGATCGGAAAGAACGTA
WI-15002	72	T	A	---	---	AAATCTCTCTTCACACACAGATGAAACTTTAATAAAATTACAAATGCACCTGAAAATGCCTTCTTGA TTTCC[T/A]TTCAGTTTAGGCCTCAAAATGGGCTCTCCTCAAGGCTGGACCTCAAAGCGCCCAGTT
WI-15000	90	G	A	GACAGAAAAA GACTCAGACT AGTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTCAGTGTCTAAGTA[G/A]TGAAGTTTGTGCAGAACTAGAAAACAAAATCCACCT

ID	No.	nt	nt	Seq 1	Seq 2	Sequence
WI-12323	68	G	A	CACAATACTT CATGTGACCTAT GAAATAA	CACTGGACATA TTCCCTACACCTG	ATTTTGTTGATGTTGGTAAATCTTATCTCTTTTTTTATACACAATACTTCATGTACCTATGAAATAA[G/A]ACAGGTAGGGAATATGTCCAGTGCAAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A	T	AAGGGACGAT TTAGTAGTCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTATTCACGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAAAACA[A/T]CAAAAAAAACACTGGGACGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100	C	A	CCTGCCTTTAT ATTGGAATTTC T	GGGAGACCATG GGTCTCT	ATTTTGTTGTTATTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAATTCCCTGCCTTTATATTGGAATTTCTA[C/A]AGAGACCCATGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCCCTTC
WI-14712	38	T	A	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGTATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCA[T/A]CTCACAATACCATATACAACATACT TCAATCACAACTCAAATATAAAATAACCTACAAAATCACATTGC
WI-13712	40	A	C	TTTACTTTGTT GTCATTTTAT TCTATTG	CCATAAGGTCT CACACTTTCT TAT	TGGGATACCCTTTACTTGTTGTCATTTTATTCTATTG[A/C]ATTATATAAGAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGGCAATATGCAATATAATATTGTGTTGTTAAAATTTATGCAT
WI-16163	35	C	T	TCTGGTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTGAAATAA[C/T]ATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAAGTTAAGAGGACTATTTCTTAAACAAGAGACAGTGTCTGACATTTATTTCAGGT
WI-13453	88	T	A	AATGCACAAA ATCTTGTCTCT TC	TCAGATTTTA CATCTCTTCT AGCA	TTTTTTATTTGCATTTGAGTGCTTTATTATTATATTGGGAATTGCAGTGATATTAAACATTTGTACAAAT GCACAAAATCTTGTCTTCTTC[T/A]TGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACTCATTGTCCAT
WI-16167	58	T	C	CGCACTCTAA ATTAGAGATA GATTTTT	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTCTGATATACATT[T/C]CATCTT ATTCACCACGAGCACCACACACGCACAGTAGAAACAGTTCCACCTGATAAATTGCACAGATG
WI-14482	17	G	A	---	---	GCAGAACCAATTAATAA[G/A]AATCTGCAAGTTTCCCCAAGAAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAAAATCGATACTAAAGGAGAGAATAAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T	C	---	---	TGTAGTTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCCATACTATGTGTATTCCCAGTATCATGTAC GCACTAAAAAAAAT[T/C]GTGTGCTGCTGGTGAGTGAACCATTGCTTAAGATAAA
WI-16156	97	A	C	TGAAGATTAA CCCAGAGTCGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAAGTATACAGAATACTCTATAAAACCAACCCTTCAATA TTACACTAATGAAGATTAACCCAGAGTCGC[A/C]TCTCTTCAAAATGCACACAATTAAGACG
WI-15012	59	G	T	GCAGCAAGAT TACATCAGTA ATGT	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATTGAATATAATAATACAGCTTTTTCATTGAAGCTTT[G/T]TACCT TACTATACTCTAGGCTATTGGAGTGTTCCCCCAC

ID	Pos			Left sequence	Sequence
WI-15100	74	G	A	...	TCTTATTCACAGCCAAGAAAAATACCCAATTATTTCCAAATAAAGCAAAAATTGGAACAGAGACTGGA GTGAGAAC[G|A]GGTTCCACCACCAAGCCCCTCAAGACAAGATGGACACGGGCAGCTGGTTCTGGGGT GCATTTCTAGTTGGACTTTAT
WI-14492	92	A	T	CCTTTATTTTC CCAAATATAA AATTACT / GTCACCATGTT ATATTTTCTTT TAAGAC	TGGTACAGAATGTTTAATTACAGCAGGGCAGTGATTCCAGTTAAATAAAATTAAAAACCTTTATTTT CCCAAATATAAAATTACTAAATTAA[A/T]GTCTTAAAAGAAAATATAACATGGTGACAGCTTT
WI-12002c	89	T	C	...	TCTTTAATTTTATCGGAATCCAGGACACAAGAAAAAACACCCAAAAACCACATGGAGACAGAAG ACGAGACACAACTCCTCCCCCAC[T/C]GCCTCCCTGCTCTCAGAGTGGGGACAAAGTGGGGGTGAGAC AG
WI-12002b	68	G	A	...	TCTTTAATTTTATCGGAATCCAGGACACAAGAAAAAACACCCAAAAACCACATGGAGACAG AC[G/A]AGACACAACTCCTCCCCCACTGCCTCCCTGCTCTCAGAGTGGGGACAAAGTGGGGGTGAGAC AG
WI-12002a	30	C	G	TCGGAATCCA GGACACAA / TGGTTTTGGG TGTTTTTCTT AG	TCTTTAATTTTATCGGAATCCAGGACACAA[C/G]AAGAAAAAACACCCAAAAACCACATGGGGGTGAGAC AG
WI-15116	96	C	T	GGGAGCCCTA GTTGCAGTAA ATGACA / CCTGAATATGC AATTATTTATT ATGACA	TTTTCATTTATTTTCCAGAAAAAGAAATCACATTTCAGTAACAACTTACATATAGAATTAAACTTTG TTCTGGAATGGGAAGCCCTAGTTGCAGTAA[C/T]GTGTCATAATAAATAATTGCATATTCAGGATTTTG TGAAATAGGTGATTGGGA
WI-12578	37	C	T	GGCCTAAAGG AATGGGAA / TCAAGCGACCA CCAACAC	GCAAAGCAAAGCTATGGAGGCCTAAAGGAATGGGAA[C/T]GTGTTGGTGGTCGCTTGATACTTGGT GCTTGTGTGCATGGAGCAGAAGTCTTCCTGGTCCATGCAGGGGCGTCACATATTTAACTGCACTAAT TTGGGCAAACTGTCATTC
WI-15153	40	A	G	CCCTTATGTTG GCATTGCA / AACCTCAGATA AGTGCAGTGTC T	ATTTCACGTTGGCCAAGATCTCCCTTATGTTGGCATTGCA[A/G]AGACACTGCACTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAATTACCATTTCCTAA
WI-15215	84	G	C	TGGCTTTAGAA TCAAATGGG AAAAGTCA / CCAACAGGGGA	CCTTTGCTCTCTGAACTGGGACCAGGAGTGTGAAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTAGAATCAAATGGG[G/C]TTGACTTTTCCCCTGTTGGTGGAAAACTCTGTGAGGGTTTGGCA
WI-15225	80	C	T	CTTGAGGACCT AGAAAGCAAA C / TTTGATTGGCA TAATCACTCC	AGGAAAGAGTGGTAAAGCAAGCAAGGCGATCATTGGATGGAATGATTATGTGTCAGGCACTTGAGGAC CTAGAAAGCAAAC[C/T]GGAGTGATTATGCCAATCAAATTGCAAGGTTGGAGATATGCTAAAA
WI-15152	51	G	A	...	AATTTGCTAGTGCAAATGGACCCAGAATTGGAAGGGCTATGTAACTACACA[G/A]TATGCACACCAC AGCCATGTCAGTCAGTTCAGCTTTCTTGTGCATTCAGT...
WI-15123	55	C	T	TGTTAGTGACA GACAGATAAA TAGGATG / TTGCTTAAGGG CAAACAGAC	TGACTGTATACCAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACTCACTGGGGAAGAAACACTGCAAACAACGAGATAAAACACAAT

Marker	Pos	A1	A2	Flank 1	Flank 2	Sequence
WI-15182	49	C	A	GCACAACCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACTAGCTAGCTGCGCACAACCAGGGCAAAATA[C/A]TGCTGGGATTAACCCATGCTAATGGGTTACCTTTATTTAGTAATCATGGGTCCCTCATAAGCATGGTCCAGATCCG
WI-15198	38	T	C	GGGCCCTTGGC ACTATG	ACTTATCCGTC	GTGGACCTCTACAAGTACCATGGGCCCTTGGCACTATGT[T/C]CTACTCTGCCTGACGGATAAGTTGGCACTTATCCGTCACTAGACGACTCTCTT
WI-12601	42	T	C	CATTTATTGAG TATTCTTGCTT TGAT	GTTGTAGTCTT ACATGCTTACG	CATTTATTGAGTATTCTTGCTTTGAT[T/C]GTCTACGTAAGCATGTAAGACTACAACATTACGACCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAAAAACATTTGTCATTCAGAT T
WI-14510	104	A	T	TGGCAAAATA TGCATAACAA AA	TTGAAAATGGT TAAACTGGCA	ATGTTGAGAGTAAATATGCCTACATATTAGTGTAAGTACACCCCAGATATTTTGGGGAGAAGAGTTGTTTGCTTTTGTGTGGCAAAAATAT[A/T]TGCCAGTTTAACCATTTCAAGAGT
WI-15239	57	T	C	CATTGCAAT AAACACCATC A	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTGCAATAAACACCATCATT[T/C]CCTGAGTCCACAGATAAGGTCCCGGAGAAGGGGCTTCCCCTCCTTTCTCGCTGGGTTGACGTTCCCAGCGAGT GAAGCCTTTTCTGGAATG
WI-12634	52	T	C	GCATCATATG AACTGTCTAGC AGT	GGACAAATTGT AAACATAGCT AATAGC	ATGAGTTATAAACTGGAGACAGCGCCATCATCATATGAACTGTCTAGCAGTATTA[T/C]GCTATTAGCTATGTTTACAATTTGTCCTGAAGGGGTCTAGATGTGTACACCCCAGAAAGTGGTGATTCCTGA
WI-15249	34	T	C	GGGCTTGACAC AGATTTTTTAAC AAAGTTCTAA AA	GGAAAGCCAG AGATTTTTAAC AA	TTTGCTTGAAGGGCTTGACACAAAGTTCAACTT[T/C]CTTGTTAAAAATCTCTGGCTTTCCTGGCTGGTGAGGAGGCACAGCTGGGGTCTTCAGGTATCCACTGGTGCCCCGCATCTGTTCCCTCCACTCCCCAG CCCACATTCTTGGCTCT
WI-12159	28	C	T	AAGACACCGT GTGCACATGC	CCCTCTCCTCA GTGCACTTT	CTGTCCGGGGAAGACACCGTGCCAAATGC[C/T]AAAGTGCACTGAGGAGAGAGGGGAGGGGTCTGTGACTCCCAAACCCTCGAATATTTTATGAATCTAAGAGTCCAGACGCAGTTCATCCACGGAGATCTGC
WI-12648	41	A	G	CCTAGTGGCAT AGTGGACATCC T	TTGCTACTAA TAAGGATGC	TCCCCAGATTGTATGGAAATGCCTAGTGCCATTAAGGATGC[A/G]GTAGGATGTGTCCCACTTTAGTAGCAACCGATGTTAATTCACTACTCATGTTAGGTGCTTACTTGGATTATCTCACTTAAAAACCACA
WI-12684	64	G	T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAAATATTCAGTAAACCATGCTGTAAACAGCTGTGC[G/T]CCATTTAGCGTTGTTGTTCCATTTAGAGAGCACAGCGGACACAGAGGAAATTTAGCATAATTCTT
WI-15260	75	G	A	AAAGGATGAA GCTAATCATG GA	TCTCTCCAGG AGCTTGC	TTTATAAGCTGAATGAAAAGAGGTCGACACAGCGGACACAGAGGGACAAAATCAAGAATGAGCTGGAACAAAGGATGAAGCT[G/A]CAAGCTCCCTGGAGAGACTCCCTGGGAGACGAGAAATTAA TCCTG
WI-15325	39	T	C	CATGTGGCTGG GAGGC	CCTTCCACCAT GATTGTGA	AAGGTTTAATGGACTCACAGTTCCATGTGGGAGGC[T/C]CTCACAATCATGGTGGAAGGCAAAAGGCCACATCTTACACGGTGGCAGTCAAGAGAGAATGAGAGC
WI-13936	123	C	T	AGTTGGCATTC AATAGCCTAT C	TGAAACTCCCA CATGGAGTT	TATTTGAGTATTTCATCCATGGCGCCTTCCCCTACTCCCCTATACAATTCTCCCAGGGTTGAGGTTAGTGTCTACCCCCATAGGTTCAGAACCTATGACCTATCTTCAGTTGGCATTCAATAGCCTATC[C/T]AACTCCATGT GGGAGTTTCATAATAA

ID	Pos					Sequence
WI-14528	62	T	G	TTTTAACTTTT TCTGGATGGTA GTAAAT	CTCGATTAGCA CTTATTATAAA AATTAAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAATATATATTTAACTTTTCTGGATGGTATAAAT[T/G]TTGAATTATAAATTTAATTTTATAATAAGTGCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74	C	T	GACTTCAAAG GAAAAGAACA AATTT	TCACTCCCCCA AGTCTTTG	TATTTCTTTCGGTTTCGGATGCAAAACAAAAATTTAAAAGAAATGTGACTTCAAAGGAAAAGAACAACAAATTT[C/T]CAAAGACTTGGGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGACG
WI-14546	95	C	A	CCAATTTCTAG TGATAGTAGA GGACTCA	AAGGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCCTGGGACCAGCCAATTCTAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTCATATACAGATCA
WI-15353	37	G	A	---	---	TTTATTGGCTGCTGTCTCTGTAATACAACATGTGGTGAAAAC[G/A]TCTTAATTCAGGACATCTTCCACCTTGTTTTGGCCTTCCAGTTGTACTGCGAAGACCAGTGTCAGGCGACATAGGCTGATAATCAGTGG
WI-14580	100	G	A	CATTCCCCATCT GTCTTGCA	CCGACCAAGAT CCCTCC	AGAATTTTTTCCTTTTTTAACAGGACAAGTAACATCAAACTTCAGAACTTCTCAAATAC CTAGTTATTATACACATTCCCATCTGTCTTGCA[G/A]GGAGGGATCTTGGTCGGCTTAACA
WI-8540	73	T	C	GGCCTGCATTT GGCTTA	GCCCTTCTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATGCGGCAACCACAGAAAAAACACACAGCTACACAGGCCTGCATT TGGCTTA[T/C]GTGCCTGAAATAAGGCCGACCTCTTGATAAGAATGTCT
WI-8039b	97	T	C	---		AAGTAGAACACAATAGAATGGCTCAAAAATATCAGAATGCACTACGCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGTTAAATATGTA[T/C]GTGTCCGTGCATGTCATGATTAAATATCCTTCT TACCACAGTCACCCTAAAGAACCAAAGCTTAGGACTAGGGACACAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTTGAGATGATGATTTAATGCCGCAGCCGACACCCACA
WI-8039a	87	T	C	---		AAGTAGAACACAATAGAATGGCTCAAAAATATCAGAATGCACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGT[T/C]AAATATGTATGTGTCCGTGCATGTCATGATTAAATATCCTTCT TACCACAGTCACCCTAAAGAACCAAAGCTTAGGACTAGGGACACAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTTGAGATGATGATTTAATGCCGCAGCCGACACCCACA
WI-8044	107	C	A	---		CACAACATTCAGAAGTTTTCTGCATTGTCTTCTCTGATGTCTCAAAAAGATTTGAGCTTTGACTAT ACGATTTCCCACACTGAACGCATTCATAAGGTTCTCCC[C/A]AGTATGATTCTCTGATGATTAATA AGCCCCGAATTCTGGCTAAAGGCTTCCCACATTCAAGACATTGTAAGGTTTTTCTCCAGTGTGGAC TCTCTGGTGTTGCACAAGAATGGAACTTCGCGGCTGAATGCTTTCCCACACT
WI-8550	32	G	A	GGGAACATCA ATGCAACAAG	TTTGTGGCTTG AGTTTACAAAT T	CTTACTACTGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAAACTCAAGCCACAAACTTAGTTA ATAATCATGGTTAAGGACATTGCCAAAGAGCAACTGATGCCTCAGTGAA
WI-8057	87	T	A	---		TATTAGATAAAACCCTTTGTTCCCGATTCAGGATGTTTAATTTGCTTCTTCTTAAACTCTGTGACTTTT CCTGGTTCAAAAGGACCAGT[T/A]GATGGACAGCAGCAGCCCCCCTGTCGAAAATGTAATCTTT GTGTCAAGGCACTCTGTGCCTCACAACTGCCCCCCTGTCAGAGGATGCGCCTTCCAGCCCTAAAG ACACTAGGGCTTTCAATGGACGGGGTGTTGCAATGGACGGGGTGTTGAAGCAGCCAGATGGTAAGG

ID	Pos					Sequence
WI-6192	91	A	G	GACTGCTAAG GATTTAATTTG GAT	TGAAGTGTTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCAACATGATTGGCAGTTGGCATATTCTAGTGAAGCAAGTGTTCT GACTGCTAAGGATTTAATTTGGAT[A/G]ATTTAATACTTAGCCATCTAACACTTCAAGCATAAC
WI-6194	105	T	A	CACATGGCAA TGATAATAAA GAAA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTGTCCTCACAAATACATTTCTCAAACTCAAAACATCATGCTTGAAATATCACTGAACTT GTCACCAAAGAAGTCACATGGCAATGATAATAAAGAAA[T/A]ATGCAGACTACACTCTGAGGATAG AGCTCTAAAGAGTAAAAACAATGGAATTTGGAAAAAATAGGAGTAAA
WI-6213	164	C	T	...	...	CATATGCTGCTTTATTTCTGTAAGGATACACTGAAACGTTAGATGATAATAGCTAATGACAGAAGTGT AGAAATGAGGCATCAGCTTCTCTAACCACTCCTACACAAGAATGTTAGTATGTATGTTCATTACATGTTT ACTTTTGATATTGTCTCATTATACTATGT[C/T]TATATAATAATAACAGTAAGTAGGTGATCC TGCATTTCAGGTAAGCGGTAGGTGGAAATCCAGATTCCTTCCTTGAGGAAAA
WI-6217	131	C	T	...	...	CGGGTTAAGAAAATACCTTTAAATTTAGGTAAATAAAGCTCAAGGAGGTGGGGCTGTGTCATCTGTGGTG TCAGTCCTTCTGGCCCCCTGGCTGTCAGTGTCGCTCAAGGCCTTGACAAGCAGCTCATTCAAG[C/T] GGCCCACCATGGCCGCCCTAGGGTCGTCAACAAGTCCAGCAGCAATCATGGCGTTCTCGTATATCGATCC AC
WI-6238	175	G	A	...	...	ATAGTCTTATTTGTCAACGAAGGCTACACGGGATCACTTCTCTGGTTTGTTTTTTTATGCTTTTTTTC TAGAAGGTATCTACACTCTGCATTTATTTACAGCCTTGTTGTATTACACAGTCAAGATACACAGTGTTA GAAACAACAAAAGTGTTGAGAAAAAACTTCTCAAAATT[G/A]GTTCCAGACTTCAGGAAAATGATT TCCACATGGTAAGGCCAGAGTCTCCAGTGTTGGTCATCCGAAGCAGCTTG
WI-6272	86	C	T	GCATTTATTCA GGGAAAACTT TAA	CTGTTTTTGGA GAAGACAAAG AA	CTTGATTTAATCAGGGCTTTGGGGTCATAGGGGGATTAGTCACTGTCACTGTCATAATAATGCATTTA TTCAGGGAAAACTTTAAT[C/T]TTCTTTGTCTTCTCCAAAAACAGCTGCTGGAACACCTCAAATTAA GGGATGTTCATCTCAAACACTTTACTGAAACTTGATTCCTTGGGCCAGAGGAAGGTCTTTACTGTAG
WI-6303	96	G	A	CCCAGAGAAG CTCTGTGTCG C	CAGCCATGGCT TTGCAG	CAGAGGACTTAATGCAATGCCTATTCGGGCAATAAATGAATACTTGATCATTCATCAGGCAAGGAAGCT TCCCAGCATCCCAGAGAAGCTCTGTGTCTGC[G/A]CTGCAAAGCCATGGCTGCAGACATCAGGGAGCT GGTGCAGTTCTAGTGTCTCGGCCTCCTGCAGTCTCCTCTCCATTCCTCTCATTCTTCTGGCCC TCTG
WI-6315b	193	C	T	...	...	ATGCTTTTGCATGATTCTAATTATTGCCTTTTCAGAGCTCTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTCAAGCCATCATCCTGCCAATCATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTAGTGT[C/T]CTGGTT CTTCCCTTTACATTCTTTGGGGGA
WI-6315	187	T	C	...	...	ATGCTTTTGCATGATTCTAATTATTGCCTTTTCAGAGCTCTGCTGGTAAAAAGTGGGGTGCCATACA AACAGTCCCTTTCAAGCCACCAGCGGTGTCTCCTGCCAATCATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAG[T/C]AGTGTCCTGGTT CTTCCCTTTACATTCTTTGGGGGA

Marker	Pos.					Sequence
WI-6375	28	A	G	GGTTATTGCA TATGGAAATC AA	AATGTGAGATC TTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAAATCAATAG[A/G]TATCTTTACAAAAAAAAGGTTAGAATAAAGATCTC ACATTTGTAAAGGCACATATGAAACATTTTATAGCAAGCACAACATCAACATACAAATCAAT
WI-6409b	112	T	A	---	---	TTGTGTCTCAACAGATGAAATTCATAACCTTGTGTTTCTGATAAGACAATCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCCTCCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73	A	T	---	---	TTGTGTCTCAACAGATGAAATTCATAACCTTGTTTTCTGATAAGACAATCAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCCTCCCACCCCTATATTTAATGCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6523	165	G	T	GCTAATCCAGT AGAGACTGAA GCTG	AGATGCTTAGG GAAGGTTGATA CAGC	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGATTTTGCAGCAGATTTCATTATAGTTACTTAA CAGCTAAATAATAAGGTGTATTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]TATCAACCTTCCCTAAGCATCTGTCGGTCCG
WI-6554	195	C	G	---	---	TCTCCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGGAAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGTGGACGTCCCTGGTAGTCTCTTTCTCACACAACTTTTCCCTGAGA ACTGTCCCAGTCAGGTGGACCTTCACAACAACAGCTAAAACTCTGAGAGAAAAC[C/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6558b	68	C	T	---	---	ATTGTAATTAAAATTTACATGGGCCTATTTATTAAGGACATTGTGTAATGTTTCCACTTGTTTAAA [C/T]AATTACAAACATGTGGCTTAAAATAATGTACAGATCAATGTAACAAGTTTGAAAAATGGGCG
WI-6558a	42	G	C	---	---	ATTGTAATTAAAATTTACATGGGCCTATTTATTAAGGACATT[G/C]TGTAATGTTTCCACTTTGTTTT AAACAATTACAAACATGTGGCTTAAAATAATGTACAGATCAATGTAACAAGTTTGAAAATGGGCG
WI-6629	75	T	C	TCTTTTCAGAG AATAAAAGTT GTCATA	TGACACAGCAT CCATTGCT	AACCAAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTCAGAGAATAAA AGTTGTCATA[T/C]AGCGACATGCTGTGTCAGAACATACTCCAATAAACTTAAGAAAAAAGGA ACTCAATGAGAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCAAAAC
WI-6644	134	T	C	---	---	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAAATCAATCAAAACTCCAGCTGTTTCTCTTGTCTTT TTACTTAGCAAAGGAAAAACTTAGTGAATGCTACTTGACAAGAAGAAAGTCATTTCTCAAGCACA[T/C]ACCCAAACTTGAAGGTGATTGAACCCAAAATAATGGGTGGGAAACACCAAATGAGGTGGAGGA ATGAGAAGATGTGTGGGCCAAGCTATCTGGTTATATTTTGATGTTGCCAAT
WI-6690b	106	C	T	ACATAAAATA TTGCAGTGTAT TAGCC	CAGACTCTGG AGCCACAGC	TGCTAAACACCACCATTATTAAGGAGAGTACTAGGAAAAACTACCAAACACACAGCATGTGAAACAGT TGGGCACGGTGGTAAGGGCACAGACTCTGGAGCCACAGC[C/T]GGCTAATACACTGCAATATTTTA TGTTTAGCAAATTATAGCTGGTCTGTGTATAACCAGAAGAGAGCGGTATCTGG

Marker	Position	Allele 1	Allele 2	Seq 1	Seq 2	Sequence
WI-6690a	28	T	C	AAACACCACC ATTATTAAGG AGAG	GCTGTGTTGG TAGTTTTCCT	TGCTAAACACCACCATTATTAAGGAGAGAG[T/C]ACTAGGAAAAAACTACCAAAACACAGCATGTGAAAC AGTTGGGCACGGTGGTAAAGGGCACAGACTCTGGAGCCACCAGCCGGCTAATACACTGCAATATTTTA TGTTTAGCAAATTATAGCTGGTCTGTGTATAACCAGAAGAGCGGTATCTGG
WI-6770	53	A	G	CAAACCCCAA AACATCACA	GCTTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAATGACACAGATCTTCCCAAAGTAATCCAAAACCCCAAAACATCACA[A/G]AATTATTCAT ACTATTATACACTCCAAAAGCAAAATACTTCAACTGCAATCC
WI-6686	151	A	G	GCATTCTTCCA AAACAAAGA A	CCTTGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAAGGTTCAGCAAATGCAGCTAGCACTAATCTTGACCAAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTAATTAGATGAAATTTAAAAACATGGTAACTCCAAGCATTCT TCCAAAACAAAGAAT[A/G]AACATTGGAATAGTCACTTACAAGGAC
WI-6761	32	C	A	GATCTAACAG CTGCAGAATG G	AAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAATGG[C/A]CTTCTTCCTTCCCAGCTTTTGTGAACAAAAC AATTCTCCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTTGTTCAGGTACAAGGTCTC
WI-6844	225	T	C		...	TAAAATACTGCCAACTAGCATTACGTCCACTCTTGCATCATTAAAAACAAAGGGTATTCCTCCTTG GTATTTTCAAATGATGCATTATACAATAAACGAAGTTAGAACTTAAAATGCACCCTGATAATATG TAAACTGGTAATTTGTTTAAAAAGCATAATAATTGGTCCTTCTTCATAAAATGGAAATTTAAA TATTTCTTCTGATAGTCTTGAGGT[T/C]ATCATTATGAGTAGTGCAAAGTGTG CGGTTTGCTCACTTTAATGGGTTTTTTTTAAGGGATTTTTTTTCAGGTCTCTTGTCAGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGGTACGACAGAGTGCTGCCAA[A/G]CACCTTAGAAAAATTACAT GACACGGAGAAAATGCGCCTCTTGCTCCTTGAAGAGCTTACAGTCTAGGGATTTGACAACTCACAGT CTTAGGAAACTGGGCAAAGTAAGGCAAAATTCTTCATCCCCTAGAGCTATTGTG
WI-6824	112	A	G		...	GTACAAAAAAAGCTGAGAAGAGAGGCCAACATGAAGTGTCAAGAAAACATTCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAAGGAGTTACATTAGTTCTTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC[T/C]AGAATAATTAAAAGCCACAAAGTGAAACTGTGTTCTGGGGCCCTATGTTGTTAGATT CTCT
WI-6889	139	T	C	GAAAAATGAG ATGCAGTTAA AATTC	TCACTTTGTGG CTTTTAATTAT TCT	TCCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACTCAAATATCTGATGAACTGAA AAGAGGTCTCTTAAACAAGATCATCATCTCCGGAAGAGAAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACTTGCCTTCCCAGGAATGTGTTCTAATTGGTTTCAAAGCACACTGGTTCC CACTTTTACCACTT[T/C]CATGACAGTTGGACAAATAGTACTACTCTTTCTAC
WI-6911	216	T	C		...	GCCAGTCTCTAGTAAGTCTCTAGGGACAATGACCAGAACCAGAGCCCCTGTTCTATATGAAGACAAAC AGGTGGCCATAGTTGGGTGGGAGGGGATACCGCTGCTATTCCCAGAT[G/C]AAGATTTGGTGGGAAGGAG ACCATGACAGATGACAAACGAACAGTTTCTCAAAAACAGAGGTATGA
WI-9413	112	G	C		...	AAAAGCTTTAAAAAAAAAGTGGTGCTATCTTTAGAAAACACTTTCAGCAAGATCAAGTAGCCCAGCT
WI-9557	74	C	T		...	ACAGCCT[C/T]GGTGCATCTTAACCCCTCCTTT

Clone	No.	Allele			Sequence
WI-9617	37	G/T			TGCTCTTTTATTTCACGTTCACACACACGCCGTG[G/T]TTGGCACAGTCTACCAAAGTGCCCGCAG CGCCACGCCTTGGGCCGGCCGGAAGGTCTCATTCGTCTCGTCTCGTGGGCACACTGTGTGGGCAGCTGCACGATGCAGCTTGCAGTGGGTCCAAGCCGGGTGTGCTGTG
WI-9657	121	T/G			AATGCTGGAGAAACATCAACATTGAGTTGACATTGTTTGCTGAAGTATAGCTACCATCCACTAT CATGAATTTTGTTTCATTCATTACAAATGATAGAAAAGCCAGATTCTCAAAATAAAG[T/G]ATAATTCTT TGTATTAAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATATCTTTTTTAAAAAGTAAAAA TTTTAGAACATATGACGCTTTCATAATTAATGCTTTGATATAGATTTGAGG
WI-13119b	114	G/C	CCTCCCAAGTA CAGGTGTGGTG T	AAAAATTAAC	CAGGGTCTTGCTCTGTCTCCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGAGTAGCTGGGACTACAGGCATG[T/G/C]ACACCACCACCTGGTTAA TTTTTTAATTTTTGTAAAGATAGGGGTCTCACTACTGTTGCCCCGTCTCAAAAAACAAACCAACTAAC
WI-13119a	51	C/G			CAGGGTCTTGCTCTGTCTCCCAGGCTAGAGTGAGGTGACACAATCAAGACT[C/G]ACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACCACCTGGTTA AATTTTTTTAATTTTTGTAAAGATAGGGGTCTCACTGTTGCCCCGTCTCAAAAAACAAACCAACTAA C
WI-13112	71	C/T	TCATAAAGAC TACAGACTTA AGCTTTTTT	TTAGAAATTTT GTGTATTATAT GGAAAAAG	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[C/T]CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAGAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACTATTTATTAATTGAGGGAATAGGCCAAT TT
WI-12988	36	C/A	TGGTACGTGCT CTACTGATGCT GTTT	CAAAGTGTACA	TGTTAACATTTTTATTGGTACGTGCTGTCTCTCAGTACAA[C/A]AAACAGCATCAGTAGTGTACACTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAAGAAGACCCAAAGGTCAGAAGGTATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCATCTTTATCTTCCCCTGTGATGAGATGTATGCACACAAGT AAA
WI-13020a	108	G/A	CCATATACAT ATATCAAGGT AAAGTCCA	CATTATTAAAC CCCTTTGCAGA	TGCTATTCATGACAGACACGTGAGACAACATTCTTATTTTACAGATGGAAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGGAACCCTGAGACTTTA[G/A]ATCTGCAAAGGGGTTTAATAAT GCAAATATCACATATTTTAACACCATATTTAAGTTTCCATTTCTTCCATTTTCTTAATAGAAAATGA TAAAAATGTTTTCCCCAATAT
WI-12837	87	A/G	CCATATACAT ATATCAAGGT AAAGTCCA	GCCATAGGAA ATGCTGTTTTT	TGTATAAAAAATCCAACTTGTTCCCACAAGTACATATGTCCTATGATTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA[A/G]TACAAAAAAAACAGCATTCCTATGGCCAGTGTTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAATGCAAATGCAAGGCAGGATGAGGCAGAAGCA AGTTGTGTGTCCA

ID		pos			Sequence
L42611b		50	G C	...	GTCCTCAGGCCCTTCTCTGGCTGCGCAGAGCCGTCTTCTCAGGTTGCCTGTGTC[G/C]TCTCCTGCTGGCCTCTAG TCTTCCCTGCTCTCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTCTGTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTGATTTACATCATAATGTATTCACCA CTGGAGCTTCACTTTGTTAC
L42611		34	T C	...	GTCCTCAGGCCCTTCTCTGGCTGCGCAGAGCCGTCTT[T/C]CTCAGGTTGCCTGTGTCTCCTGCTGGCCTCTAG TCTTCCCTGCTCTCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTGTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTGATTTACATCATAATGTATTCACCA CTGGAGCTTCACTTTGTTAC
WI-1172b	TGAAGAAATG GCTGATACCA A	179	C T	ATGTGCATTT TCACTGCAG	TGAACGTGTGGTTAAAACTAGGCAATTGGTTAAAATCAATTAAAAAACAGGCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTCTGCTTC AAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/T]CTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a		17	C A	...	TGAACGTGTGGTTAAAA[C/A]TAGGCAATTGGTTAAAATCAATTTAAAAAACAGGCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTCTGCT TCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	GCAGATTGGA AGTGTGAAAA A	35	G C A	CACTTACATT CTGAATATTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAGAGTCTAAATATTCAG AAATGTAAGTGCTGCCCTCCAACTGTTCTTACCCACTTGGAATTTTGAAAACTAGATTGAAT TCCTTTGCAAAACCGTTGCATCATGATCATCATGGAGACCGTTAATTAATTAAAAGACACATTAAACATGG CCTGGTG
WI-1231b		141	G A	...	TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTATTCCTCTTCATTAATTTTCTT TCAC[G/A]TTATTCCCTCACCCTGAACGCGCCCTTCTTCCTTCGTGAGTGACATTTAAAATCCACTTTAC ACATTCGGACC
WI-1231a	GGCTCTTTATT CTCCTTCTTTC C	126	T C A	CGTTCAGGGTG AGGGAATAA.	TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTTATTCCTCTTCATTCCTTCA[T/C]TAATTT CTTTCACGTTATTCCTCGTGAGTGACATTTAAAATCCACTTTACA CATTCGGACC
WI-472	ACATACATAT CCATTATACA G C ACAGAAAG	114	G C	GACCTTTCTT TCCAGCCC	GAAGGCAGGACTGTGTTTTGGAGGACAAAAAGTAAAATCTTTTTATATCTTTAATTTTTATT TTTTTCAGGCATATAGACATACATATCCATTATACAACACAGAAAG[G/C]GGGCTGGAAAAGAAAG GTCAAGTGAGAGATTTCAGATATTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

Marker	No.			5' sequence	Sequence
WI-478	46	C	T	GCATGTCTGTG TTACTCTATTT TGTTC	AAACCACTGCAACCTTCAAGCACATGTCTGTGTTACTCTATTTGTTC[C/T]AGCCACCTGTGGCATTCCAAAATATGATAATCTCTGCCACCATACTGCTTAAACACAAATAGAATCTGGCAGCAAAATATAGCAAATGCCACAGATAAGCTTACTTCTAAATCAAAGCTACCATCAGTACCTTAGCACATTTAAAAATAAAAACCAACACTGCCCA
WI-533	29	T	C	ATCACAGCAG AGTACCTTTCT AACT / CCTTCCAACCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTAACTT[T/C]ATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGACTGTTCTGTTGGTATAATGACCCTGTGTCCAGTTAATCCA
WI-601b	112	T	A	...	TCACTTATCTCTTTTTTGTGGTGAGAACACTTAAGAATCTAAGAATGATCAATTTCAAATAAAGATGGTAGTGAGCGAACAGAAGAGGTTTCATTGACTCCTAAACTGAGTAC[T/A]CAAAAACGAGCAGGTGCTCACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74	C	T	...	TCACTTATCTCTTTTTGTGGTGAGAACACTTAAAATCTAAGAATGATCAATTTCAAATAAAGATGG[C/T]GAACAGAAGAGGTTTCATTGACTCCTAAACTGAGTACTCAAAAACGAGCAGGTGCTCACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107	A	G	CTCCTTCACAA CCTCACCA / CTTCCCGGTAA GCCAAGT	AACAAAAACAGACACCCTCCCCACTGGGCTGCCCTCCTTCCACCAGTCCACAACCTCACCA[A/G]ACTTGGCTTACCGGGAAGCATAAAGCCAAAGCCATTTAGTCTTTATTGCAACATGGTCTGCTGCAATAC
WI-919	36	G	A	ACTGCTTGCTT GTTGATTTAAT C / TTATTCTAATC CCACATGACAG C	ACTCACTGCTTGCTTGTTGATTAATCAACCTAGCC[G/A]GCTGTCATGTGGGATTAGAATAAAATAAACACAAAAATGAAAACACCAGATTCTTTTTCAAGGCACACGTAAAGATAATAACTTCAA
WI-991	37	A	T	...	TGCATTCATTATGCACCAAATAATAACTTCTGTACAT[A/T]CATTATTGTATTTCATTATCACAAAATTATGAGTGAGGGATGATTGTTATCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCTTTCCCAAAGTCACAAAGTTAGTGACAGAGCCGGGATTCGAATCCATCAACTTGAATCCAGAGAAAATGTTCTGCATCCATCGTACAACACTGACTCCTTTTCTCCCTTTGAAAACAAGGC
WI-1011	70	G	C	CAGTATCTGA AGTTTTTGTCT CCCA / AGGAACACCTA CAAAATGACTT CT	CTTCCTGACCTGTTTGCAGTGGATACTGTTTTGGAAGGCTCTGTCTCAGTATCTGAAGTTTTTGTCTCC[G/C]AGAAGTCATTTTGTAGGTGTTCCTGGCGTTTTGCTACGTTTCCATTTTCTCTAATACACTGCCGTCTTAAGGGAGGGCTTGCAGAGCATTTATCAGATGGCTGTTTTGCTGCATTATCGTGTCACTGAAG
WI-5381	178	A	T	...	TTCATGCAGAAGGTCCATGAGTTTACAGAATCTCAAGGAAGAAGAAAGGCCCCTCAGAGAGGATGACACCAGAAGAATGAGAGTGGCTTGCTCATGAAAATTGGACAGCATGTTCCAAGCAGAGGGAACAGCAGGAAGAGAAAAATCATATCTATCCACGTGCAGAAACTGGCAATTAGTTTTGT[A/T]TACTAAAACACAAATGTTTAACTTGGGGTCCACAAAACAAGGATATGTTGGCAAATGTGTATTTCTGTGATG
WI-5791b	76	G	A	...	CTATGTATTCCATCTAGCAAAGCAAGACTATTTGGATAAGTTTCACAAAGATGAGAACAGGTCCTAGAACCCTCAG[G/A]ATCGAAAGGAAGTTCATCTCAGTCCATAGACCCTATCTCACTGACCCAAAAGGTAAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTGCCACCCTGTTTGTTAGGAA

ID	Pos			Flank	Sequence
WI-5791a	44	C	G	...	CTATGTATTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTT[C/G]ACAAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAGTAAAGAACTTACACTACAGATTGTGCATTTCTTATTTGCCACCCTGTTTGT TAGGAA
WI-5406c	120	C	T	...	CACTCTGCTGTTGTCCATGGGTGCCACAGAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACC[C/T]TATGAGCCCAC ACTTCTCATTTCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGAAAAAGAGAGAGGCAA GG
WI-5406b	118	C	A	CCAGGATGTC AAGGTGAGAA A	AATGAGAAGT GTGGGCTCAT A	CACTCTGCTGTTGTCCATGGGTGCCACAGAGACTCTTCCACAGAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAA[C/A]CCTATGAGCCCAC ACTTCTCATTTCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGAAAAAGAGAGAGGCAA GG
WI-5406a	42	A	G	...	CACTCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCACAGAAG[A/G]GCCACTTCCACAGATGCAACAG GCCTTTTGAAGGAGCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCTATGAGCCCAC ACTTCTCATTTCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAGAAAAAGAGAGAGGCAA GG
WI-5798	48	G	C	TTTATTCTCCC TTGTTTTCTTT TG	ACTGTTAGAAA ACCAGTATTT TCAAT	CCATTCCTCTTCCTCCTCCCTTATTCTCCCTTGTTTTCTTTG[G/C]ATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54	T	A	TCTTCATGAAT TCATCTTTCAG TTT	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT[T/A]AGATCGGAT CATGAATTAGTCCAGGCTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C	T	TCCCAGAGAA AAATCCAAGA G	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCCAGAGAAAAATCCAAGAG[C/T]CTTAAACCATATTTGTGTTTA GAAACTCCTGTGCCAACCACTCTTGATGTGAGTGAC
WI-5481b	131	A	G	TGTCATTTATG CTGCAGTCG	TTACTTCCAGG CTCCAAGTATT	AAGCCAATTTCACATTAGTTGATGAATTTGAATTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTTCAAGAGGTAGTATATGTCTGAAAAATCTATTTGTCATTATGCTGCAGTCG[A/G]A ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTCACAATTA
WI-5481a	29	G	A	CCAATTTCAC ATTAGTTGATG AATTT	CCCATGCATTA GATACTGTAAA ATT	AAGCCAATTCACATTAGTTGATGAATTT[G/A]AATTTTACAGTATCTAATGCATGGGCATCTGTTTC AACTCTCTGTTTTTCAAGAGGTAGTATATGTCTGAAAAATCTATTTGTCATTATGCTGCAGTCGAA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTCACAATTA
WI-5492	38	T	C	...	TCATGAGTCTTTCTTCAAAGATGCTTGTTAAAGTCCCA[T/C]CAAAGAAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

ID	#				Sequence
WI-5826	134	T	C	...	TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTTCTATTTCATGCTTCACATTTATTTTTT TTTCACTTAGTTAAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTATACATATTCTTTAG[T/C] TTTCAAATTAAATGCCACCATAGAAATAATTTTCTAACCAACCAGCCAAACAGCCTCACTCTTCCTT CCTTGGTGCATTTACTCTTTACAC
WI-5546	40	C	T A	CCCAATACTTT TTCAGGTGAA A	CCTGTATTTTA GCAAACATGGG / CCTTATAACCCAATACTTTTCAGGTGAAAAAAAGGGAAAA[C/T]ACCCATGTTTGCTAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAAATTCTGATGTGGGAAATAT TAGAAAAATTAAGCGAGAGGCA
WI-5552	97	C	T	GGCACCAGCCT TTTTAGAGT	TGCACAAATTG CCCAGG / TGTTTGTTCTGCACCTCCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTTGATTGAGCGGGTATGGGT GGGGCTATCGGCACCAGCCTTTTTAGAGT[C/T]CCTGGGCAATTTGTGCACTAGTGTCAGA
WI-5836b	161	C	T	...	TAAGTTGATTTAAACACTCTGTGCCTCAATTTCTCACCTATAAAATAAAGATAATAGTATCTAAAA AAAAGAGAGAAGAATTAAAAGTGGATAGACATGAATAACTCTGATGATACTGGTTGTATCCCTGAA TCCTGCAATATACACATGCTCATGAT[C/T]CCATTTTGAAAAT TAAGCTTTTTGAATTGTTTTCCA ATG
WI-5573	58	C	T	GTTCATAAGG AGGTGGGGA	TGAACAGTTGG AGAGTAATGTG TC / TCGGGTATTAGGATGCGTTCACCCTCGATGATGATGGGCGTTCATAAGGAGGTGGGA[C/T]GACAC ATTACTCTCCAACTGTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G	A	...	CAGGACCTTGGAGCCCTTGGAGCGTTCCTTCGTGTTTGTCCTTCCACCCTCACTCTTTCTCTGCCTGGGTGGAGC CTCTCTCAGGCTTCCTCTATGCCACGCGTCTATCTTCTATATGGGGCAATATCCCAATGTCCCATTC[G/A] TTTTGCCATTTCCTGTATATCAAACAGAGAAGCAGAGGGTGG
WI-5850a	92	C	T	...	CAGGACCTTGGAGCCCTTGGAGC CTCTCTCAGGCTTCCTCTATGCA[C/T]GCGTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCCTGTATATCAAACAGAGAAGCAGAGGGTGG
WI-5612b	125	A	T	CTATTAATGA GCATCGTGTCA TTC	TTCTCTTGAGA AACCTAAAAC ACTG / TGCCTGATTGACACATAGTTATCTGACAGTAAATCATTCTAACATCACAAATATCTTATTTCTGCCTG TCACACTAATTTGCAAAGCATTCAATTGATTGACTATTAATGAGCATCGTGTCATTC[A/T]CAGTGTT TTAGGTTTCTCAAGAGAATTATGCTGTTCTTCCTGTAACTCAAGTA
WI-5612a	44	T	A	...	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATTCATAACA[T/A]CACAAATATCTTATTTCTGC CTGTCACACTAATTTGCAAAGCATTCAATTGATTGACTATTAATGAGCATCGTGTCATTCACAGTGTT TTAGGTTTCTCAAGAGAATTATGCTGTTCTTCCTGTAACTCAAGTA
WI-5636	26	A	C	GCCAATTTTAT CCGCAATAAA	CATCGAGGACT TTGGGAA / TGAGAGCCAATTTTATCCGCAATAAA[A/C]TTCCCAAAGTCCTCGATGGGAGGCATTTCAGAATCGGG GCAGGGGGAGGCAGAAGGGTGAGACAGATGTGAAGAAC

Marker	Pos	Allele 1	Allele 2	Left Flank	Gap	Right Flank
WI-5865c	103	C	G	CATAGCATGG ATAATATTAT ACAGAAAAA	...	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCATTC ACTGACTCACTCGCTCTATCAAAAATTAAA[C/G]AAATATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCTTCA GAGAAGACAGAGACAACTAAATAAATTCCAGG
WI-5865b	99	T	A		...	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCATTC ACTGACTCACTCGCTCTATCAAAAAT[T/A]AAACAAATATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCTTCA GAGAAGACAGAGACAACTAAATAAATTCCAGG
WI-5865	165	T	A		...	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCATTC ACTGACTCACTCGCTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGGAACTC AGAGAAGCCAGAAAAAATGACCAAGACACAGT[T/A]CCAGTCTCCATCTTCAAAAGGTCACAGTCCTTC AGAGAAGACAGAGACAACTAAATAAATTCCAGG
WI-5874	76	T	G	CCTAGTAAGTT TCAGTCATTTG ATATGT	...	CTCAGACATTCATTTCATTAGTTGTTAATTTTGTGTATTTCATAGCATGGATAATATTATACAGAA AAAAAATT[T/G]TACATATCAAATGACTGAAACTTACTAGGTAGCAATTGTTTGTCAATTTGCT
WI-5752	36	A	T	CAGCCTCTCAG TTTTTTCCATC	GACAGAAAAG AGAGTAAATT ATGAAAAA	CATGGAGCCGACGTTCAGCCTCTCAGTTTTTTCCATC[A/T]TTTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTTCGTATTTCAACTCTCATTGCTGATTGGATGGTCATAAAATATGGGTGATTC AGAAAATAAGTAAATG
WI-5760b	61	C	G		...	TTAGCAGAAACAACAACAAAAAATGTCACAACACTGCAGTAAAGAAGTGTTTTCCCGATAAATA[C/G]C CATTAGGTATTAGATAAGCATCCCATAAAACATTGTTGAAAACGAAGCCGAGTTTTCGATTCACACA GTTGTCTGTTTTAAACCTCTCTAAATCCGATAAATAGCCATTAGGTATTAGATAAGCGGTCCCACGAAA CATTGTTGAAAACGAAGCCACGTTTTCCGATTCACACAGTTAGTTGTCTGTT
WI-5760	187	G	A	TTCTCACCATG GGGAATCTTG	...	TTAGCAGAAACAACAACAAAAAATGTCACAACACTGCAGTAAAGAAGTGTTTTCCCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAAACATTGTTGAAAACGAAGCCGAGTTTTCGATTCACACAGTT GTCTGTTTTAAACCTCTCTAAATCCGATAAATAGCCATTAGGTATTAGATAAGC[G/A]TCCCACGAA ACATTGTTGAAAACGAAGCCACGTTTTCCGATTCACACAGTTAGTTGTCTGTT
WI-5944	52	A	G		GGGTGGGATCT AACTTGCA	AATATCTGGCCTTTTCTTCTTCTTAGGAGGAGATTTCTCACCATGGGAATCTTG[A/G]TGCAAGTTAGAT CCCACCCTCACTATTGAGAAGCTAAAAGTGTAAGACTACTCATTTCTCAGTCTTCCTTGCTG
WI-5967b	1148	C	T		...	GAGTTTAATGAATCCTGTTCCCCTCCTAAAAACCTCCTGTTCCCCAACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTTGCCCAAGTCATGGAGGAGATGCATGTAATTGTGATCATTCAAGAGTGTGAG TAATGCTTGGTA[C/T]TTGCTCTGTGTGCCGTATCTGCTCCAATCACCCATTCACCACTTTATTCCTATTAT GCTGAATGAAACGGTTATATTACAG

ID	Pos	A1	A2	Seq A	Seq B	Main sequence
WI-5967	165	C	T		---	GAGTTTAATGAATCCTGTTCCCCTCCTAAAAACCTCCTGTTCCCCAACTTCACATTCAGCAGATATTCTTTCATGGGTTATTTGCCCAAGTCAGTCAGGAGATGCATGTAATTGTGATCATTCAAGAGTGTGAGTAATGCTTGGTACTTGCTCTGTGCCGTAT[C/T]TGCTCCAATCACCCATTCCACTTTATTTCCTATTATGCTGAATGAAACGGTTATATTACAG
WI-6093	53	G	C		---	GGGTAAGATCCAGAGCACAGGTGAACTCGCCGGTATTGAAAGTCTTTGGGCCA[G/C]GTCTGTAATGATCTGACTTCTCTCCCAGAACCCCCTCTTCTCGGAAGTTCCAACTGTGCACTGAGCCCATTGTAGGGAGCATTTGAACCAAAACCCAGGACGACACTGCTGACATTTGACTTTGACTTCAGCAAACCTTGATTGACGGTGACACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80	T	C	TGAAACCCCA GAACAGTG	CTTCTTAATTA AGCATCTACA AGGTACTT	GACTCTGTCTCAAGAGAAAAAAAAATTGAATAATATTAAGCACTTCTTAATTAAGCATCTACAAGGTACTTA[T/C]CACTGTTCTGGGGTTTCAATCCTCTTCACCTTTAGACTTCAGGAAATTCTACAAGGTACTTA[T/C]CACTGTTCTGGGGTTTCAATCCTCTTCACCTTTAGACTTCAGGAAATTCAGAAAAATGCATGAAAACAGGATTGTTACATGCAGAGAAATAGGGGGAGAAAATAGGGGAGATAAAATTTGTCTTTCTC
WI-6450	45	T	G	TTGTTTGAAAT GTGTGGTACTT CT	CCAATGACTT ATTCTATATCT TGTCACA	ATAGGACAGTTTTTCTTCCAATGACTTATTCTATATCTTGTCACA[T/G]AGAAGTAGTACCACACATTCAAACAAGAGCCAGGCTATGCCCAGGGTGGGATTATTTCACGGTCATGGTAATGCATGTAAGACTATTTTTACTTGGCCTTCTCTTTATGCCATAAAACAAGGTATTGGTCTATTCAACAAACATGTGTCAATACAG
WI-6461	88	C	T		---	CAGTTGTCATGTCCCTCTGGTACTACTAGAAATATAGTCTTATAGAATGTGGTTAGAATAAAGCCACAAATTATTCTATAAAACAACA[C/T]AAGGAACGAGGCTCAAAAGTGGAACAAAACGGCCTTAGTTTCTAAGTGGAAGACTAAGACGATATAGGAAAAATATAATCCGTGACCTCTTA
WI-7466c	141	G	A	AGTCGCATGCC AATTTATAATT AATTTATAATT	TTTTCACAGTC AATTTATAATT ATTGTTCCTTT	GAAACTATCCTTAGTGTGGTGCCACATTTTCTATTTCTGATTCTTTGGTCACACAGGGACTTTCTGGGCTATGAAATAGTCTATTCAGTGAACTAGTTATCATAAAAGACATGCAAAAACCTTTCACAGTCTTTGTATGAAATAAATGGCATGCAACTTTCTGATTTAGCCTGACAGG
WI-7466b	80	T	C	GACTTTCTGGG CTATGAAATA CTGTC	TGTCTTTTATG ATAACTAGTTC ACTGAA	GAAACTATCCTTAGTGTGGTGCCACATTTTCTATTTCTGATTCTTTGGTCACACAGGGACTTTCTGGGCTATGAAATAGTC[T/C]ATTCAGTGAACTAGTTATCATAAAAGACATGCAAAAACCTTTCACAGTCTTTGTATGAAATAAATGGCATGCAACTTTCTGATTTAGCCTGACAGGATGAAATAGTCTATTCAGTGAACTAGTTATCATAAAAGACATGCAAAAACCTTTCACAGTCTTTGTATGAAATAAATGGCATGCAACTTTCTGATTTAGCCTGACAGGATTGTTCCTTT
WI-9814	104	C	A		---	TGCTTTTTAAAAATAACAATGACCACCTGACACCATAGTCTGTCTCCATTGCCAGTCTTCCTCAGTAGAATAAGACAGGGACTTTGCTGGCTGCTATCT[C/A]TTCCTTCCTTCAGAAGAGCACTTGGCCCCTCATAGGCATTCCATAGATATTTGTTGAATGAATGTGCTTTTGCATATTGATTCCTACATTTGATACATTCTCAGGAGGGGACATTTGGCCTAT
WI-9720b	55	A	G		---	CCTCTAACAAGAAAAACTTGACTTCCTCAACTCAAAATACCCTTCTCTAATAATTT[A/G]AGTAACCAAAATATTCCTTCAAATAAATTAATCTTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCACCACC

Marker	Position			Sequence
WI-9720a	47	A	G	CCTCTAACAAGAAAAACTTGACTTCCTCAACTCAAAATACCCTTCTCT[A/G]ATAATTTAAGTAACCA AAATATTCCTTCAAATAAATTAATCTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC
WI-9825	123	A	T	CACGCTCTAAGGCAGGATGTGGCTTATGAGATACTTGCATTGTCTGTCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGTGCT[A/T]GAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAGAGAGAACTCACCAGGGTTTAGTTTGCATT TAAGAATTGCCAGTCTTTTTGTCCTGCATCATCTTGAACATTAATCCACATG
WI-9748	74	C	G	CCACTTCAGTAAATCAATTGTAGCACTTATTTCTAAAGATTCTAATTTTTATATGTTACCCTTT GTCATT[C/G]TCAGACCAAGTACATGTTTCACACAGCCATCTTCTTTCCTGGAATCTTTCAGAAT TACAGTTATGATGTCCTTTATATTCCCCA
WI-9943	91	T	C	TGAGGCTATGATTGCAGATTTGTAGTGACTAATACTTATTAAGCAATTCAATGTTGTGGGCACTGTT CGTTGTGTTTATATCCATCTTC[T/C]ATTTAATTTTCTACTGAGCAGAAAAAAATGTATACATT AACCTTTGCTCCCTATTTGTACCTTTAATATTGCATTTCACACCTTCTTTTTGTCATTAGGGA AGGGGCCTTCACAGATCCGTCAGCTCAACTGCCTCCTT[T/C]AGTGAGCCTGTGAACCACCCAGAC GGCTGGTCATCAGTGTCATCCTCCTTTCCGGACAACTATCTTTAAAGAAAAAAAAGAGTGT CTTTGAATGTATCCATTTTATCCCCAAATAATCTTGTTTAATAAATTCCTTATTAGGCCAAATCCAAT GTGCTGAAATATCTGCCAAGCATGTCATTCTACACAAAAGGATTTGCAAA
WI-9891	39	T	C	CTCAGAATTATTCAGATCTTCCCCAAATGTCATGATTCTTGTTCTCAACATCCTATTTTTCCTCAAAC ATTTATCTAGCCTGTA[C/T]AAGTCATCCAGTGAGGCTGTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897b	84	C	T	CTCAGAATTATTCAGATCTTCCCCAAATGTCATGATTCTTGTTCTCAACATCCTATTTTTCCTCAAAC ATTTATCTAGCCTGTI[A/T]CAAGTCATCCAGTGAGGCTGTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83	A	T	AGATAACCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCACACCTCACCGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGGTGCTTGGACTGGCGCAGGGGAGTTCAGACAC[C/A]AGCCAAGAAAAGCC TGATATTAAGAGGCACTTGCATTAA
WI-9935b	115	C	A	AGATAACCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCA[C/T]ACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGGTGCTTGGACTGGCGCAGGGGAGTTCAGACACAGCCAAGAAAAGCC TGATATTAAGAGGCACTTGCATTAA
WI-9935a	42	C	T	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCTCCCCATTCCTTTGTCTTGA TTCCCCAAACCCAAGGTTCTCACCCAATCTGATCAAATGCTGACTAGGTCATGGCTGTCAGGGTAA AGCATTATGA[C/T]AGACACAAAGACAAAGAGGTAAAGTTGCTGCTCCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGTGGAGCAAAGG
WI-9983	146	C	T	

ID	Pos					Sequence
WI-10019	139	A	T	TGATGTAATGC TATGTAGCAA ATCT	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTTGAGTATACAGCAATCTATTTGTTTATTTATGTGTGCTATAAATCAATGGTTCTA ACATTCAAATAAGATCTTTTGCTTCTCTGCTCAGATGCTTCAATGATGTAATGCTATGTAGCAAAT CTA[A/T]TCCCCCTAAGCACAGTAATCAAGGCCTTCTACCCCA
WI-10020b	122	T	A	GCGAGAAAAG AAATCATGAC TTT	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAATTTAGGC ATGCATAGAGAATAGCAGTGTTTTTATTGGCGAGAAAAGAAATCATGACTTTT[T/A]AAAAATACC AGACTAATGATTAAATTAACAGTCCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10020a	39	T	C	TGTCATCTTGA CTCGTATTAA ATAAATT	AAATTCTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTA[T/C]GTTAACTGGCTCTGAAAAGAATTA GGCATGCATAGAGAATAGCAGTGTTTTTATTGGCGAGAAAAGAAATCATGACTTTTTAAAAATACC AGACTAATGATTAAATTAACAGTCCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10064b	170	C	T	CCTTTAGATAT ATTGTGATTGT TTTACATG	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCCAAGGGTAGCAGGATCAGGGAAGGCATTAATAAAT ATAATTTGCAGAGCATCTCTCTCCTATGCACCAGATATTGTGGTGACACTCTGTTTAATCCAGTATCC CTACTCCTTAGATATATTGTGATTGTTTTACATG[C/T]GAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10064a	54	C	A	GTAGCAGGAT CAGGGAAGG	GAGATGCTCTG CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCCAAGGGTAGCAGGATCAGGGAAGG[C/A]ATTATAATA AATATAATTTGCAGAGCATCTCTCTCCTATGCACCAGATATTGTGGTGACACTCTGTTTAATCCAGTA TCCCTACTCCTTAGATATATTGTGATTGTTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T	C	TCTCCTGTCCC CAAACTCTT	ATTCTTGTTGT ATTGAATGGAA TTAA	CCAGGGGATTCTCCTGTCCCCAAACTCTTA[T/C]TTAATTCCATTCAATCAACAAGAATTTATAGAA TATGCCACCACATGCCACAAAGACACCCTTATATTAGT
WI-1319	40	A	T	TGGCACTTAG AACATAGTT ATTCTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACACATAGTTTATTCTTT[A/T]ACCATAGGGGTGTGTGGCTTATCT TTTACCTGGCATGGCTTAGGTCCTGTTTATAATTTGGTATCTTTTGCCACAAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTAACATTAACACTGGTCAGATGTGTTAAAACTTGTTGAACCTGCGAGC
WI-10316	104	T	C	CTGTTGATTTT CTACCTCTATT CTCTT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACTTAGTGAGGTGTAAATCAGAAGCATCTATATTATTCACCAGTCACCACCCTG GACTATAGTCTGTTGATTTTCTACCTCTATT[T/C]TAAACTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAAGGATGTTTAAAAGCCCAGCC
WI-2572	61	C	T	---	---	AGTGAGTTGTGCACAATTTTGGAGACATTCTGTGACCCCAACTTAAAACACTTCTCCCACA[C/T]AC AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA

ID	Pos			Seq 1	Seq 2	Sequence
WI-10368	31	C	T	TGAAGCAACC AGGTCTTGTT	CAAGATATTAT ATTTATTCTCT AAGAGGGG	GAGGAACTGCCTGAAGCAACCAGGTCTTGTT[C/T]CTACCCCTCTTAGAGAATAAATATAATATCTT GAGATAGGGAGGAGGCAGCCTGAGGACAGTCTGGGTTTGTTCTACCCCACTGGAAGCAGAATATCC TTCAAAGCTTTTCCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATGGATTGCCTTTCAGGG T
WI-10391	32	A	G	CTGTCTCAGGT ATGACTCCCA GA	GGGAGGTTAGGA GTCAAGAAGTT	CCTCCGTTCTCTGTCTCAGGTATGACTCCCA[A/G]TCAACTTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTTCCCAGGGGACGACCATCTGACACAGCCTTTTGCTTGCTTGTGACAAACAGAACATTGCAGAAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146	A	C	GTTACCCAGA GTCTTCTAATA GCAA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTATATGTTATGCCTGACTTAGCGGGTGCTCAATAAATAATATTATTCTTTTTCATATT TTCCAATTATTAATAACTAGAATTTCACCAACAGAATTTTAAACATTTTAAGTTACCCAGAGTCTT CTAATAGCAA[A/C]AGCTACTGGAAGCGGCAAGAATTTAACCCT
WI-10567b	82	A	C	...	...	AGCGATGAAATTTATATGTTATGCCTGACTTAGCGGGTGCTCAATAAATAATATTATTCTTTTTCATATT TTCCAATTATTAAT[A/C]CTAGAATTTCACCAACAGAATTTTAAACATTTTAAGTTACCCAGAG TCTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAATTTAACCCT
WI-10567a	60	T	C	GGGTGCTCAAT AAATATTATT CTTTT	AAAATTCTGTT GGTGAAAATTC TAG	AGCGATGAAATTTATATGTTATGCCTGACTTAGCGGGTGCTCAATAAATATTATTCTTT[T/C]TCAT ATTTTCCAATTATTAATAACTAGAATTTCACCAACAGAATTTTAAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAATTTAACCCT
WI-11153b	84	C	G	CAAACTTCAA ATTGCTTTAAG TACTTTA	AAATCCAACA GTCAAGGTCTT C	CGTTGGGAATATTTCTATCTCACCTAAATATGCGTGATAAAATATACATTTAACAAACTTCAAA TTGCTTTAAGTACTTTA[C/G]GAAGACCTTGACTGTTGGATTTTGAGTTTTCTTATTCTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33	C	A	GGGAATATTTC TATCTCACCTA AATTATG	GCAATTTGAAG TTTGTTAAAAT GTAT	CGTTGGGAATATTTCTATCTCACCTAAATTATG[C/A]GTGATAAAATATACATTTAACAAACTTC AAATTGCTTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTGAGTTTTCTTATTCTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125	T	C	CACAAATGTA ACAAGAAATTG ATCC	CCATGGCTGTA GTCCCAGT	GTTGTGAAACTCCAGTATCATTCCCTCAAACCACGCTTAAATCACAAATCACTTTTCTTTCCTGTA GAGCTCAAACTCAGTCTGAATGAAATTGCTGCACAAATGTAACAAGAATTGATCCTA[T/C]ACTGGG ACTACAGCCATGGCTGTAGTCCCAGT
WI-11163	58	C	T	CAAGTGAATT ATGACCAAAA TGAGA	TGTCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAACACACACAAAAAGTTTCACCAAGTGAATTATGACCAAAATGAGA[C/T]AAAT TTGTTAAAAAAAAACCTCAAATGAAAGAGACAAATATAGTTCAAAGATTCAGGTTCAATATTGT
WI-10656	59	T	G	...	...	ACCTACAAAATAGGGATAGTCATGGTGTTGGCAGACTTTCTTCTTTCTTTTGT[T/G]CTCTTA GAATCCATTTGCTTTTGGCCAGCATTCCCTCTCCCATATTTAAGGAGGAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCGTCGTCTTCCCAATCCAGAGGACGTACTATTCACCCCATGGGGTCAT AGAGAGGGATTAAACAGGGTGATGCCTGCAATGGGAATATTTGAAAACC

Marker	Pos					Sequence
WI-11169b	154	T	G	TTAACCAAGA GTTTTTCATTC TTTTT	CTAACTTAAAA ATCCTCATTCA AAATATAA	CAGCATAGAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAAAGAGCAGACA[T/G]TTTATCATGTGTTCTGATAATTTTTTATATTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95	A	G	AATAAGTGAA AGTAACTGAC TTGAAAAA	AAACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGAGGCTGTTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAAAATTTAAGCCT[A/G]AAGTAGTGCTTTTTAACCAAGAGTTTTCATTCTT TTTTTTAAAAAGAGACAGACACATTTTATCATGTGTTCTGATAATTTTTTATATTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25	A	G	...	...	CAAGTGCTTGGACCTTGGATAGGTC[A/G]ACCGGCTGAAGGTTGGACAGTTGTTGGTTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTGTTCCTTTGGGTTACCACTAGGGGTCACTAAAG AGAGAAGATGGGGAGACAGTCTCAATCTTGTCTAAATAATTCCAAAATAGCCATGGGGTTTGGACAAAATAC AAGGTTAGTGTGTCTCTCTAACTTTAATGGGCATA
WI-10686	133	C	T	TGCCCCTGTCC TTCATGTGTAG AAGG	CAATCTCTAAA ACACA	AATAACCTGTGGCACATAAGGCAAATACTGAGCCCCATACAGAGTGTTTATGTTAATATTATGAAA AAAGTCAAGAGAACAAGATGATATAGTTCTGCTAGAAATCTGAAATCTGATGCCCCTGTCCAAGG[C/T]TGTGTCTCACACATGAATTGAGAGATTGAATGAAAATGGCAAAATTCAGAAAATGGG
WI-11175	77	T A	A	AAATGATTCTT CTGTTCTCACA TCTGCTCAAAG TTCTTTTTGAA A	AA	GGTAGGATGATTCTAGAGATGCCACTTACAGCCACTGAAATATATTGCCTCCCAAATGATTCTTCTG CTCAAAGAG[T/A]TTTTTAAGTTATCTACTTATTATTATTCTGCTTTTTCAAAAAGAATGTGAGA ACAGTACAAAATGTGTTCAGTATAGCAAATTAAAATTAATTAAAAGTAAGAAAAAGAGAGCCAATT TGGGC
WI-10694	144	A	G	TGCAAATGCTT TATGAGTTTTC	GGCATTTGTA AAGGAGGAAA	TAGAGAGGTCTTTCAGTTCAGGGGTTGGAGGGGTGGTGAGGTGAGATTCACTCTTAGAAGCACTGGC TATGTTACAGAAAGATAAACTCTGAGAAGAACTCAGTTCTAAAGTGTTCAGTCTTTGCAAATGCTTTA TGAGTTTC[A/G]TTTCCTCCTCCTTACAAAATGCCATCAATTCCTCAAGGAAAAAAAAAGCTTTCT T
WI-2716	23	T	C	TGAATTCATCC AGAAAAACAG CC	TCTCTTTCTC TCTTGTTGTCA TTC	GTGAATTCATCCAGAAAAACAGC[T/C]GAATGACAACAAGAGAGAAAGAGAGAATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCCCAGTGCATGGAGCAGTG
WI-10719	115	T	C	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	CAGGGCCCAACTCTGTCATTAAGTGTTTAGAACAGACACCTCAGTCACACAAAGTTTCTCTTGTATGT GCCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCTAGT[T/C]GGGCTGCTGGCAGTGCTT TTCCAGCCTGCTGCCCATAACTAA
WI-10721	40	A	G	TGGCTCTGCTA GCTTGCCA	GAAACTCCCAC ATAAATAAAT CTCA	CAACCAATTCAGATTTAATTTTGGCTCTGCTACTGCCA[A/G]ATGAGATTTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCCTCTCCCTGCTTAGGTTTGAAGAAGTTGAA

Clone	Pos			Seq 1	Seq 2	Sequence
WI-11204b	88	T	C		...	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAGGGTG AAAAGAAAAACTTCACCTTT[T/C]ATTTAAAGTAACACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAATTTTAATTGGGAAGAGATTAGTAGTCGAATCAGAAAATAATTAATCAGAAG GCAACATC
WI-11204a	80	T	A	GTAAAAAGGG TGAAAAGAAA AACTT TACCTTT	AAGAACAATG	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAGGGTG AAAAGAAAAACTT[T/A]CACCTTTTATTTAAAGTAACACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAATTTTAATTGGGAAGAGATTAGTAGTCGAATCAGAAAATAATTAATCAGAAG GCAACATC
WI-10732	80	C	A	GCTGTGTCTTC ATTGGTTCACT	CATAACAGAA	ACATGTATTTCCTTAGTGGTCAGCCTTCCTTACCCCCAAGAATATCCCTGGTTATTGCTGTGTCTTC ATTGGTTCACT[C/A]TTAAAGTTCTGTTATGCATTGTCGTTCTTGAGTCCACATAGGTGTTAATCATTCCA CACCACTCTGTTTAAACTGTC
WI-11206	127	A	T	GGTTGTGTTT CTGTATGTGTACA ACTC	GAGTGACAATC CTAATGGTTGG	TAGTCTTTTCTTTGTACGAGTGTCATAAAGAATTACCACTCTGTCACATTTGTAAAAGATAGCACAG AGAGAAGCATTACAGGGCACAGCACAAACATGAGGTTGTGTTTCTGTATGTGTACAGAGTGACAATC CCATTAGGATTGTCACTCTCATATAGACAGAATTCAGTGGTGGTGATTTGAATTCAGTGGTGATAAGTCTA
WI-11215	68	C	T	...	...	GAAAAAAAGTTTAATTGGATTGCTTAGTTGTGTCTTAAATTGACCTACTTTCAGATTTATTTAGT [C/T]ATTTTTCTATAATATTTTCTTGTAAGTGATGGATTTTCTATAAATTAAGGAAACAGATATTT ACACAGAGAAGACACAGGATTGCTTGAATTAGTATAACATTCTTATTCCAAGCCCCATTCCACCATGT TT
WI-11219b	89	G	A	GAGAGAATAT TCCAAAAAGT AGAGAAA	GGTCCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAATTGGAGGATAAAAATTGAGAGAATATTCCAAAAAGT[G/A]AGAGAAAA TTAGAGGCCATTCTATACAGGAGACAAGAGATGAAAAATAGGAGAAATGAAGGGAGAAAAATCCAC TCCAATATTTGAATAATAGTTATTCAAAAAAAAAAGAAAAATGAGGGGAGAAAAATCCAC AAAACATCTC
WI-11219a	18	G	A	...	...	ATGAAAAATGCATTAGAA[G/A]AATTGGAGGATAAAAATTGAGAGAAAAATTAGAGGACCATTCTATACAG AAAGACAAGACAGAAGAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAAAGAGGCAAGAAATGAAGGGAGAAAAATCCAC AAAACATCTC
WI-11222b	136	G	A	CATACCACTGC GGCTGG	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGAATCATTTACACTACCGAAATCAGCAAATGCTAAAATTGGGGCTTTGGATTTTTGT TTTGTTTTTCCATAGACCCCACCGTTGAACTATTGTTAAACATTTACCACCACGTTAAACTTCGTAATTGCTTTCACAGGCTACTGGA AAGCC

Marker	Pos	A1	A2	Seq 1	Seq 2	Sequence
WI-11222a	25	C	T	GCCACAGTGG AATCATTTAC A	TTTTAGCATTT GCTGATTTCG	AGCCACAGTGGGAATCATTTACACTA[C/T]GGAAAATCAGCAAATGCTAAAATTGGGGCTTTGGATTTT TGTTTTTGTTTTTCCATAGACCCCACGTTGAACTATTGTAAACATTACCAGCATACCACTGCGG CTGGGTCACAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTCACAGGCTACTGGA AAGCC
WI-10775	39	C	T	TTTATGCCATA TTAATTCATTA CACTC	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTGTTTATGCCATATTAATTCATTACACTC[C/T]ACATCATATTTCTTAGCAAATACA TCTAGACACCTGGCACTCAGTAGGGATAATCCTGGCACGATAATCATTGTATCATTAGACATTGCA GGAACCACCATATGGATGGATAAATGTTGTTGTTAATGAAGGCAAGCAATTA TTGCATGCATTTATACGAAAGGAATTAAAATATCTTCCTTATAGTTGAATTTAAGTAAAAAATAAA GTTATACATATAATACAAAAAAGTTGTAAGTATAGTAACAAATGAATTAGAAAATTGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA[A/C]GACTATAGTTGCTAAGGATATTCCACAAATTAT TTCATGA
WI-11226	165	A	C	...	...	...
WI-10778	62	A	G	GCAAGGGAGG AACATTTACA G	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAAACGTAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG[A/G]G TCCATCTCTGATGTCACCAGCAGGGCCAGGAAGGGGTTGATCTGGAG
WI-10789	21	C	T	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGGA	TGGGACACACTGCTCTAGACC[C/T]TCCCAGGGTCCCTCAAAGGTGGGTGTAGAGGCCCTACTGCCCT GCCCTGGGGACGCAGAGGCATCAGGGCTTAGTCCTCTGGGGACAGTGAAAGGGCCACCACC
WI-10810	58	C	T	CATCTTCATGG GCAGGAATT	CAAACCCTAAG AAACACAGAA ATG	ACAGAAAAATGCCTAGGTCTTGTAGCAAGAGGAGAAAGCATCTTCATGGGCAGGAATT[C/T]CATTT CTGTGTTTCTTAGGGTTTGTGGCTGGCCATCAGTTCAACTCAGCCCCTGTCCCCTGATCCAGCCAACATT TCCGTAACTACCCCTCTAGAAGTCATGCAAAGAGAAATGATGA
WI-10828	23	T	C	...	...	GGACCAAACAGAATTACTTGGCAT[T/C]AGGGTTTCTTAAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACACATGTGATGAATATTTCTTAGTAGAG GACTTCTAAAAGGCTATAAATCTGATTTCTGAGCAGGAGGGCAGATGAGAGAAGCATGTGAGT AGGGCATATCTAA
WI-10832	91	G	C	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	TATGCCTTCCCAACGAGCCATCCACGCTGCTCTTAGCACAAAAAATAGAATACATCATTCTGAATG GGCACATTAATCTGCAGGCTCTCC[G/C]TTTCTAAGTCACCTGCAGTTAGGTCTGCGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGGAGGGCAGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGTTCGG
WI-10834	96	C	T	AGAATTAACT GTTCAAAAGT GTGTTAAT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAAATTGCCCAAAGACCATTAACAAGAGATTTAATAGTTAAAGCCAAAACTATA AAGAATTAACTGTTCAAAAGTGTGTTAAT[C/T]CTTAATACCAATTTTATAGGGCCACCATTAACTT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24	T	C	...	...	GGATGATGTTTCTGTGGTGTCCCTTTA[T/C]AAAGCCTCTTGCATCCCAAATGTGTAAATTATTATTTCT TGGTATTTCTCGCTCTACCCATAGTCACCTGTCAAGTGTTCCACCCT

Name	Pos	A1	A2	Seq 1	Seq 2	Seq 3
WI-2296	81	A	G	TGTTACTTTGA TTCTTTGCTCT GA	GCAAATCACAC AGCTAACTGG	TGGAGGGGTTAGAAATGCAGGTGGCATCCTAGAAGGTCTCAGGCTTTAGAATAAGTTGTTACTTTGA TTCTTTGCTCTGAC[A/G]CCAGTTAGCTGTGTGATTTGCAGAAGGTTACATTTGTTGTTG
WI-2300	77	G	T	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGTCTTCCCTGGAAATTTCCTTTATTGAGCGGGGCAGGTGGTAGGCACAGAAGC CAGTCATAC[G/T][T]GCTTTAAAGCA
WI-2371	55	G	T	GTCTGTGTCTT CCCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTCCAGGGAAAGGTCTGGTCTTGTTCTTCCCAGCTTCT[G/T]GTGGTGGCT GTCAATCTTGACATTCCTTGCGACGCTGTATAATCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCCGTGTGTCGTG
WI-2395	122	A	C	GAACATATTT GTAGAAAAAT TACTATCCAA	TCACCTTCTA TTTATTCTGAA TTCA	GGGGGCACAATTTAGCTACAGTGCATATTAAAAAGATAACATAGAATATCATAATAACTTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTACTATCCAA[A/C]CTGAATTC AGAATAAAATAGAAAGGTGAATCATCTTATATCATTAAAGAAGCTAAATTATTAGTAACAATCTTTA CATTTACACAAACCCA
WI-2437c	192	G	A	...	...	CACCAGCGCCACCCTACAAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAATTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCCTTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179	G	A	...	...	CACCAGCGCCACCCTACAAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAATTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCCTTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128	G	A	...	...	CACCAGCGCCACCCTACAAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAATTCCCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71	G	A	GCAACCTACT GACAATTTAA TTTTAGTT	AACAACTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTTCCTTAGACCCTCCAGAAAATAATGCAACCTACTGACAATTTAATTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123	T	C	TGTTTAGGAA ATAATGACAA GAAAAA	TGGTTACAACT GTACCAAACAT G	CTGTAACCTACACACATCCTCCTGTAACCTCTAGGTTACTTGTAATACAAAACACAATGTAAATGCT ACATAAATAATTGTCATACTATATGTTTAGGAAATAATGACAAGAAAAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCAGCCATTTTCCCCAATATTTCAATCCACCAGTTGGTTTAATCCACAG AAACCACGAATG
WI-2886	46	C	A	CAGAGTCTGG GGGAGGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAGAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGGAAGA[C/A]AACGAGATAAAGCATG GCAAAGACCACGCTGAAAGTATCCCAGGGTGCTGTATGTGCACATAGGAAGGATCACTTACCTCAGCA TAGGAGGAGGGGCTAGGCAGGTGCAAGGAAGTGTCAGAGAAGAAACAGAGGAGCGTT

ID	Position	Allele 1	Allele 2	Left flank	Right flank	Sequence
WI-2906b	77	T	A	---	---	CCTGAACACCTGGAGCACTTCCCTCCCTCCCTTGGACACCTTCATTCTTGCTGGAATGCTCTTTCCCTCG[T/A]AGAGCTTGCTTGGCTGGCTTACTTTTCTTTTCCTTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTGCTGACCAACAAA
WI-2906a	50	A	C	GACACCTTCAT TCTTGCTGG	AGAGCATTCCA GGCAAAGT	CCTGAACACCTGGAGCACTTCCCTCCCTCCCTTGGACACCTTCATTCTTGGCTTGCTTGCTGG[A/C]ACTTTGCTGGAATGCTCTTTCCCTCGTCGAGCTTTGCTTTTCTTTTCCTTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTGCTGACCAACAAA
WI-1736	175	C	T	---	---	TACTCCTCATTCCTCATGTCCTCTAGACGTACTCAGATTTCCATGCCCTGAAACATTTATTTCCTAAATTAGATTTCCCACCCCCAGCACTATTACACAGAAAACAGCAGTTTGGAGTCTGGCTCTTAGAGAACTTACTTAAGGACAGTGGTTTTCCCATCGTCGTCTTCCA[C/T]AGAGATCTAGGGTGTCTTTGGAACCACCTTGG
WI-1851	136	G	A	GCATTGAATT AACTATAGAT GTGTTAAGTA	CACTAGCAATG TTAAACTGAAG TTG	AATACCCCACGTCCTAACACCATCCAACTGATCATCAATCAGGTTTTAACATATTAATCTGGGGAGGACACAAAACATTTAGACACATGCATTGAATTAACTATAGATGTGTTAAGTAATTAATATTAACATGGTA[G/A]ACAACTTCAGTTTAACATTGCTAGTGATTCCATGTGGATACCCATGTACCTTCTTACATCATGTGA
WI-3000	62	G	A	CCCAAAACAC AGAGACCCC	GCCACTATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTCAGCACCCAAAACACAGAGACCC[G/A]AGAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
WI-1754	177	G	A	TTTTCTCCCTT CTTAAAGAGA TAGTC	AAAGTCGAATT GCCTCTGG	ATGGATCTGCTGCTCAATTATAGTCCCAGATAAACAGCCCTTCTCCCCGCCACCCCGGATTATTTACTTAAGGGTTTAGCAAATTCACCTGACAAAGAGTTAGGTTCAACATTGACCCTCATAAAGTGATTTTTTCTCTTTCTGTTTGTTTCTCGTCGTTCTTAAAAGAGATAGTC[G/A]CCAGAGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37	T	A	AAATTCAACC ACAGATCTAT TAGATTC	TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAATTCAACCACCAGATCTATTAGATTC[T/A]CACCCATCTCAAAACTATCACATCAAAGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140	G	A	GTGGAGTGGGC AGATAAAGA	TCACTCAAACT AGGGCTTGG	CAAGCACACATTCAGGCAGTGGGCAGTGGGCAGTTGGGCAGTAGCTTGCGCAGCAGAGAGGAGGAAGAAGTTCAGACCGGTTGGGTAGGATAAGTGGATCCAACCCCTTTGTAGGGCAGGTGGTGGGAGTGGGCAGATAAAGA[G/A]CCAAGCCCTAGTTTGAGTGACACTGTGGGATTCAAG
WI-1775	47	C	T	CCTGCATGGTC TTTTCTCTG	AGTTGAGATTT ATGACAATGAT GTAAA	ACTCCACCAACAGTTTGTGAGCCAACCCTGCATGGTCTTTTCTCTG[C/T]TTACATCATTGTCATAAATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55	G	A	AGCATATTCA TTGATTTCCTT ACAT	GAGGACTTAAA AAGGAGCATTT G	CTGCCCCTTTTACATCCAAAGCCAGTTACTCGAGCATATTCATTGATTTCCTTACAT[G/A]CAAATGCTCCTTTTTAAGTCCTCAACTTTAAAGCGGAAGTTGAGACACTAGAATTCCTTAGGA

ID	Pos					
WI-3416	33	C	T	CCAAGTTGTA GCATTCAGAA GTC	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCCTCCAAGTTGTAGCAGCATTCAGAAGTC[C/T]CTCTTAGAGAGGTAGTTGTGCTCGTCGTTAAAA TATGTTTTCAAGATAGTAGTATCTCCCTGTGTCACTTCCTCCAAACAACAAGTGTACCAACAGCATTGTTAAG GAAATGTGCAATGCTTGCTACCTGCTACCTCTGACGCACACAACATAAATCCCATGAGCCCATCAGAG
WI-3453	70	C	T	TTCTTAGGCCC ATCAGAGAA	TCAATTTTCCC CATGGACTTC	TCCTATTCCTACACAACACAGAAATTTAACAAATCAGCTACTCTTCTTAGGCCCATCAGAG AAT[C/T]GAAGTCATGGGGAAAATTGATGCCATGTGAATTGGAGAAACAGACAGGCATATGGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109	G	A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTGAACAAACTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTATTTTAATGAGGTGGT[G/A]TGGGAGAAAATTGATGGTTGCG TAGTTGAGTTTTCTGTCCACC
WI-3474a	90	A	G	AGTCAGTTTCC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTGAACAAACTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAG[A/G]TGTATTTTAATGAGGTGGTGTGGGAGAAAATTGATGGTTGCG TAGTTGAGTTTTCTGTCCACC
WI-3502	79	C	T	CCTGGGTTTCT GGATGTCT	GGGTGACCCTG TCCTCA	TTTGACCCCATCACATGAGAATAAACCATAAGAAATGGTGGAAAAAATAAAACGGGAGAGAGACCTGGG TTTCTGGATGTCT[C/T]TGAGGACAGGGTCACCCCAC
WI-3600b	146	G	C	GGTTTCTAACC TGGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCCAAGTTCTGCGCAGCAGTGTCCTGACTCCTGCCGTGTTCCAGAGTCTGATTATCCATGCCCCTG ATAGTTCTGTGAGCCACCTAAACTCGTTCCTGCTTAAGTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCT[G/C]ATGGAAGGCTGCACTGGATGAGGTCACAAA
WI-3600a	78	T	G	CCATGCCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCCAAGTTCTGCGCAGCAGTGTCCTGCCTGTTCCTGACTCCTGTTTCCTGCTTAAGTATCCAGAGTCTGATTATCCATGCCCCTG ATAGTTCTG[T/G]GAGCCACCTAAACTCGTTCCTGCTTAAGTATCCAGAGGTGGTTTCTAACCTGG ATATAAACATCTGATGGAAGGCTGCACTGGATGAGGTCACAAA
WI-3678	125	G	T	---		TAAATCATGCTTATTTTTCACAAGGTAATCCACTCACAATAGGCAATTGATGTGATCTCTTCTGTAA GAAAAGCTCTCCATGCTCTTCCTGAACCTTCTACTGTCTGTTATGATGCACCT[G/T]CTGTTTGG ATAGATGGTTGATAGGAGATGGGTTGTTAAAGACACAATTACCTTGTGTTCAGGCGAGAAATAG ACTCTCTCTGTAATCACTGAATGAGTTCCAAAAGCCTTTATGTCTTAC
WI-3687	67	A	C	---	---	AAAGCGATGTTGAGATACCACCATTCCATGAAAAAAGTAAAAAACACACACAAAATATGACATAAAA T[A/C]AAAAACTACTATAGTTTATGAAAAATGACTTCCAAAATTCAGAGAAAAGTCACTTAAACAGG ATTCTCAATTCATTCCAGAATACTCCTGTCATTCTTAACTTTGACTGCACAG
WI-3735	72	T	C	CCTCAGTTATG TATCAAATGA AAAAC	GGCTCACCAAT CATTGTTTT	TCTAAAATGTGAAACCAAAGAATCCTGACACGACCTAACTGCCAGTCCTCAGTTATGTATCAAATGA AAAAC[T/C]CACACCGGTTCAATGAAAAAAACAATGATTGGTGAGCCATGTCCCCTTATTTAATGAAAA GATCTTGGGCAATTAACTC

ID	Pos	Alleles		Flanking	Sequence
WI-1819	51	C	T	...	GAAAAAGCAGGAAGCCAGGCAGGACAAACTTTTGAAAAAGTCTTTCAGCAC[C/T]TTCGTGTGGATCCG AATTTAGTGTGATTGGCAGGCAATGCGGGGTAACATGTTCCAGTGTTTAACTTGCACAGAATTGC CAGAATAGCGATTGTTTGACTTGTCCAATTAATGAAATGTGAAAAAAAAGGGGTGGTAACTGTT AAGCCTGCTGCAATGTTTAGACACGATGTTTGGGGAGGTGGAATACC
WI-3746	116	G	A	...	GGCCTATTCACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCCAGGAAGATGGTTGTCTCATCATCTCTGTCTCTGC[G/A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T	C	ACAGTCATTT AGTCTTCCTGA CAA / TAAGATAACC ATACTAGGTAC ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGAACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAGTGGAGAAGCCAGCATTCTAATCAGCTCAGTGATCTGCCAAACCAACCCTTCTGCTATAG CATC
WI-3898	25	A C	G	TGACCAATGTC TTTAGAAGCA G / TCGTCGGTGTC CTCTCC	CAATGACCAATGTCTTTAGAAGCAG[A/C]GGAGAGGACACCGACGAGAGACACAGGAAGGAGGTGAG GTGAAGATGAAAGCAGTGTGACGCGCCACAAGGTGAGGAAGAGCAAGGGTTGCTGGCCACT
WI-3901	114	A	G	...	GGACCATTGTCCCTCAGAAGTACATTCAAGCGCCTGGACCTGCGTCCTCACACTGTGACCTCAGGCA AGTCATGTCTGCTTCCTGCAACCTGCCTCACCTGACAAGTGC[A/G]TATCATGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	99	C T	C	TGATTCTTCTC AAGACTCACA CC / TCTAGAAGCAA TGAAGGATGG CAAAAGAG	CTGAGGAGATTGATGCTACTTACCTGAGGAAACTTTATTACCTCCCCTGAGTTTGTTGCCTTGCAA GACATTGCTGATTCTTCTCAAGACTCACAGC[C/T]ACCATCCTCATTGCTTCTAGACCTATAACTAG ACTCAAGTCCCAGCAGCCCTTAAAGGTAAGGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G	A	CCAAGAGCGT CCTATGAATC A / AACAGCAATA ACAGGAACAA ATG	CCACTCCCAGGCCAAGAGCGTCCTATGAATCAT[G/A]CATTGTTCCTGTTATTGCTGTTCACAGAGT GGCAACTCTTGCAAAGGGGAGGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84	A	T	TTGAGGTCTTA GTCATTGCATG ATTGTT / TGAGTTCCTAT TAAGTGACAAT	TAATTCACATTGCTCTTGTTTGTGCATTTATTGCTCTCTTATGTGAAACACAATCACCAACATTGAGG TCTTAGTCATTGCATG[A/T]TGTATAAACAATATTGTCACTTAATAGGAACTCAAGCATAGTATGT ACATTTATTGCTAACAGCAG
WI-4160	117	A	G	CCTATAATTTA GCAACAATAT CAACAGAA / TGCAGGTAGAA TTTTCTAATAT AGCC	TCCTCTTCTGTGTAATAGGAAGTCTGATTAGATGCCTTTGAGGTTAGGTTGGCTTCTAAGATGGTAATT ATCTGTCCAAGTTTTTGTTCCTATAATTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	32	A	G	GGTGAGAGTC AAATTGATAC AAACA / ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGGAGAGTCAAATTGATACAAACA[A/G]TCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAATATATACCAGCAGTGTGGTCTAGCAATTCACTGCTAGCATTACCTTACCTAACATAAATGAT

ID	Pos	A	B	Probe 1	Probe 2	Sequence
WI-4177	68	T	C	TGAATAAGCA CGTATTAAATT CTACCTA	AAGGCAGCAA ATCATGATG	ATGCCTGGCGATATACTTTCCAAATGACTAGTAGTATGAATAAGCACGTATTAAATTTACCTATTATATTTA[T/C]CATCATGATTGCTGCCTTCTTTCCAAATTTACTACAAATTGTCACATGAGGCACATGATCCCATTAACCCAAATAG
WI-4199	51	A	C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAAACCACTCCCAAGTTAGTCAATATAAAAAA[A/C]CACACATATTGTTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAAACAA
WI-5163	24	C	T	CTGTCACTGGT CTGCCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCCACTGGTCTGCCTGT[C/T]GGTCTGTTCCTTTCAATGTTCAACTGCTTGTATCTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGGGCCTTTGTAGACCAGAGTTTTCTTGGAAATTGCAACATTTGGGCAT
WI-4250b	117	A	G	---	---	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAAGTGCTAAAGCAGTTTAATAACAGGTTCAATATGAGTCTTGTGAAACAGGGGTGGGAAGGATCCTGTAAAAGG[A/G]TAAAATATTGTTTTCCATAATAATTGAAGATGTG
WI-4250a	94	G	T	TCAATATGAG TCTTGTGAAAC TAGG	CTTTTACAGGA TCCTTCCCAC	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTTCCACCAAGTGCTAAAGCAGTTTAATAACAGGTTCAATATGAGTCTTGTGAAACAGG[G/T]GTGGGAAGGATCCTGTAAAAGGATAAAATATTGTTTTCCATAATAATTGAAGATGTG
WI-4255	68	G	C	TGCTCCCCCAT AGTTGTGTAAG G	GGCCTACTTCA	TAAATGTCCTGGGGGAGATAATAGGAAAGGTCCCATCCCTCTGATACCTTGGTTGCTCCCCATCACCT[G/C]CCTTACACAACTTGAAGTAGGCCCATCCAAACACTGGTCAGAAGAGTAATACTGTCGAC
WI-4256	57	C	T	---	---	ACAGCCTCTTCAAATGGCACAATCAAAAGCACCAGTAAAAGCAGAGGCAAAATCTGG[C/T]CTCACCATTGGAAAGTCTTCTGAAGGATAAGGGAGTGAATGACTAGCTAGAAGAGAATGATTGGCCTT
WI-4325b	71	C	T	---	---	AGTTCACTGCTGCTAGATGAGTAGACCATGTTGTCTTGTTAAATGTACATGGGCAGGAC[C/T]GGAAAGATG[C/T]TACTATAGATAATCTTTTTAAATGACTCTTCTTGGTCTTCTTCAAGATATCACCAGCCACCCAGGACACTGCCATATCT
WI-4325a	58	C	T	---	---	AGTTCACTGCTGCTAGATGAGTAGACCATGTTGTCTTGTTAAATGTACATGGGCAGGAC[C/T]GGAAATGGGATGCTACTATAGATAATCTTTTTAAATGACTCTTCTTGGTCTTCTTCAAGATATCACCAGCCACCCAGGACACTGCCATATCT
WI-4347	158	A	G	---	---	TGGGCAGAAGTCGGGTATGGCAAGTCAGGGTGGGTTAACTTGGATGCCACTTCTGCCTGTCACCTTCTCTAGACTCTTGACCCTGCGACGGAGGATCCCTGGCCTCTGAGTTTTATCATCTCCCACCTCCAGCCCAGGGCCCTGTATCTGTTCAGGCCCC[A/G]GAATCGTCACAACTGTGGGAGGTAGGAATGACGAGG
WI-1936	117	T	C	---	---	CCAGTCTCTAGGCTGCAAGGACTCAATTCTGGGGCAAGTCCTGTGGTTGTGTCGCTAGGGTCAGAGGCGCAGCGACCTGAGGGGACGACACACAAACCAGTGGGACACCAGGGGTACTTGTATCACC[T/C]CTCCCGCAACCCCAAGCAGCACAGCTTGCAGCTCCAGGAAAGACTCCTTACTTCCACTTGAGAAAGGAGAGGGAAGAGAAAAGAGAGGACTTTGACACACAACTTGGA

Marker	Pos	A1	A2	Left flank	Right flank	Sequence
WI-5204	54	C	T	...	...	TAGATTTGATTGATGACAATAGGGAAGGAAGCCTTTGTTGTTAAATTGGGTTTGAAAGAA[C/T]GAAGAAAAATGGAAAGGGAAGAATTGACAGAAACCAAGAGAGTGTTGAGGGGCAGCAAATCCCAGTTTGACTGGAATATAGAGTGATGTCAGGGTTG
WI-5215	70	A	G	AGATAATTTTG TAAAGATAGTT TTCGC	GGACCTTAAT ATTTAACAGA CTCAAAAA	TTTCCCTTATTTATTTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAATAT[A/G]GCGAAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTAGCACATTTCCTGTAGTCAAGGTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112	T	G	TTGTATCAAA GAGATGGGGT ATATAA	AATTAAAGAA ATCTTTACATG GTTCTTT	CCCTGAAATGTGCTTTGCTTCTCCTCCAACTCTCTAGGGAACTTTTCCATGTCAGGTGAAGGTTTGAAGAGTACTTTAATTAACTTGTATCAAAGAGATGGGGTATATAA[T/G]AAAGAACCATGTAAAGATTTCTTTAATTAGTGAATTTCATCAGGGCTCTTCCACTGTCTATCAGTAAA
WI-4456	49	C	T	AGTTGAATTA TTCAGAAAAT TATAGTTCC	TTTCCTGTTAT GCATGAACTTG	ACACATTTCATTTGCTTTAAGTTGAATTATTCAGAAAATTATAGTTCC[C/T]CAAGTTCATGCATAACAGGAAACACCAGGTTGGGGCAATTGAATTGT
WI-4461	49	A	G	TCACTGTTATT TTAAAATTAT CCTTCC	TTTGACCTTC ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAAATTATCCTTCC[A/G]TGAAATTGGTGAAAGGTCAAAGAATGAAATTCCCACTTTAGATTTCTTGGAAATTTATTTGCGATGATAATGCAATGGGC
WI-4465b	75	G	A	...	...	CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGT[A/G]TATAAAAGAAAACAGTTAGTAATTCACCTTT[G/A]ATATTCTCTTTCTGTATTCTCTACCTCAGGGAATC
WI-4465a	41	A	G	AAGCCAGACA ACACGAAAGT	GGTGAAAGATT ACTAACTGTTT TCTTT	CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGT[A/G]TATAAAAGAAAACAGTTAGTAATCTTTCACCTTTGTATTCTCTTTCTGTATTCTCTACCTCAGGGAATC
WI-1949b	160	T	C	GAGTGAATAA ATGAATGCCA TAATC	TGAGAGGTGGG GACAAAAA	GGGGTTAGGACCTCGAGATCTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCAGTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGTCATGGCTGCTGAATATATGTGAAGAAATAAAGGAGTGAATAAATGAATGCCA[T/C]CTGTGTTTTTGTCCCCACCTCTCCACCTTTCCCTGGCACA
WI-1949a	86	T	G	CAGTGGTGAG ATGCTCTGAGT	CCATGTCAGCA GCCTTG	GGGGTTAGGACCTCGAGATCTTTCAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCAGTGGTGAG[T/G]ATGCTCTGAGTTCATGGCTGCTGACATGGTCATGGCTGCTGAATATGTTGTCCCCACCTCTCCACCTTTCCCCTGG...CACA
WI-4529	64	T	C	CCAAGTAAGT CTATCATTCTG AAGATG	TTCTAAAAATA ACACTTCCTGA AAAA	TGAGAGAGTTTTTGGATTATTCATCTCTGCAACACTCCAAGTAAGTCTATCATTCTGAAGATG[T/C]GAGTTCTTCTTTTATATCCTATGATTATTTTCAGGAGTGTTATTTTAGAATAAAACTCCTGGGTCCCATCCCAGGTCCAGGGTCAAGAGATGGGCCCTAGGATCATTT

Name	Pos	Allele 1	Allele 2	Sequence
WI-4540	110	A	G	AGCTTTTCCTTTCTTAAAAATTGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTATTGCTCGGTAACAGTACTTTGCAATAAGCACCATGTGGCATCC[A/G]TGCATGGCTGCATTGTCCAGTCAAATGAGACAACTTCCTAT
WI-4582	226	T	C	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAAATTCACCAAACACCACCTGCTCCAAATGTCCATGTTAATGCAATTAGGGAGACTCCAGTAGCATTCAAGGCCAGTTAACTTATCCTGTACACAAATAACTTTATGGGAGACAGCATTGTAATTCAAATCAATAAAATGACTCGGTTGGCTGTACAAGCATAAACAGAAACGCTTGCAAAATATGGTT[T/C]CCTCCTTGCTAGAAACCATTTGAT
WI-1965	105	G	C	CAAAGGTTAGTTAACTTGGGGGGCAAACACAAAGTTATGAGTACTCAATAACCTATGTTCAAGGGTAACCAACACCTTTTGCCATTGAGGAAGTGTTTAAAG[G/C]AGAGAGATGACCCATTCCTGGGCTTCTTATATGACACCATTCCCACACAGATGTGGAGTCATTTATTTGGTTGGTTATGACAGTCATGG
WI-5248b	99	C	T	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTTGAGCAACCCAGAAAATTAAAACGCCTACCATTTTCACTGTTTTCTATTGACCGTACTG[C/T]TCTTGCTTTTTTTCCCTTCTCTTTTCTGCCCTCTTTAACTATT
WI-5248a	38	G	C	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGTTA[G/C]AGCAACCCAGAAAATTAAAACGCCTACCATTTTCACTGTTTTCTATTGACCGTACTGCTCTTGCTTTTTTTCCCTTCTCTTTTCTGCCCTCTTTAACTATT
WI-4596	69	T	A	CATTGGTGGGTCCAACTTCTCCGGTGACATTACTCTGTTGACTTGCTCTGAAGCAGCAAAGCACTGTGAC[T/A]CATTATTAGGCCCATCCTCCTGAGCCGCCTACAGCAATTGTAACATATGGCATGGGACATATCTCGAGCCCATCAAACTATTGACAAGATTCTCCTTTTAACAA
WI-5252	119	A	C	GAAATAGGGCAAAATTCAATATTAAGAGTCTTGGGAAAAGGATTGTGATGATCATTGAATCTGTTTAAAATACAGAATTAATAACTGAATACCTGTGTGAATCATTGTCTTT[A/C]TACCATGTACATATTATATGAATTAACAATGTAAAATAGTAGTACTAAAGAAAATATTGGGCCCT
WI-4606	61	A	G	TGCAAAAAGGAAAAATGATAACCAGGACTGTTGTTCAAGCAATGCTAGAAAAATTATGCCTA[A/G]CCAAGTAGCAACTTAAGCACCTAAGGCAGAATGAAAGTTTCTCTCTGTCATTAAGTCCTCTATTCAATTACCATTTATCGGGGTAATTAAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAATTACACGTCTTTGCTATGCT
WI-5257	77	C	A	CAATGAGAAGTTACCAGATGCGGGCAAATTAAGCATATGAAAATACCAAGTGTTGGCAGAGGCATGAAGCAAAGAGG[C/A]CTTTCATCTGCCCCTGGTGGTTTTCAGTAACTGCAACATGTCTTTGCCTCCCGGATGAAAGATACCCTTCTATGACTCAGCAATTCCACTCCTAGGTATGCACCCTAAACATGGGTGGCAAAT
WI-4649	50	C	T	TCACTGTTTAGAAAATTTCTTCCTCCTCCAGTGAGACCATTCTTCCGAATG[C/T]GATGATTTCTTGTAAGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGCTACCTGAATTGTATTTTTTAAAAAATCCTCCCAATATTG

Clone	Pos	A1	A2	Flank 1	Flank 2	Sequence
WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT	CTGAAGTGTTA AACTGGATTTG	GTCTCTT G — AACTGTGTGGTATGTATGTTTGTTGTATTTTTCTGGAGAGTCAGTTACTCTCCACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTAATCCTAGAAGCACAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTAACACTTCAGTAACGTT
WI-4677	82	T	C	TCCAAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	CTT — AATTCAGATTTTGAACACATGTCGACATTTGGAAAAAATTGTCCAAAGTGATTAGGTGAAAAAT GAGTTGAAATAAATG[T/C]AAGTTGAAATAATGACACTGTTGAAAATGATGAATCTGCTTTCAATTCA CATGGAAAGGAGACTAGAACACAGCAGGTTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGTCTATCATGAGGAATTCTGTGAGAAATTTTCACCTGGCAATTGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTCAGTGACATTCTTTCTTTTGACGGAAGAAAACTTCAA[C/G][TT]CGAGAAGGGCTTAGATTATATCGGCTGAAGCCCATTCTG
WI-4722	88	G	A	TGCACTATGG AACACCACAC G	AATATGGAATC TGCATTCAGTT G	CTTCCCATTCTGCCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGGAGATTTATTTTC TGCACTATGGAACACCACAC[G/A]CAACTGAATGCAGATTCCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAAATGGAGCCATGTAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCACTTTGATGGTTGAGATTTCAGAAAACGTGAAATTATTGAGTAACCATGGG TCAACTATGAT[C/A]CAAAACAGCAGTGTTGTCTAAAAAATATGATAGTTTCTCTCCTGTCCACC GCAATGAAAAGGAGTT
WI-2028	176	T	C	TGTTTACGTTC CCTGTCTCATC	GGTTGGAAACT CAAATTACCTA GAA	GAA — GACTACAGCGGCACAGACAGGCATTGTGTGGCCTGCACAGGTGTTGGTTTGTTTGTTGTTTAAGTTAGATT TGAATCCTTAAAGAGAAAAGTGGCTCTTCAGTTACTACAGACCTCATCATCCTGGTTCTCTTG CACCCCAGTCCACTGTTTACGTTCCCTGTCCATC[T/C]TTCTAGGTAATTTGAGTTTCCAACC TGTGG
WI-2033	183	T	C	GGGGTGCTAGA ACTAATCCCTC A	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGCTCCACATTCGCGAGATTCAACCAACTATGGATAGAAAATATAGTATTCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAATTTCCAAGGTTATACAGGACCAGTGTTGGAATTT AGCATTCTGGGTTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGAACGTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGGTGGAAGGACAAGAGTTGAAGCAAAGGACAAAGGAGATCAACTGGG TAGAATAACTTATATGCATCGATCCACCAGGCCTCCTTCCACCATTCTCCATCCTCCTACTTTCTACTCTGA[T/C] AGGCAGACTTATATGGAAAAAGGGA
WI-2034	150	T	C	CCACAGTGCA CCAAGGAC CC	GGGTAAAGAT AGAGTGCGAGGT	CCACGACTATGTCTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCAAGA CCTCCTTCTGCGGGTTTCAGTGAAAGACGATGAACTCCTTCATCTTCTCACAGCAGCTGGACTTCACCA CAGTGCACCAAGGAC[T/C]GGACCTGCACTCTATCTTTACCCCTTCCGACACCAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C	T	TGTGCTTTAAA GTGTGTAAGT ATTAATTAG	ATTCCTCTG AAAGAAACAT CA	TCAGGTGACAAGAAAAGTCACATTCTTCAATCACTCACCATTGTCTGTTATTGTCTCTTGCAGTGT ATCCAAGGATGTCACTTTGGAACTCTGTAGATCAGAAAAACTGTGCTTAAAGTGTAAGTATTA ATTAGATTCTATTTGATA[C/T]TGATGTTTCTTCAAGAGGAAATTTGTGTAAGAGGATTCCCATT TGCATTCCATTGGC
WI-4782	113	C	T	GATGCAGAAG ATAACTAGAA AATGC	GAACTCTTCTG GTTATTTTTCT GTTC	TCATTGACTTTTAGAGTTCCTTCAGTCTTTATGTCTTATTTCTTTAGGAAAAACTAGGCTAGGAGAA CACAATTCAGGTTCTCTCCAGATGCAGAAGATAACTAGAAAAATGC[C/T]GAACAGAAAAATAACCA GAAGAGTTCATTATGGTTTTTTCCAGAACGATTAC
WI-4788	65	A	G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAATT AAAATTTTGGC ATAA	AGGAGAGTTTTGGCTCTCTTTCCGGACTCTTGGAATTCAGTGCATAGAATCATCTTGCTAAGTTCC[A/G] TTGAAAAAAAATTATGCCAAAATTTTATTTCCAAACTTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
WI-5300	38	T	C	TCCCAGAGAC CACTTCATTC	CTACTCTTTCT ATTTCATAATC CAAAAA	CTTACTTCCAAAGTGTTTTCCCAGAGACCACTTCATTC[T/C]TTTTGGATTATGAAATAGAAAGAGT AGGTGTTATTATTCTCTTTTACCAAGGTGAAATTGAGGCTCAGAGACAAGGTAGATGAGAGCCCA AGGTCAGTGACAGAGCCA
WI-4818b	121	G	T	TGATAATGGG GCCCTGTT	CCTTCCTTTTA TATGTATGCCA GA	TATAATGTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAAACAATCTTATATA ATAATTATTCAAGAAGGAAATATACATATGGGGTGATAATGGGCCCTGTT[G/T]TCTGGCATA CATATAAAAGGAAGGCTAA
WI-4818a	43	A	G	TTGCCATAGAC TAGGTTATGTC C	CATATGTATAT TTTCCTTCTTG AATAAAATT	TATAATGTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCC[A/G]CACATGAATAAACAATCTTAT ATAATAATTATTCAAGAAGGAAAAATACATATGGGGTGATAATGGGCCCTGTTGCTCTGGCATA CATATAAAAGGAAGGCTAA
WI-5317	139	T	C	TTCCATTTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTTCCATTTGTTGATTCTTTTTGTCTGAGCCCTTAGAGATCTCCTTTAAAATTAATAGCAAGGTTAAT AATATAATAATGATGTTATATATACAATTTCAACTCAACAGGAATTCCATTTCTGGTAGCAGGT ATA[T/C]GGGACTCATTTCTTTCTTTCTTTGCATCTATTTCTAGGTTATTTGCAGCGCCGAGATCTACCCAGG
WI-4888	56	G	A	GCAAGATATA AAGATTAAGA AAAGATAACA CA	CAATTCCACTA CCTCATTTATT CA	AAATGAGTAACCAAGTTACTCGGCAAGATATAAAGATTAAGAAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAATTGCTTGATAAACTGGAGTAGTGCCTT
WI-5328	44	A	G	...	...	AACATTTTTAACCATGCTACATTTACAAACACTGAAAGACAG[A/G]AAAAAAAGAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAAGAAAAAATATGAATCAGAAAAGGAAAGAAAT AGAAACACGTGATACTGGAAGGAG
WI-4897	93	A	G	...	...	GCCTTTTTGAGTTTAAGTCTTTTGAGTGGTGTCTTTTTTCCCCCACTAGGTACTCTCGGGCCCAAAT CCCCAAAAGAGAAAATAAGCCGCTTGG[A/G]GATAAACACATCTTC
WI-5345	29	G	A	...	...	CCCTGCTATAGGTCAGTTTTAAAAATCCT[G/A]CCTGCTATGGTTTGCTTGTTGAAGCCACATCCACT GAGGTATATTCTGTCTGCATTTTCTATATCACTCAGCTTCTATATCACTCAGCTTCTATATCACTCAGCTTCTGTTCAGAGATCCACTCCATCAACTTGCAG

Marker	Position	Allele		Sequence
WI-5370	143	T	C	TGCATGTGTTACTTCTTGGAAATCATAAAGGGATCTGAGAGCCTACAGTATATGGCAACATTAACCAAT CTTTTGAAAATTTACCTGTATCCATCCATCGTGTTCATTTGCAAAAAATAAGATGGTACCTTAACTA ATAAAACAA[T/C]TTGAAATTCTCTGTACCAACTTTGCTTTTC
WI-9711b	423	T	A	GATCTCCTTCATCCCTCCCAGAGAGGAGAAGAGGAAACACAAGAAGAAACGCCTGGTGTGCAGAGCC CCAATTCCTACTTCATGGATGTGAAAATGCCCAGGTGAGGAGACGGCTTGCTGTATCCTGATACTCTTAAAATTTGAATG TGGACCTCAACAGTTGGAAAATGTTGTAGTGTTAGCTGTCTGTATCCTGATACTCTTAAAATTTGAATG CAGTTTCTTCGCCTGTGGGAAAATATTTCCCTGATACTCTTAAAATTTGAATG
WI-9711a	390	C	A	GATCTCCTTCATCCCTCCCAGAGAGGAGAAGAGGAAACACAAGAAGAAACGCCTGGTGTGGGGAAAGCAC CCAATTCCTACTTCATGGATGTGAAAATGCCCAGGTGAGGAGACGGCTTGCTGTATCCTGATACTCTTAAAATTTGAATG TGGACCTCAACAGTTGGAAAATGTTGTAGTGTTAGCTGTCTGTATCCTGATACTCTTAAAATTTGAATG CAGTTTCTTCGCCTGTGGGAAAATATTTCCCTGATACTCTTAAAATTTGAATG
WI-9702c	345	G	A	GGAGGAATTTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTTCATTCCAGTGTGCTACAGCATCTGATAG TTATACTAGCTTTAAGAGGTTTCATTCCAGTGTGCTACAGCATCTGATAG
WI-9702b	344	C	T	GGAGGAATTTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCTAACTTTAATGATCTCTGTGACTT AGAGGTGAATCAAGCTGATATTTTCATTCCAGTGTGCTACAGCATCTGATAG TTATACTAGCTTTAAGAGGTTTCATTCCAGTGTGCTACAGCATCTGATAG
WI-9702a	179	C	T	GGAGGAATTTCAGGGTGAATGGACTGCTCCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCTATTCAGCAATTCTCAGTTTATT[C/T]TAACTTTAATGATCTCTGTGA AGAGGTGAATCAAGCTGATATTTTCATTCCAGTGTGCTACAGCATCTG CTTTTATACTAGCTTTAAGAGGTTTCATTCCAGTGTGCTACAGCATCTG
TIGR-A003N21	49	C	A	TATAGTATTTAACGAAGCCTAGAAGCACGGCTGTGTGGGTGGTGATTTGGT[C/A]AGCATATCTTAGGT ATATAATAACTTTGAAGCCATAACTTTAACTGGAGTGGTTTGATTCTTTTTAATTTATTGGGA GGGTTTGGATTTTAACTTTTTTAATGTTGTTAAAATATTAAGTTTTTGTAAAAGGAAAACCATCTCTG TGATTACCTCTCCAATCTATTGT
TIGR-A004V30	203	C	T	AGAATGGCTACTTCATAGGCAGAGCAGCCACTTTGGCTAATTTTAACATCCAAAGCTAATAAAT AATCAAGAAGAAATAGAGAACATTAACAAAATAAATTATGTTCTATTGGGAATACCTAATATCAG ATACTAACAAGTACAGTACAGTGATAAGAATAAAAAAGATAATAATAACTCACACATACCTTCTAGGTTAGTAGA AAAG[C/G,T]CTTCTTAGGTTAGTAGAAAGTT

					Sequence
TIGR-A004W22	232	C	A	---	GGATAAATCAGTACAATAATGGGACCTTAAAACTGCTGTGTGATGCAGGAGTGGAGGGGCTGGGCAGTG CCCGAGGCAGGGGAGGACAGTGGGACAAGGGATGCTCAGTGGTGGAGCCACAGCCCTGGGCTCTGGA TGGGGCATGGGAATGACCAGGTTCCCACATCATGCACAGCA[C/A]CTGGAGATGTCTCTAAAA GCCTGCCCACATTGGTGGTGCTGCCCCCGCCTA
TIGR-A005D24 b	138	C	T	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAATTCTCTTTGAGATAATTGATTTCATATTC TGTGGCTTCAACCTCCATTCCTGTCATCTTGATTTCACTCAAGATGCAGCTCCTAAGATTATT CTT[C/T]TTTCACCATTAGTTTGATTATCATCTGGATTTTAATAATTAAGGAAACAAT GTTATGTTAAATTCATAAAACTCCTTCACCTTTAATAATTCATATTC
TIGR-A005D24 a	123	A	G	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAAAATTCTCTTTGAGATAATTGATTTCATATTC TGTGGCTTCAACCTCCATTCCTGTCATCTTGATTTCATTCCAACATCTTATAGAGAAAT[A/G]AAAACCCAA TTTCTCTTTCACCATTAGTTTGATTATCATCTGGATTTTAATAATTAAGGAAACAAT TTATGTTAAATTCATAAAACTCCTTCACCTTTAATAATTCATATTC
U03735	74	C	G	---	TGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGGAGGGGTCTGGGCCCAGTGCACCTTCCGGGGCC GCATCC[C/G]TTAGTTTCCACTGCCTCCTGTGACGTGAGGCCCATCCTTCACTCTTGAAGCGGAGCAG TCAGCATTCTTAGTAGTGGGTTTCTGTTCTGTTGGGATGACTTTGAGATTATTCTTTGTTTCCTGTTGGA GTTGTTCAAATGTTCCTTTAA
U39840b	42	T	C	---	GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGGAGCAAGAGAGAAAAA[T/C]CAACAGCAAAACCACA CAAACCAAACCGTCAACAGCATAATAAAATCCAACAACTATTTTCATTTTCATGCACAACC TTGCCCCCAGTGCAAAGACTGTTACTTTATTATTGTGTATTACTACAAA GACGGGCCCCAAAACCAATTTTTTCC
U39840	56	A	C	---	GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAATCAACAACTATTTTCATTTTCATGCACAACC CAAACCAAACCGTCAACAGCATAATAAAATCCAACAACTATTTATTATTGTGTATTACTACAAA TTGCCCCCAGTGCAAAGACTGTTACTTTATTATTCATTGTGTATTATTACTACAAA GACGGGCCCCAAAACCAATTTTTTCC
WI-8997	41	G	A	CCCC GCCCCACTTGCT TGTTTGTACGC AGTGCTCA	GTGGCCATCGATCTGGACCGTCCCCTGCCCACTCT[G/A]TGAGCACTGCGTACAAACATCCA AAAGTTCAACAACACCAGAACTGTGTGTCTCATGGT
WI-7008	180	A	G	---	TATACCACTTCCATTTGATGATGGAATGCTGTCTTCATGACCAACTTTATGGCTAGATGGGTCAGAA AGCACCCAGTTCATGGATAGGCAGTTCAGGTCACATATGGTGAACCCAGAGTCAAACATTCAG TTTCCACCAAAGCCCAGTAACAGGCCAAGCCGTGTCTCTCAAAAG[A/G]AGAGTAGTTATCTGCGAGA AGATGGCAGGGCGCCTTGCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACCT
WI-9005	26	C	T	TCCCAAAAGTC TTAAGAAGAA AAA CGAATTTGCTG GGGAATCT	GGTCCCACGAATTTGCTGGGGAATCT[C/T]G[T/T]TTTCTTCTTAAGACTTTTGGGACATGGTTTGACTCC CGAACATCACCGACGCGTCTCCGTCTTTCTCTGGGTGG

Marker	Pos					Sequence
WI-7593	46	G	A	...		TTTTTGTTTGCTCTGGACACCCACTGCTGCTCCCAGGATGAAAGGAGAAAGGAGAAAGGAGAG[G/A]AATGAGAATCAGTTTGGACACTTCCTCTTGAAATAATAAGAATCAACAAGTTACAGTCATGTTGGGGACTTCTCTCTCCAA
WI-6962	78	A	G	...		AGTGCATCTTGGGGGAAAGGGCTCCAGTGTATCTGGACCAGTTCCTTCCTTTTCAGGTGGGACTCTTGATCCAGAGA[A/G]GACAAAGCTCCTCTCTATCCCCTCTCATGCTGAGCTGGTGTATAATCAAGACAGAACCAAGTCTCCTGACTCCTGGCCTTCTATCCCCTCTCATCGATAAACATTCTCCACAGCCTCACTTCATTCCACCTATTCTCTGAAAATATTCCCTGAGAGAGAACAGAGAGATTTAGATAAGA
WI-7059	43	C	G	AAGGCACCCA GCCATC	GCTCCTCGCTG GGTCA	GCAGAGAAGAGAACCATGCCAGGGGAGAAGGCACCGCATC[C/G]TGACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGGTGAAATATACCAAATTCTGCATCTCCAGAGGAAAATAAGAAATAAAGATGAATTGTTGCAACTCTTAAAAAA
WI-9063	53	A	C	CACTTCACTGA AAGACACCAT TT	TCTACTTCTG CCCTTGGGT	AGCAGCCATCACACATGATCTGTTTTCACCACTTCACTGAAAGACACCATTTAT[A/C]TACCCAAGGGCAGAAAGTAGAACTTACTATTCATTAAAATGTTTGACACAATTGGAATTGTC
WI-7079	293	T	G	...	GACAGATTTT GACCTAGTTCC TT	AAGGGGCATTGAGACTATAAAGCAGTAGACAATCCCACATACCATCTGTAGAGTTGGAACTGCATTCTTTAAAGTTTATATGCATATATTTAGGGCTGCTAGACTTACTTTCTATTTTCTTTCCATTGCTTATTCTTGAGCACAAAATGATAATCAATTATACATTATACACCTTTTGACTTTCCAAGCCCTTTTACAGCTCTTGGCATTTCCTCGCGTCTGTGAGGTAACTGGGAT
WI-9074	38	A	G	GGTAAAAGTT CTTTTTGCTCT AAAAG	...	TGGATGCCGAGGTAAAAGTTCTTTTGCTCTAAAAGAA[A/G]AAGGAACTAGGTCAAAAATCTGTCCGTGACCTATCAGTTTATTAATTTTAAGGATGTTGCCACTGGCAAATGTAACTGT
WI-7104b	249	C	T	...	...	GGAGTTTGCCCCCTTCCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGGCTTGACCAGTCACGTTGGGAGAAGAGAGAGAGTGCCAGGAGACCCTGAGGCAGCCGGTTCCTACTTTGGACTGAGAGAAGGGAGCCCCAGGCTGGAGCAGCAGTGAGGCCCAGCAGAAGGGCTTGGGTTCTGAGGAAGCAGATGTTTCATGCTGTGAGGCCCTTGCACCAGGTGGGGGCTCACCAGGTCACCAGCAGCATCTTTGC[C/T]TT
WI-7104	157	C	A	...	...	GGAGTTTGCCCCCTTCCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGGCTTGACCAGTCACGTTGGGAGAAGAGAGAGAGTGCCAGGAGACCCTGAGGCAGCCGGTT[C/A]CAGCAGAAGGGCCACCAGCACCAGCATCTTTGCCCAGGCTGGAGCAGCCTTGCACCAGGTGGGGGCCCTCAGAAGACTCA[C/T]TGCCAGCTCAGCCCTACACCAGTTTCCACC
WI-8974	34	C	T	CCTGAGCCCTC AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCATTTAGTTCATGCAAGGCAAAAGGCAGTGCCATGCAAGCTGTTTAA
WI-9161	61	C	T	CCTAAGCATTG CCTGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTACCCCCAACCTCATTTTAGTTGCCTAAGCATTGCCTGGC[C/T]TTCCTGTCTAGTCTCTCTGTAAGCCAAAGAAATGAACATTCCA
WI-9014c	93	T	C	...		CCCTGTTCCCATGCTGACCTGTGTTTCCTCCCCAGTCATCTTTCCTGTTCCAGAGAGGTGGGGCTGGATGTCTCCATCTCTGTCTCAACTTTAT[T/C]GTGCACTGACTGCCAACTTCT

ID	No.	Allele 1	Allele 2	5' flank		3' sequence
WI-9014b	44	C	T	...	...	CCCTGTTCCCATGCTGACCTGTGTTCCTCCCCAGTCATCTTTC[C/T]TGTTCCAGAGAGAGGTGGGGCTG GATGTCTCCATCTCTGTCTCAACTTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206	C	A	...	...	TCTGAGAGAAATGACTTGTGGGAGACACCCTGCAGATCCTCAGATCTCATGGGTTGTGACAGACCCTGCGTGCT CAGTGCCCTTTAAGTGCATCCGCGTCTGCTGACTTTGAGTGGGATCAACATCTGTCCTTCCCTTCCCATTCAACAC TCTTTTTGGCCCCAGTATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA A[C/A]ACACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56	A	C	...	...	TCTGAGAGAAATGACTTGTGGGAGACACCCTGCAGATCCTCATGGGTTTGTGACAG[A/C]CCCTGCGGT GCTCAGTGCCCTTAAGTGCATCCGCGTCTGCTGACTTTGTTGGACACCTACAGCTTCCCTTCCCATTCAA CCCTCTTTTTGGCCCCAGTATTCATGGCTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA CACACACACATTCTTGCTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54	C	T	...	...	CTGAAATCCCCCTCTCTGCCCTGGCTGGGATCCGGGGGACCCCTTGCCCTTCCCTT[C/T]GGCCTCCCAGCC CTACAGACTTGCTGTGTGACCTCAGGCCAGTGTCCGACCTCTCTGGGCCTCAGTTTCCCAGCTATG AAAACAGCTATCTCACAAAGTTGTGAAGCAGAAGAAAAGCTGGAGGAAGGCCGTGGGGCCAAT GGGGAGAGCTCTGTTTATTATTATTGTTGCCGCTGTTGTGTTGTTA ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAAAGTAGAGATAATAATCA[G/A]
WI-9171	62	G	A	CTAGGACCCC ATTCTCCTATT	TCTAGAGGGTA TATAGGACAGG ACTG	TTCTTTACAACCGATGGTAATTAAGCTTGTATTCACAAGACTTCATGC
WI-9174	47	T	C	T	CCATGTTCCGA AAATACAGGG A	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATTCTCCTATTTA[T/C]CAGTCCTGTCCTATATA CCCTCTAGAAACAGAAAGCAATTTTTAGGCAGCTATGGTCAAATTGAG AAGGCCAGATGCACATCCCTGGAAGGACATGTTCCGAGAAGAAGAACAGATA[A/G]ATCCCTGTATT TCAAGAACCTCTGTGCACTTATTATGAACCTGCCCGTCCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTTCTTAAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-7753	52	A	G	CCACTTCTCCC TCTGACCTAGG T	AAAGGGAAAG	AAAGAACTACAGAGGACGACGATGTCCAAAACAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCCGCA[G/A]ACCTAGGTCAGACTTTCCCTTTCATCTT
WI-9186	76	G	A	CGCA	GGTGTGTGTGG TAGGGGG	TTGGACAAACCTAGAATTTCTCCCTTTATGTATCTCTATGGATTGTGTAGCAATTGACAGAGAATAA CTCAG/AATATTGTCTGCCTTAAAGCA[G/A]ATACCCCTACCACACACCCCTGTCCTC
WI-9193	94	G	A	AGAATATTGT CTGCCTTAAAG CA	...	TTTGGATTGATATCGTGAAAATCCTCAGCCGAGAAATTGGGCTGATTG[C/T]GCTTTGGTTTAATACAT CTTTCCCTAAAGAAGATAAACACAAAATCCATTCCAGGTAGCTCGGCACCAACTAAGAA
WI-9015	48	C	T	...	...	GGAGCCAGGAGCAGCAGAGGGTCTGAGAGAGGGGAAGAGTGCCAC[A/G]GTCCCTAATGACACCCACTCCTAGCC CTGAGGCTCGTGCCCCTCGACTGGGGAAGGAGTCCAAGGAGGGGAGGGAGCCACTCCTCAATGC
WI-7254	37	A	G	AGGAGCCAC	GGAGTGGGTGT CATTAGGGA	GGTCTGAGAG TCAATGGCTCCCCCCTGAAATCAAGGA

ID	Pos				Sequence
WI-9231	32	G C	CAGGTCCCCCA GATTGA	CACTTGCCCAC ACTCAGAC	GTGACCCTGTGAGGTCAGGTCCCCAGATTGA[G/C]GTCTGAGTGTGGGCAAGTGTGTCAAAAGGGGGC TGCCCCCCAGGAGGATGAGGCTGAGAGGGAGTTGAGGCCGAGGAAGTCA
WI-7836	120	T C	CAAATAAACA ATGCAACGTTC C	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTTGGGAAATAGAGAGTTGAGATAAACACTCTCATTCAGTAGTTACTGAAAGAAAACTCTGCTA GAATGATAAATGTCATGGTGCTATAAACTCCAAATAAACAATGCAACGTTCC[T/C]GATTTCTAAT CTTGGTTCTGAGAGCCATTTGGTTTCAGTTGTGTAGCAATCCCATACCAGCT
WI-7286	65	T C A	CAGCTTCAGCT TAACTGACAG	AAACAATCTA ACCAGAAAGCT TAA	TCCATTCCTTTGGCCCTGCAGCATGTCATGCTCCCCAGAATTCAGCTTCAGCTTAACTGACAGA[T/C] [GTTAAAGCTTTCTGGTTAGATTGTTTCCACTTGGTGATCATGTCTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91	T G	CTAAGCATGT ACGTGAATTTT TAAAT	CCCAATTTTA TTAAAAGTTTA CATCTAT	CAAATTCTTGGAAATATCTCAAATGTTAATAACAACATAGAATTTTTCTCATGCATACTATTACTACT AAGCATGTACGTGAATTTTAAAT[T/G]TATAGATGTAAACTTTAATAAAAATTGGGGTGTGG
WI-7860	50	C G	A		GAAGATTAAGGGAGGGGTGTGCTCTGTGGTCTCCTCCCCCA[C/A,G]TGGGGAGAGACC TGTGATTTGCCAAGTCCCTGGACCAGCTACTGGGGGCCTTATGGGGTGGGGTGGTAGGCAGG TGAGCGTAAGTGGGGAGGGAAATGGGTAAGAAGTCTACTCCAAACCTAGGTCTCTATGTCAGACCAG ACCTAGGTGCTTCTCTAGGAGGGAAACAGGAGGAGACGTGGGGTCCTGTGGAT
WI-9064	29	A G	CGTACCTCCAA ACATAATTGA GTTC	GCTTGAGTGTA AGTCTCGCGAGA	CAAGGCGTACCTCCAAACATAATTGATTC[A/G]TATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGGAGGGCCTGGCTACGTCTCTCTGCCACTCTGCTTTG CACACTTGTCGTTCTTCAGTGCTGCTGAGGGTCTGGCCAGGGGTCTGGCGGGGTAAGCCGGGGTTCCACA GGGCCCAGCCCTGGCCAGGGTCTGGCCCCCAGGTAGGCGGAGAGCAGTCCCCTCCCCTCAG[G/T]AACT GGAGGAGGGGACTCCAGGAAATGGGGAAATGTGACACCACCATCCTGAAGCCAGCTTGCCACCTCCAGT TTGCACAGGGATTTGTCCTGGGGGCTGAGGGCCTGCCCCACCCCGCC
WI-7307	128	G T	GAAATGTGAC TTCACTTTGGT	CAGGTAGAATT TTCTGTCCATT G	GAGGAAATGTGACTTCACTTGGTG[C/T]CAATGGACAGAAAATTCTACCTGTGCTACATAGGAGAA GTTGGAATGCACTTAATAGCTGGTTTTCACACCTTGATTTCGAGGTGGAAA
WI-9274	25	C T	G	G	AATTCCTTTCTGGTAATCAGGCACATGATGAACTTTGATTAGTAGGTCTGTGATTAAGTTCTTAAAT TGTTTTGCAGTGTCTTTATGTTTATTATCAGGTATAGGTGGACCTAAATCCTTATCATCATCTTTATT AATTCAGCCAGTGTATCCGTGTATCCACCAGTTTTTGTTTATGTTTTATGTTTTAAGTAACCTATAGCGATGA
WI-7313e	266	T C			AAGGTGTAATATCGTTTTGTTAAACTGAATGAAATGTATAGCGATGA AATTCCTTTCTGGTAATCAGGCACATGATGAACTTTGATTAGTAGGTCTGTGTTAAGTTCTTAAAT TGTTTTGCAGTCTTTATGTTTATTATCATCAGGTATAGGTGGACCTAAATCATCATCTTTATT AATTCAGCCAGTGTATCCGTGTATCCACCAGTTTTTGTTTATGTTTTATGTTTTAAGTAACTATTATATCTCTGGATTTCATG
WI-7313c	256	C T			AAGGTGTAATATCGTTTTGTTAAACTGAATGAAATAGAATTGTATAGCGATGA

ID	No.			Sequence
WI-9281	68	G	A	...	ACTGGTGGGAGGACTGTGAGGATCCCAGGATTCAGTATTCCTGGCCCAGAGGGCCCTTGCTGCTGGCTACTGG[G/A]TGTTAGTTTGCAGTCTGCTGTGTGCTTCCCTCTCTTATGACTGTGTCCC
WI-7848	142	A	G	GCTAACACTTT TTAAAACCGT CTC / CATTTATTTTG GACA	TTCTGAAAATATAACCAGCCATTGAGCTATTAAAACTTGTAATTTTTTAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAATAAAACATTAATGCTAACACTTTTTAAA ACCGTCTC[A/G]TGTCTGAATAGCTTTCAAAATAAATGTGAAATGGT
WI-9304	70	G	A	GTATATTACA ATGATCACCG ACTGA / CCCCACAGAAC TATTGTAAAAC AA	TCACGTTTGGTGCTTCTCAGATTTCTGAGGAAATTGCTTTGTATTGTATATTACAATGATCACCGACT GA[G/A]AATATTGTTTACAATAGTTCTGTGGGGCTGTTTTTGT
WI-7933b	314	C	A	...	TTACAGAAACTTGCCCTGTGCCTGTGTCCCCATGCTAGGGCGGGAGGGGTCTTTCCTTCCTTCTCTTTCC TACCTACCCCTTTCTTCTTGGCCAGGGCCCTCGTATCCTACCTTCCTTGTCCCTGGGCTGGCTGCAC AGAGGATTGCCCCCTTCTTTCAGAGCGTGGCCCTCGAGCTGGGGAGGAACCATAGCTCCCT AGTCTAAGGGACCATGGCTGCCTGCCTTGGGGAGGAACCATAGCTCCCT
WI-7933	96	G	C	...	TTACAGAAACTTGCCCTGTGCCTGTGTCCCCATGCTAGGGCGGGAGGGGTCTTTCCTTCCTTCTCTTCC TACCTACCCCTTTCTTCTTGGCCAGGG[G/C]CCTCGTATCCTACCTTCCTTGTCCCTGGGCTGGCTG CACAGAGGATTGCCCCCTTCTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTAGTATTTTGCA CAAAGTCTAAGGGACCATGGCTGCCTGCCTTGGGGAGGAACCATAGCT
WI-7374	182	T	A	AAATGAAACTT ACGTTTTGTTG CCAACAACAT TG / CCTCGCCA	CCCAGATGTGCCCATCACGTTTTTCTGAGGCTTTGTACTTTAGTAAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTGACTTTGTTAAATATTTGAAATGTAAATGAAAAGAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTTCTAGCTGTGTTGAAGAATATATTGT[T/A]CAGAAAACACAAGGCTT GAT
WI-9343	78	C	T	CCAACAACAT CCCTCGCCA	GGTCTGCTCCTGCTACCTTGACCCTTCCCTTTCCTCTGCTTCTCCTCCTCATCATTCCCAACAACAT CCCTCGCCA[C/T]ACACAACAACAAAACGTAAGTTTCATTTGGGCAAA
WI-7386b	104	T	A	...	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAAACAATTGTTA[T/A]GTGTTTAGAATCAGAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75	A	G	...	AAGAAGGAGCTCAGTTACGGGGGTTTTTAAAACCTTCATGAAAACCTGAAGAGTTCACTTTTGTTATTAT GCTCTTA[A/G]TGATTTACAGACTGATGCCAGACAAACCTTGGGAAGA
WI-9360	79	T	C	CTTTAGAAAA TCTGCTTTAAC TTGG / A	CTTTAACTTGG[T/C]ATTCCTCTAATTGTGTTCCCTAGGAAATGACTGTCCCAAG
WI-7423	107	T	C	TGCTGGGCTGT GGTCCAGAAGA GTTCC / GCCCG	TGCTCCCGTGCCCATCTGCAGTGGACCCCAGGCACCCCCTTTGAGCGAGTGGGGTGAACTGCTCCTT GGCAGGGATTGTGACACTGCATTGCTGGGCTGTTCC[T/C]GCGGGCTCTTCTGGACCTTGCACCGTG GATACCAGGCCATGTGCCATGGTGATTTGGGTGGGTGAAATAAAGGCATACTGTCT

ID	Pos	Alleles	Sequence
WI-7424	131	T A	CCAGGAGCACTAGAGAGGGAGGAAGAGCAGAAGTTAGAGAAAAAAGCCACCGGAGGAAAGG AAAAAACATCGGCCAACCTAGAAACGTTTCATTCGTCATTCCAAGAGAGAGAGAGGAAAGAAAAA [T/A]ACAACTTCATTCTTCTTGCACGTTCATAAACATTCTACATA
X86400	118	A C	TCCTGCAAGAAGTTCTCAGCCTTTTGTGCAATAAAGTACAGCTTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACTTCTCTAATTTAAGTGAGA[A/C]TCTTTTAAACACCT GTTAAATTAATGTAGCAGTCTGAGAATCTAAAATTATGTACCACTCGTTTATTTGTTCATTCATCCA TCCCTTTCCCATGAATATTTCA
WI-8053	242	T A	GTGGCCACTACATGTTATAGAAACCATCATCTTGTCACAGCACAGTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAAAGTGTCCCATTAAAAGGGACTTTAATCAACCTAA TAAACTCTAATTCTGCTGACTTTTAAAGATCTAAGGTCATTCATTTAATACATGCTGAAAAGGGTCACA ATTAATTCTTTGATCTTTTTACTCACTGTTAACTTATATAA[T/A]TTCAGAAC
WI-6190	165	G A	TACACAATGAATTGCTTTTATTTCGGTATGCATCCACATTTCAGCATTTAGTGGTCCTGAACAGCAAG TGGAAAGACGCAGCAATTTGCCAGGAGGTCAAGCCCACCAATTTCGGGGATCGTGCTGTGCACACGGG GTTCCTTCTTAATCCCTGCTGAGGATCTTG[G/A]GAAGCAGCAGCAAAACCAAGGCATGCA CCGGATTCAAGGTCTTTTGTTCAGTTGTCAGTTCAGAATTCCAAACTAGACCCCA
WI-6275	148	G C	AACAGTCACCACCAACCACATGACAACTCGCCAGGCAAGGCCTTGCTTCCCTCCCTCCTTTGCGTCCC ATGTGCCTAGTCAGCAAGGTCGGGGAGGCACCGATGTTAGCTTCGCCCAAGGGAGTATTACAGAGA GAGGCTTGGGAAA[G/C]GGAAGGAAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTCAGTAACTGGTATGTCTGAA
WI-6421	41	G T	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTTTGATTGT[G/T]TGGGCTTCCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGAACCGTACCTGAGAGGGGGATGGGGGCTCTCTCACAAA GAATATTTGGGGCAGAAACCCTGGAACTGGCCACCAGGGACATCCCAAATATCCCCTCCTCCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215	T A	GGGTGAGACGGGTTATTGTGCACATTTACACAGCGTCCAGCGTCTCGGGGCTGGCAGCGGCCATGCTC CTGTGTGGTCGGGCTGCTCTACAGGGCGTTCACTTTCTTCATCAACTCATGTACAGTCAGTGCTCCAA GGTGATGGGCTACAGTGCTGCCATCGTGCTCATCAGTGAGTCTGTACACACATTTTACATAAATTACACGACTC ATACATGAAAAA[T/A]AGAGCCTAAGGGCCTGATTTAATGAGAAAAAA
WI-9420	202	G A	AACTTGTTTACAAAATAGGCTTTGCAAACTTCATTCATTACTGAATTGTAAAGTCAATGCAATCATCATCAG TAAAAATATGTACCAAGGAAATACAAATTGGATAATGATCATTTTCATGCTCAGGAGGAAGAACAGCAC AGAAATAAAGGATACTGCACAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTTCTTCACACAG [G/A]GCATTCTTTCTCACCTTAACTGCAGCTGTGCAAGATGCCTCAGTGTG

WI-9448	184	G	A	---	TGGGGCTGCTTTTAGACTTCATTTCTAGAGACAGCAGCACCTAGTGAGAGAGGAATACCTGGGAGAGAGAC TGCCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTGGATGCCAGTCCAGTCAGATCCC TTTTAAGAAAAAATGGGCTGGTTCCAAGGCCATGTCCTAACGTGCCCGTGAGCAG TCTCTGGCTTGGATTTTATCCAAGCGCATGTTCCTAACGTGCCCGTGAGCAG
WI-9470	204	G	A	---	ATGTCAGAAGAGACACAGACAAGGAGTTTTTCCCTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAAATCAGATTCCAGCGTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCAGATTCCTACTAGAGCCGCTGGGGACACTGATGAC AA(G/A)GCAATCAACTCAACTCATCTCCTCACCAGGGCTCACCTTCCCAAG
WI-1245b	201	G	T	---	GATGATTTCTGAAGTCCTCCAGCAGCCCTGATTCTCTAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGGT TTATTAAATTTCATTTATCATCTGGACAGCCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC TJCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T	C	---	GATGATTTCTGAAGTCCTCCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGT(T/C)GCCTGATGCAGATCTGTGTGAGCATGTGCTGGCATCACAGGGGT GGTTTATTAAATTTCATTTATCATCTGGACAGCCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G	A	---	TTCAGTGATAAGGACAGGTCTAGAACAAGCGTTCCAACCCTGGCACCAATGACAGTTTGGACCAAA TAACTCTTGTTTCAGGGACTGTCCTACACATTGTGGGGATGTTTAGCAGCCTCCGTGGCCTTCTACCCA CTAGATGCCAGCA(G/A)CACACAACACCCCTCCCCAACAATGCAATGAAAATGTCTTTAGACATT GCCAAATATACCTTGTGGGGACAAAATGGCCCCCTGATTGAGAACCACTGGTT
WI-5385	110	G	A	---	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAAATGGTGACTCCAATGGTGGGATTTGAAGAGG GAAGTCTCGATAATTTTAACATATAGGTTTCTGCCAGGAATCG(G/A)CAATGCTAATCTATTGCTTAA TTCTTTATCAACAGACTCTTGAATCAATTTAGAGATACTCAGTGACCCCCATGGCTAGAGTTCCTGAC CCCTGCTACGGGAAACATTGAATGCA
WI-5403	199	T	G	---	ACCAAACCGTTGGCAAAGGCTCCCCAAGACTCACCACCCAACTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCATAAATATAATTTTCCAGTAGTAGTTACCAGGCACCAGCCTAT TGGAAGAAATCATAAATGTAACCCTACAATGTATTGCTCTCTGGCTTGGTGCCAGGCATAGAGTT(T/G)]GGCCTACAACCCATTTATCATTCATTGAACCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G	A	---	TGGTATTTTCCTTTCCTAAAATGTTATGATTAATTAGTGTCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAGAGAAAAATAAAGTATAGTTGAAACCTCTAACAATTTAGATTTTTAAGGCCTAG GGAAAGAAAAGAAGAGAGCCTGGGAA(G/A)AGGGAATGAAAAGCACAACCAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAGGAAAGTTAAGT

Marker	Pos			Sequence
WI-5801a	48	A	G	TGGTATTTTTCCTTTTCCTAAAAATGTTATGATTAATTAGTGTCTTTGT[A/G]GAATTTGAAAAAATGT AAATCAGAGAACAGAAAGAAAATAAAGTATAGTTGAAACCTCTAACAATTTGAATTTTTAAGGCC TAGGGAAGAAAAGAAGAGAGGCCTGGGAAGGGAATGAGAGAAGCACAACCAGAAAAAAAGTGTGT GGCTTAAGGGAAGCCAAGGAAAGTTAAGT
WI-5696	61	C	A	TTCTATTTAAATCCTGTGCCCCATTGCAAGACTGCATTCAGTCTGCATGAGCCTTAGTTTC[C/A]TAA AAGCCCCCTCACACGCCGAGGAGGACAATGTTCAGAACTAAATGACTGCAGGTGAGCAATTCTCTGTATTA TACAAACTGGGACCAAAGATGACTTTATAATAGTAGCAAGAGGACAATCAGGCCAGACTGGGAGGACC TTATAAATAGATTATAAGGCTGTGTGGTGAGTTTATTTTAACTT
WI-7461	153	C	T	TATTACTTAGGTTCATAGAGCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCCC AATTCTAACGCTCTCCTCACTTCCCTTGGGTCCCCTGGCCCGGGCGCCTCAGAGATGACACTTAGGCTGCACATTCCCTG TGGGCAGGGACTGTGTCTC[C/T]GTTCCCGTGTGGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
WI-9716	221	G	A	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAACTCTGAGGCTTTAATGGTCCCTTGTCTCTCTAAC GCTTTTGGTATACTTTCTCTTTCTGAAGACCAACCCTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTTCAGATGTGTACTTCCTACACACTCAATTGATGAGTTAGGCTCTCTTCATCT CAATTGAAAATTCTAGAA[G/A]AAAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49	C	T	TTTTCGTTAAGTCTTGTGAAGCCACACAGAAGTGATCTACTCCTTTAC[C/T]AAGTGTTACTTTGCA TATATTTATGGGGATGATTCTATCCTACTTAAGATTTTCTCTCTCCAGGTTAAATATTCCATTTCCT TTGTTCAGGAGTTTCTTATTGGCCTTCTTTCTAAACCCTTAACCATTCTGCTTATTCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31	A	C	GAAAACCTCGTTGGCTCAAAGGAAAACTGTAG[A/C]AAATTCTTTTTTTATTTTTGTTTTTTTAACTC AAAGAGAGTGGAGTTTGCATTGACCTTGTCATTGGCCACGCTGCTCTTTTGTTTGGTGTAAATCCTCTAGT GGGCACTTGCAAAAGCAATTTAGAGCAAGGTGGTGGCATGGCAAAGGTGGTGAGGTTGCTGAAAAG TAGCAAATGGAAGAAAGGTTAATGGA
WI-10312	41	A	G	AAGGCCCAGTGGGAAAAGCAGACAAAACACTCCAAGAATAC[A/G]AGATATAAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTCATGCTGATGAGGGCATGTCAGACAAAAGACACATTGGGTCT TGAGGGTTGAATAGGAGTTGTCTGGTGAGTCTTGCCCAGTCCCATAGTAGGTGTTCCAATAAATAAAC AGTGACTAAACTGAGGTAGAGTCACAGAAGAAAATTTCA
WI-11152	179	C	T	GATTCTTTGCGACATGCGACAGAGCAGATACGGCAAGGCATCTTGGGCATTGGAAGGAAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAGTTAAGGTCTCGCCACCAGGGACCTGGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGGACAAGGTGGGACAAAAGGCTTGTCA[C/T]TCTGTCAGAAACATTGAA AACAGCCAGTACATGCCCACTGATAGA

ID	Pos			Sequence
WI-1968	167	A	G	TGGTGAGGAGCTGTAAGGCTGAAAGAATAGTCTCTGCTCTGGTCTTTCGTTGTTGGAAATGGATGAGTCCT TTTACAAAATTTTCCTCTTGCCATGGGTGTTATGTTTAGAATCATGGAAGTTGGAAGACTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGT[A/G]TGAACTTGAGCAAGTGTCTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198	G	A	GGGTTCATTTAACAGCCTTCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAACAACAACAACATTAAACTCCTCCCCACTCTA CCCGCCAAAGTCTACCTTTGGTTCTTTATTTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCATTTTCAGAAAAGCAGTATA
WI-4823	164	C	A	TTTATCTTTCCAAACCATGTGTGTTTCTTCACATACTTTACGTAATTTTAAATCATGTCATTTAATTA TGCACTTACTTGTTGGCTACCAGACATTGCTTCCAATTGTAAATTCCCTAACAACAGCAAGCATAACT GATGTGTCCATCTTTGTATTCCTAAAA[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCCTCTCTGT CTTCCTCTGTTTCACCTCCTGTATTCCCTATTCAGCATTCAATGATTA
WI-4860	72	A	G	AAAAAAACAACTTCATTTGACATTCTAAGAAGATAAAGAAAAACAACGATCCACTGGTGTTGTTGCTT GATTT[A/G]GGAGATAAAACCTGATCTCTAAGAAAATTAAACCAAAGCAGTACACTAAAATAGCCT TTGTGTGTTTTCAGGAAAGAAAGCCAATCCAACTAAGTTGCTAAGAAAATAATGTTTCATATCA CTCTAAACTTCCACATAGAGCATTAATATAGCA ... TGAAAGGACCAGTTCGAATGCCTACCCAAGGTAAATCGGAGGGCAGGAAGTAGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCGGCTGCC[C/A]AAAATTGTTAACACTGATGC TGTCTACAAACGCACATAGAAATCGGTGGTAGAATCGGTAGTAGCTAATGTTTAGATA TGATTGTTGAATTATTGTTGCTGTGTTCTTGGTG
WI-9705	111	C	A	CAAATAATCTCTGCTTAGAAGTTGCTCTCTAGGGCCATGGATTCATGTAAGGGTGGGGCAGGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGAGAGCGGGGGTGAGGGGAGAGATCGTGGGTTCATGAGATCCCAT CTTGGGCAATACGGTGGAGCCAATGAAGACCAGGTAGATGAT[A/G]TCCTCCAATTTCAGGGGGCTCCC GTGGGATGGTGGAGCCAATGAAGACCAGTAGATGATGCCACCTAGAGATG
TIGR-A004Z48	177	A	G	GGGGATTCAATGTGTCTGTCTCATCCAATAAGCCACT[T/G]CATGACCTCAGCCCCCATACTCTTCTTCCC TATGTTCCCAGAGACAGAAGATAGAACCTGGCCCCTTCCTTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAAACCACCAGCTCCCATGCCAAAATAGAAACGATGAGTGGCTGGGATCCAATTTCTATGGGAGCC
U17579	34	T	G	TGGGGAGAGGGGATCCTTTCTAGTTGA
WI-7747b	88	T	G	GTGAGAGCGAGGCTGAGCCTACAGATGAACTCTTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTTAATTTGAT[T/G]AAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAGTT ATTTCTTGTTGTTTGTTGGGTATCCTGCCCAGTGTGTTGTTGTAAATAAGAGAGATTTGGAGCACTCTGA GTTTACCATTTGTAATAAAGTATATAATATTTATTGTTCTGA

WI-7747a	44	T	C	GTGAGAGCGAGGCTGAGCCTACAGATGAACTCTTTCTGGCCTGCT[C]/[C]CTTCGTTAACTGTGTATGTAC ATATATATTTTGTTGTTTGGGTATCCTGCCCAGTGTGTTGTAAATAAACAGCTTCATGCCTTTGTAAGTT ATTTCTTGTTTGTTTGTTGGGTAATAAAGTATATATAATTTTTTATGTTTTTGTTTCTGA GTTTACCACCATTTGTAATAAACTAATACTGGTGAAAATTTACCTAAAACCTTGGTTATT
WI-7189	197	T	C	TCCAGAATTTCCTTCTTCAGCTCATTTGTCTCTCACAATTAAGGGAGTAGGTTAAGTGAAAGGT CACATACCACCATTATTCCCCTTCAAACAAATAATATTTTACAGAAGCAGGAGCAAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAGTGGTTATTTTATTTTATATTAAGCCTACAACACATTTTT[T/C]AG
WI-7850	57	G	A	AGCCCCAGCTGGACTCATGGATGTGCACCCTTTGCTCCCGTCCTTCTGCCTCTGG[G/A]CTCATGTA TCTGCGCAGCTCTGGTACCCTCTGTGGGTGCCATCTCTACCTCTGACACAGACTGCCTGCCTTGAAGCT GAGAAGGCACAGGGCAAGGAGCCAAGGACCACAGAGCCTCAGCCAGCCCAGGATCCGTCCTCCTCATTT ATTGGTGATGATGAATGGGAAATCAGGGGGGCGTGTGTCTACTAGAGCC
WI-7907	69	G	C	CTCTTCTTCTTCATCCCATCACACCCCTAAATAGGTCAGGTGAGGGAGGCTGGGAAGAGGTGGGAGGAGG G[G/C]AGAAGTGAAGGAAGATAGGAAGGATATTACCTCTTCTGTTATTTTTTTAAGAAAACATTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCCACTGTTAGAGGCCTAATTTTTATATCTATATAATATTAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAATTATTGTCAAAGTTTAAAT
WI-7919	242	T	C	GAAGGCAGCTGGATCCACTTCCCGCCAGTCCTTGGGGCAGCGTTTGCTGTGGAACACGAGAGCTCCTCCT CAGGGGCCTGCCACTCACCTTCTATTCTGTGTATGATGTATTTGGTTAAACACTGTCAAATAATAGAGAT GTGCCAGATTAGATTTCTTACCCTAATCTGTTAATATTGTAACTTTATTCCATTGAAAGTGTCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAA[T/C]ACAACTTT
WI-7928	101	T	G	CTCCCTTCCTATGTCTCTCAGCAGCACGTTGGGGCACACTGTTCATCTTCTGACCGTTTGCTGGCCTA TTCCCCTGCAGTGCAGTCAACATGTCAAAATTCA[T/G]ACAAGAGGAAATTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTTGCACTTAAAACTGAAATTCAACTCTTTATATAGGATTTTCTTTT CTATCTCCATCTCCTCATTAAAAAATACGTACATTTGGAGGTAATGGTA
WI-7936	131	T	A	TTTTGAGTCAAAGACTTAAAGGGCCCAATGAATTATTATATACATACTTGGTTATTTCTGAA GGTAGCATTCTTTGGAGTTAAAATGCACATATAGACACATACACCCAAACACTTACACCAAAC[T/A] ACTGAATGAAGAAGTATTTTGGTAACCAGGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99	T	C	TACACGTTCCAGCCCGGTTGCCCCACTCATCTCGCGCGCTTTGCTTTGGTTGGGGGGCAGATTGGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTCATG[T/C]AGCCCAAAGTACAGCCCTGGACCACCCCTGGTGTG TGTAGCTAGTAAGATTACCCTGAGCTGCAATGGGACAGTTACACTTGACAGA CAAAGATAGGTGGAGATTGGCATGCCATTGAGAACTAAGAGCTCTCAAGTCA

Marker	Position	Allele	Allele		Sequence
WI-7805	101	A	G	...	TTCTAGGCTGTACAGTCTGATGCATGATTTTTTATAAATATTTCATACTCTTGTGTGAATTTGGATCTTTTTACTTTGAGCATATATTTTAGAATATGTGT[A/G]TGTTAAAGGATCTCCACAATGTCTGCAGTGTGAAGGCAGGTTCATTGTGGAATAGTTTAACAGTCAGGAAGGCTAAACTGGTCAGTATTAATGTGTAGCCCTACCAAAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137	G	T	...	GGCCAGGAGGATTAGCAACAAGGATTCATTCTGTTACTTACTTGCCCCTTTTATCTTTCCCTCTTGCCCCAGTCGTTCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTTGCCTTGGCAGTGCT[G/T]CTACTCCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAGAGACTAAATCTGCAATATATAAAGAGCTCCTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAAATGTCATCAG
WI-140	252	C	T	...	ATTTGAAGAGATTTGGAGGGCTTTGCAGAGGAAAATAGATTTCAATTGGATCCCCAAACTATAATGACAAGTTTTAATTAGGTGTGATCAAGGCTTCTAAAAGTGAAATGCAAGTTGTTACCAGTAAAGTTTATATCTTCCATTCAGCCCAGCTCATTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGATCATCTGGCAAGGATGAAAATTTAGTTAAAAATGTGTCATTGTCTGTATTGGCATTCCT[C/ GAGGTCTTCAGCAACATGGAAGCCCTACTGCTTCAACCCGAGTTCCCCGGATCAAGTGCTGGCACCCATGATGGAAACTCTTGCCATGGTTTAGTACCCTGGACCAAGTAGTCATTCCATCCTGACTTTAAAATTCTAAACAGCCTTTGATGGGACAAATCTCTGCTAAAGACTAACCACTTCCTTATCTTATCTTCAGCTACCTGCTTCCCTTTC[C/T]GTTTAACAAGCATAGAATATTCTGAAACAACT
WI-198	218	C	T	...	TTCATGGTCCCAAGACAGAGATTTTAAAGAAGAAAAATAAAGCCTCATCTCCTAACTATGACTTGGTCGGAAGCCAAGAACCTACTTCAACATTGACCCATAAACCCTTCTCTTGAGATGATGGGCTGACTTTTTCAATGCATGAGTTTG[T/C]CCAAAGGCTTGATGGAAAATCTCAACATTGTTACCTAAGAAAGAGGGATGTATCTTACTTTGTTTAAAAACTGCATATGCCTTTATTTTGTTTTAGTTCCC
WI-205c	146	T	C	...	TTCATGGTCCCAAGACAGATTTTAAAGAAGAAAAATAAAGCCTCATCTCCTAACTATGACTTGGTCGGAAGCCAAGAACCTACTTCAACATTGACCCATAAACCCTTCTCTTGAGATGATGGGCTGACTTTTTCAATGCATGAGTTTG[T/C]CCAAAGGCTTGATGGAAAATCTCAACATTGTTACCTAAGAAAGAGGGATGTATCTTACTTTGTTTAAAAACTGCATATGCCTTTATTTTTGTTTTAGTTCCC
WI-205b	146	T	C	...	GAAGACTGAGTTCCAGGAGGTTGCAGCCGTTCTCTCTGCGGCCATATGGCTAATAAGGAGCTTGAGCAGGGGATTCAACCTGTTTGCAACCCAAGTNCTTCCAAGAGGTCTCAGACTACCTCCTCCATCTCCCCCTCTCCCCACAACACAAATACAGAGATT[G/C]AATTCAGGAGGCCAGTTTCTAGGTGGCTTTGAGCAATCATACACAGTAATCTCTTGGTGTCTTTAGTTTTCTCAAATGGAAATGG
WI-234	165	G	C	...	AGCTTTTGAAATCCAAAAACCACAT[A/G]CTTGACTCTCTTGTTGTAACATCTATCCCTGAGGCAGAAAATACAGAACACCCTGTTGGCTGCCTGAAAGACCTCTCCTGAAAGACATGGGGCGGGGAGACATCGGTCAATGTATCAAAAGCATCTCTGCCTGAAAGACCTCTCCTGATGACTGGGCAAA
WI-276b	25	A	G	...	TCTGGCAAGGGCCTTGTCTGTCTTATCCCTATCCCGCTATCCCTGATGACTGGGCAAA

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WI-276	25	A	G	AGCTTTTGAAATCCAAAAACCACAT[A/G]CTTGACTCTCTTATCCTCCTCTTGTTGTAACATCTATCC CTGAGGCAGAAATACAGAAACACACCCTGTGCTGCTGCCCTGAACGGAGGAAGGGATGGGGCGGGAGACAT CGGTCAATGTATCCAAAGCATCTCTCGCCTGAAAGACCTCTCTGAAAGACTATTAGGAGC
WI-427	59	G	A	TCTGGCAAGGGCTTTGTCTTATCCTCCTTGCTATCCTGATGACTGGGCAAA TTTTCCCAATCCACAGGTAAAACTAATATAATGGATGTATAGAAACTACTTCC[G/A]GTTT TTTCCCCTGGGGAAAATATTCACAAAACATTTGTGGTCTGCAATCAGGTTAAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGGCCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGTGAGACTTTATGT ATTCATTTATTAGAGCCAGGGTCTTGCTCTGTCACCCAGCTTCAGTGCAGT
WI-562c	106	T	C	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA[T/C]AAATGGTCCTTTATTAAAAAAAAA AAAGNTATCTAAAGAGAAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106	T	C	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA[T/C]AAATGGTCCTTTATTAAAAAAAAA AAAGNTATCTAAAGAGAAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103	T	C	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAGCCCAGAAAGGAAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATT[T/C]AATAAATGGTCCTTTATTAAAAAAAAA AAAGNTATCTAAAGAGAAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141	A	G	GTGTAATTTGGTGGCTTTGCAACTTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCTCCATGACTCTGGTACCTCCATCATTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141	A	G	GTGTAATTTGGTGGCTTTGCAACTTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCTCCATGACTCTGGTACCTCCATCATTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136	A	G	GTGTAATTTGGTGGCTTTGCAACTTTTCCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT[A/G]CATGATAATGACCCTCCATGACTCTGGTACCTCCATCATTACCAATGTGAGAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT

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WI-611	66	G	C	TTCAAATTTAACACCATTGGGTATATTATATAATTTTNGCTCTATCCATAGTTCTAACCCTCTCTCT[G/C]ACAGTGAGAGACACCTGCCTTCTATTGTCGTTCCTGACGTATTAACGTATTCGATCAGTCAGTCACCCATCTGGAACCAAGGTTCATTTCTGCTGACCCCTCCTCCTCACCCTACTTGGGCTCTCGACTTCCTTTCCTGGGCTGAACCTTCTCTGTGTGGGCTGTCCGCCTCTCCTCGTCTTGGGCTCCAATAC
WI-681b	156	A	G	TGAAGCCCCTCTCTATACCCAAGTGTCTTTATCTTAAAATGCTGTGGTGCAAGTATCTACCCCTTAGGGATATTGTGAGAATTCATACAGGGGAAGCACTTGTNCCTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCAAGCAGATTATATGTCAGACACCACGNATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
WI-681	156	A	G	TGAAGCCCCTCTCTATACCCAAGTGTCTGTGGTGCAAGTATCTACCCCTTAGGGATATTGTGAGAATTCATACAGGGGAAGCACTTGTNCCTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCAAGCAGATTATATGTCAGACACCACGNATGTCCTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
WI-867b	119	G	A	AATCTTAACAGCCACTTTCAGTCTCTTAATTCTTTTGGAGCCTAAGATCAGTGCAACCCTCCAAGGCTCCCCAGGTATCTGGCACATCTTTCCCTTTCATCTCC[G/A]TTTGTGTGTTTGGCCAAATAATATCTCCCCACAAGCACACTTAGAAACTTAAGTGCTATGGTTTGAATGTCTATGGTTT
WI-867	113	A	G	AATCTTAACAGCCTTTGATGCCAAAGCCACTTTCAGTCTCTTAATTCTTTCCCTTTC[A/G]TCTCCGTTTGTGTGTTTGGCCAACCCTCCAAGGCTCCCCAGGTATCTGGCACATCTTTCCCTTTCATCTCCTAATCCTGAAACCTGAGAAAATGTTATCTTATGCCAAATAATATCTCCTAATCCTGAAACCTGAGAAAATGTTATCTTATGCAGTGCTATGGTTTGAATGTCTATGGTTTGAATGTCTTAGAAACTTA
WI-867	119	G	A	AATCTTAACAGCCTTTGATGCCAAAGCCACTTTCAGTCTCTTAATTCTTTCCCTTTCATCTCC[G/A]TTTGTGTGTTTGGCCAACCCTCCAAGGCTCCCCAGGTATCTGGCACATCTTTCCCTTTCATCTCCTAATCCTGAAACCTGAGAAAATGTTATCTTATGCCAAATAATATCTCTTTCTAATCCTGAAACCTGAGAAAATGTTATCTTATGCAGTGCTATGGTTTGAATGTCTATGGTTTGAATGTCTTAATTAGAAACTTA
WI-871b	123	C	G	TCATCAGACCTGAGATTCAGCATGAAATCTCACCAAAGGTACCACCACTTGTAACCTTGTCCAAAACGAATCTCAGTTTCTGCATATGTAAAATGGGAATGATAAGTTTGTAATGCACTGTTATGGCCTGAATTGTGTACCCGAGAGAAATAAATGAGACATTGAAGTAAAGTTTGTAATGCACTGTTATGGCCTGAATTGTGTACCC[C/G]AACTGTTTAAAATTCATATGTTGAAGCCCTAACACACCCAATATGNCTGTATTTGTACATAA
WI-871	123	C	G	TCATCAGACCTGAGATTCAGCATGAAATCTCACCAAAGGTACCACCAAATGTAACCTTGTCCAAAACGAATCTCAGTTTCTGCATATGTAAAATGGGAATGATAAGTTTGTAATGCACTGTTATGGCCTGAATTGTGTACCCGAGAGAAATAAATGAGACATTGAAGTAAAGTTTGTAATGCACTGTTATGGCCTGAATTGTGTACCC[C/G]AACTGTTTAAAATTCATATGTTGAAGCCCTAACACACCCAATATGNCTGTATTTGTACATAA

WI-884	198	T	C	AGGTTCTGGACTTGATGCTGGGAAACAATTGGGTNCTGGAGAATTCCTATTTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTATTAGGAAACTTTCCTGATCTATTGGGA ACTTCCTCCTAATAGATCAGGAAAATCCACCTCACCTCATTAATCATGGACAACNNAAAAGGAATA[T/C]G ATCCCGCATGCAACATTTATTCAGTGAAAACATGATGAAAAATGAACATAAT
WI-921b	205	G	A	CACTTCCCAAGGGCTCTGGGGANGAGCGGTGGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCGAGGGGCTCTGCTCTGAAGCCGGACACGTGCACACAGGGACAGTTATACTGG CAGTGATGCCTCTCACGCCTGGCCCCCAAGAAAAAGTCTTNGCCAGGAAAAAGCACGATCCATCTAC TCT[G/A]GGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCTTCCGAG
WI-921	205	G	A	CACTTCCCAAGGGCTCTGGGGANGAGCGGTGGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCGAGGGGCTCTGCTCTGAAGCCGGACACGTGCACACAGGGACAGTTATACTGG CAGTGATGCCTCTCACGCCTGGCCCCCAAGAAAAAGTCTTNGCCAGGAAAAAGCACGATCCATCTAC TCT[G/A]GGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCTTCCGAG
WI-945c	90	G	C	GGCTGGGATGAGAGGTCTACTTGTGGTACTGGAGGTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGACTAAC[G/C]CATGGCAGTAGTGGGCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGGTT TTCTCTGGTCATAGAATCTCTTAAAAGGAATCATGACAGATTTCTTGGCTTTA
WI-945b	90	G	C	GGCTGGGATGAGAGGTCTACTTGTGCTACTGGAGGTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGACTAAC[G/C]CATGGCAGTAGTGGGCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAACAAAGTTCAAACANTAGGTGCAGCACANNNGGGTT TTCTCTGGTCATAGAATCTCTTAAAAGGAATCATGACAGATTTCTTGGCTTTA
WI-960b	167	C	T	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACCACAGGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTTCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCT[C/T]CTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155	G	A	TTGCTTCAAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATTGTTTTTGAGTACAT ATCAAGCACCACAGGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTTCTACC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181	T	C	TCCCACTGAGTGATGGCTTTCAGTAGTTTTATTATGATGTGCCTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGTATTACTTTGGGAGAAATGCTCAACTATAAAATATTGCTTCTGACCCTTTCTGTGTTC CTTCTTAAAGATACAAAATAAAATGTAACATTAGACCTCTCACTA[T/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTCCATTATTTTATTGCTCTGGCTTCATTTTGTAAATNTG

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WI-1147b	204	G	A	TTTGCCATTATTTGAAGATAACCCACACCTTGGTGTCCAGGGTTTCACAGGTATTAGTGGTCAGTCACATAGGCATATAGTACCTGTATGACTTCTATTCCAGCCACGCGCAAACTTCTCCTCCTGGCTCCTGAGCCAAAAACAGGCATTACCATAAATCACTTTGTTAGGGATGAACTTATCTGGCCAAACTGATAC[G/A]GCATGACCCACAGCCTCAGGTATATAAAACACTCTCACAGA
WI-1158b	147	C	T	GCATTCAGAGGGTTCGTTAATGACATTCACTGAGGCCCTGTCTATGTCCAGGCCCTTGGTGTTGAAGACGCAAATCATGAACAAAATGAAAATACATGTGATGGTCTCCTGAGTGTGTCAGGT[C/G]GCCAGGTTAAGTGCTGGGG[C/T]TCTGGGGGTCACATCCTGGGTCCAAACTGCTTTGCTATG GCT
WI-1158a	124	C	G	GCATTCAGAGGGTTCGTTAATGACATTCACTGAGGCCCTGTCTATGTCCAGGCCCTTGGTGTTGAAGACGCAAATCATGAACAAAATACAATGTGATGGTCTCCTGAGTGTGTCAGGT[C/G]GCCAGGTGGCTAAGTGCTGGGGCTCTGGGGGTCACATCCTGGGTCCAAACTGCTTTGCTATG GCT
WI-1304	124	T	C	AAGTTTACAGAAGAAAAATACCAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCATCATCTTCAANGTNCCCACAGACACTTATCCCCTAGACAGCAGCCATTCTTTTGAATGN[T/C]GNCANTAAAAATGATTTGAAATTGGGAATAAAGCCCTCCCTCTAATGATTTGACAGTGTTAGACCTTGCCTAG GGC
WI-1305d	202	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTTCTTTCCATT[C/T]TATGTTGGTAAATATAAAGATTGTGCAAAGTATTTAAATATCGTCTGATTATACCACTNATGTCTNACAAAATNACACTGTTTAANTGNNATAACATCCACTGCTTTCANTAATTNACTCCACTNATGTACAGNGANTCATAACAGCCCTGCCTACCA [T]AGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTTCTTTCCATT[C/T]TATGTTGGTAAATATAAAGATTGTGCAAAGTATTTAAATATCGTCTGATTATACCACTNATGTCTNACAAAATNACACTGTTTAANTGNNATAACATCCACTGCTTTCANTAATTNACTCCACTNATGTACAGNGANTCATAACAGCCCTGCCTACCA TGCAGGGCGGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153	T	C	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTTCTTTCCATT[C/T]TATGTTGGTAAATATAAAGATTGTGCAAAGTATTTAAATATCGTCTGATTATACCACTNATGTCTNACAAAATNACACTGTTTAANTGNNATAATTGTGCAAAGTATTTAAATATCGTCTGATTATACCACTNATGTCTNACAAAATNACACTGTTTAANTGNNATATTGTGTCCACTGCTTTCANTAATA(T/C]TNACTCCACTNATGTACAGNGANTCATAACAGCCCTGCCTACCA TGCAGGGCGGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202	C	T	TTCTCAATTCCAATCTGTGTGTTACTTTATTTCTTTCTTTCCATT[C/T]TATGTTGGTAAATATAAAGATTGTGCAAAGTATTTAAATATCGTCTGATTATACCACTNATGTCTNACAAAATNACACTGTTTAANTGNNATATTGTGTCCACTGCTTTCANTAATTNACTCCACTNATGTACAGNGANTCATAACAGCCCTGCCTACCA [T]AGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248	A	G	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAAATGGACAATCTTGTNGNNNNNTNG GGCTGGGTGACTGTGCCTGGGTCATTTAGAAGCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAGACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCT[A/G]GC
WI-1306	240	A	G	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAAATGGACAATCTTGTNGNNNNNTNG GGCTGGGTGACTGTGCCTGGGTCATTTAGAAGCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAGACTGTGCCTAAGGGNGAGAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTT[A/G]TCTTCCTAGC
WI-1307b	118	T	C	GACAAGGCTGGTACTAGTTTCCAATTCCAAATCTATGTACACTTTCCTCTCCACTTTCTCAAGTGGACA GATTTCTGCATTATACTGCTTGGGGAGCAGTGGTGTAGGCAAT[T/C]GTGAGATTGTCTTT CCTACCCTCTTAAATGTATCTTTNCTAATTATNATGCTAAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTTGTTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1307	118	T	C	GACAAGGCTGGTACTAGTTTCCAATTCCAAATCTATGTACACTTTCCTCTCCACTTTCTCAAGTGGACA GATTTCTGCATTATACTGCTTGGGGAGCAGTGGTGTAGGCAA[T/C]GTGAGATTGTCTTT CCTACCCTCTTAAATGTATCTTTNCTAATTATNATGCTAAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTTGTTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1325b	169	T	C	GAGAGATGGCCAAGACAAAGCAGAGGGAGAGAAGCAACCNTCTGTGTTTATCGCAGCAAGCN ATGTGTCTCCATACCCAGAAATGAGCATGTCGTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCCTTGCTC[C/T]CTTCTTACCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCCCACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165	C	T	GAGAGATGGCCAAGACAAAGCAGAGGGAGAGAAGCAACCNTCTGTGTTTATCGCAGCAAGCN ATGTGTCTCCATACCCAGAAATGAGCATGTCGTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCCTTGCTC[T/C]CTTACCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATTCCCACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162	T	C	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCCTGTTATTGTAAA ACACCAAGTGCGGTTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGT[T/C]GAAGTTGGGTAGCTACCAGGCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAG
WI-1327	175	C	G	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAAGAAGTCCTGTTATTGTAAA ACACCAAGTGCGGTTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGTGGTAG[C/G]TACCAGGCCTCCCCAAATGTAGT TCTTGNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAG

WI-1341b	136	G	A	TATCAGCATGATTGTGGCTGTTGGACACAAAGTCAATTTGTACTTTGNTGCNNNTCCTTTCTNTT ACCTGATCCACTATCTTCTCTCAAGATCANGTTCAAATTTGGCTNCTTGTTNAATTATACCCAAGC [G/A]GGATTGTGATGGATCTGTTATTTCCTGTGTCTTGGAACAGCAGAGTCGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTCTGTTCCCCAGCCCACTTAGCAAGTGT
WI-1349e	192	G	C	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTAGTGCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGATTTCAGAAAATA
WI-1349d	264	C	A	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTAGTGCTGAATTTCCATCTCTGA[G/C]TTCAAA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGAATTTCAGAAAATATGAT
WI-1349c	192	G	C	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTAGTGCTGAATTTCCATCTCTGAGTTCAAAATA
WI-1349b	264	C	A	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTAGTGCTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGAATTTCAGAAAATATGAT
WI-1349	264	C	A	CTGACAAATGTCATATCTCACTCCTAAAACCCACAGGTCATAGAATCAGTTAGCTACCCTCAATCCA GCAACCCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTAGTGCTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAAATATGATAGAAATTGTGAAGTACTAGAATTTCAGAAAAATGAT
WI-1403b	57	C	T	TGGTATTTGGAATGGGGTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TTCCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGACGTAGAGTAAGCCATAAAAATATACGT AAAGTTTACATCAACAACATAATTCTTGCCCTGACATCATGCATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCCAAAGTGCCAAAAAGGGGTTGTATCTGATTTGT
WI-1403	58	T	C	TGGTATTTGGAATGGGGTTCAGACTCCGGGTTCTGGCTTTGGTAAGTTGCT[T/C]TCCGAA TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGACGTAGAGTAAGCCATAAAAATATACG TAAAGTTTACATCAACAACATAATTCTTGCCCTGACATCATGCATTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCCAAAGTGCCAAAAAGGGGTTGTATCTGATTTGT

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WI-1417c	31	C	T	...	CAGGCCGGAAGAGAGATTCACGTGGAGAGATGTC[C/T]TTGGCCAGGCGGGGGCGGCAGATGTGAGCCCACGGG GGTGACAGCAGCATGCCGCTGCTGGCAGTTGGAGGGCCCAGAAGGAATCCCAGTGGCCCTCTCAATGACTTG GGGTCCTCGACTTCGGAAGTTTAAGGGGCTCGCGGTCTCAAAAAGCTGGGTCCGGTTTGAGGCGGGTTGC AGGCGGAGGCCCTTAGGTCGTATTTAATGTTTGCTTTGTAGAAAAGTCGC
WI-1417b	31	C	T	...	CAGGCCGGAAGAGAGATTCACGTGGAGAGATGTC[C/T]TTGGCCAGGCGGGGGCGGCAGATGTGAGCCCACGGG GGTGACAGCATGCCGCTGCTGGGAGGGCCCAGAAGGAATCCCAGTGGCCCTCTCAATGACTTG GGGTCCTCGACTTCGGAAGTTTAAGGGGCTCGCGGTCTCAAAAAGCTGGGTCCGGTTTTGAGGCGGGTTGC AGGCGGAGGCCCTTAGGTCGTATTTAATGTTTGCTTTGTAGAAAAGTCGC
WI-1729	172	A		...	CCATGAGCAAACAGCATGTTCTACTCTGTGATGTGTATGTTAGGGGGCATGTATATCTGTATTTCT TTTATTCTCTCCAAAAGAAATTTCATTATGCAAAACATTATCAGGCAATGCAATGCTCGTAATAAAGA TGTTGGAGAACTGAAAAAGAGAGAGCTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGTATGTGTCCTCCGTGGTNACCTTCTCTCCACCACCTGTGTTTTT
WI-1732b	122	T	C	...	TGCCTTACTTCTTTGTTCATTCCCACCATTACATTTGTAAATTGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGTCAACCCTT[T/C]ATTCAGTCT CTGCCACATGTCTAGTAACTGTGAGTGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACTACTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1732	114	C	T	...	TGCCTTACTTCTTTGTTCATTCCCACCATTACATTTGTAAATTGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGT[C/T]AACCCTTTATTCAGTCT CTGCCACATGTCTAGTAACTGTGAGTGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACTACTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1750	97	A	G	...	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTCCCCAAAAAAGGTTTTAAAATCTGTGTTGGA CATAAATGTTGAATTTGCAGTTGCACCTTGG[A/G]TTAAGGTGTGCTGTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31	A	G	...	GGTACACAAAGAAATGCTTCTGGAAATCTCAC[A/G]TAGCGCCTTAACATTTGGCTGAGTATTAATC TGTACATGTAATGTGAACCACCATGGGCAAAGAACAATTCCTAGGAAAAGTACAATTAC TGGGAAACTGTAGAACAAATAATTCTCATAGTTTACACATAGCTGGAATCACTCATGTTCCCATCA ACTGGAGAGACCTTGTTGTTGGAGTACGGGACATTCAAGAATAATCATAAAAAT
WI-1803c	77	A	G	...	CCACTCAGTAATAATAGTGTTGGAGATAAGTAATGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGAT[A/G]AGTAGGGTAGAGCTAGAGCATCACACTTGGGAGGACATATTCGGAGTNAGATATCCTG GGTGCTAATTTCAAATATCTACTAAAGCATGACTTCTAGAAATTACTTATTACTCTTGTCCTCAA GGAAATGGGAATACCTATATAATACAGTCTTATTGAGGAAATAACTGGAATCA

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			CCACTCAGTAATAATAGTGTTGGAGATAAGTATATGGTAGGCACATAATAATTATTTCAGGCAGAA CCATTATGAT[A/G]AGTAGGGTAGAGAGCATCACACTGGGAGGACATATTCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTACTACTACTAAAGCATGAGTGACTTCTAGAAAATTACTTATTACTCTTGTCCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGGAAATAACTGGAATCA
WI-1803b	77	A G ...	TTTACTTGGGGATTTTTCATAGCTGATCATAATTTGATAATTCACTTCTTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[C/T]CTGTCCCCAGTTTATTTT AAGGTTTTTTCATTGCACCTGATGCCAAAACAAAACCTCAAAAGACCTTGAGTGAATTTGAGCT CGTGTAACAACTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGTGTGGCT
WI-1837b	112	C T ...	TTTACTTGGGGATTTTTCATAGCTGATCATAATTTACCATTTGATAATTCACTTCTTTTTCCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[C/T]CTGTCCCCAGTTTATTTT AAGGTTTTTTCATTGCACCTGATGCCAAAACAAAACCTCAAAAGACCTTGAGTGAATTTGAGCT CGTGTAACAACTGGGAAGTCTGGGGAACGTTTTAGCTTTCTGTGTGGCT
WI-1837	112	C T ...	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACT[G/T]GAGAATCTGAATATTCAGCACATACAAGTGTGACAACCACTGTTTAGTAT ATTTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1840b	79	G T ...	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACT[G/T]GAGAATCTGAATATTCAGCACATACAAGTGTGACAACCACTGTTTAGTAT ATTTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1840	79	G T ...	GGGCTCACTTCATCAGAGCACATATCACGTGATAGTCTGTTTCCTCTTTTCATAACTTACTCCCCG CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTTA[C/T]GTCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTTAATAGTTCTTGTTGAATTTCTTGTGTGTGCGACCCTGTGCCTTCT CAAGAAAAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
WI-1879b	110	C T ...	GGGCTCACTTCATCAGAGCACATATCACGTGATAGTCTGTTTCCTCTTTTCATAACTTACTCCCCG CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTTA[C/T]GTCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAATAGTTCTTGTTGAATTTCTTGTGTGTGCGACCCTGTGCCTTCT CAAGAAAAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
WI-1879	110	C T ...	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCCTGCCCCAACGCGCACAACTAGGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAACTGCCATGGCCATGAGAAAACCACTTTTCTTTGCTCC
WI-1900b	119	C T ...	

ID	No.			Sequence
WI-1900	119	C	T	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGGG[C/T]GCTCTGAGAGGT AAAGTGCCCTGCCCCAACGCGCACAACTAGAGAGAAACCACTTTCTTTGCCT GACTTCAGATCTGTGTGCTTAACTGCCATGCCAT
WI-1943c	165	C	T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAAGACCAGCGC[C/T]CTCTGAAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943b	165	C	T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAAGACCAGCGC[C/T]CTCTGAAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943	164	C	T	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGGTAGGGAAAGACCAGCGC[C/T]CCTCTGAANCTGGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1960c	270	A	T	CCAGGTGAGGCTGAAAGAAGGAGGAGGCAATTGCTGTTGGGAGGATTCTGGAGAAGCACCCT GCAGAGCTTCATTCAATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAAATGCACCTCCCAACTTT
WI-1960b	270	A	T	CCAGGTGAGGCTGAAAGAAGGAGGAGGCAATTGCTGTTGGGAGGATTCTGGAGAAGCACCCT GCAGAGCTTCATTCGTTTCAAAAGTGTCANGGTGCNTCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAAATGCACCTCCCAACTTT
WI-1977	203	T	C	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTTCATAGAGTNTGTTTTAGTCTCGTAATAATACTGTTGCCCTAGGAAGGTTGTT TTTCCTACTGCGTCTGTGAAAGCCTTCCCCATCGAAAGATGATACAGTACTTTCCAGTTATGGAGATTT[T /C]TAACAATCAAACACTGGCTGAGGCTGTTGG
WI-2012	102	T	C	AAATTCTAGAAGCCAGAAGTCAGCTCACGATTTATAAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTTCTTAATTCTGCACAAAACTAGCTAAAAATC[T/C]TTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACTTTTTCTACTCTCATT GGCTTCACCAATGCTTCCCACTGGATC

ID				Sequence
WI-2013	127	C	T	CTTTTAGAGGTGGTCATTCGGTTCCCTTCTGGGAAAGTGATTCGTGTTAAGAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACTGACACT[C/T]CTCA CCAGAAAAAGAGAATACCCATCATGAGGAAGAGAAATGACTTTGTTCAGTTATGCTCCGGGTCC CCTTTCACTCGGAGGGATATCTCAGCTTTCTGAGCCCCTGGTTACTGCAATCC
WI-2032c	166	G	A	ACCAGACATCCCATCCAGGAGTTAGTCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACAC[G/A]TGTGGGACCTCTGTCTCAACCTCCGACTTTCAC AGATCATTGGTTAGGCTCACTTCCTGTAATTGCTCTGTTTTCAAAGGG
WI-2032b	219	C	G	ACCAGACATCCCATCCAGGAGTTAGTCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACAC[C/G]TGTGGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA[C/G]CTTCCTGTAATTGCTCTGTTTTCAAAGGG
WI-2032	219	C	G	ACCAGACATCCCATCCAGGAGTTAGTCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA[C/G]CTTCCTGTAATTGCTCTGTTTTCAAAGGG
WI-2054b	188	C	T	CGTTTCTTCTCTACATCTTGGGGNACATAAAGANGAAGAAGNAGCTGTCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAAGACCCAGGCTCAACAGAACTAATACCTGC[T/C]GTTCCTCTGCCTCCAC TTTTCATGGTGGTTGGCACAGCNAGGAGAAATTTACTGGATGGGCTGTCTT CAGCCCTATCCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGTCTT
WI-2054	183	T	C	CGTTTCTTCTACATCTTGGGGNACATAAAGANGAAGAAGNAGCTGTCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAAGACCCAGGCTCAACAGAACTAATACCTGC[T/C]GTTCCTCTGCCTCCAC CAGCCCTATCCTTAGGCTCAAGGAGAAATTTACTGGATGGGCTGTCTT
WI-2573d	129	T	C	TGGGATTAAAACCCTGTTTCTTCTTCCCAGTGTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTCCGTTGCTTT[T/C]TGA TATCATCTGATCTTCCCAACCAGGGCTTATTTA[C/T]GCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGGCTGGGACGAG
WI-2573c	165	A	C	TGGGATTAAAACCCTGTTTCTTCTTCCCAGTGTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAAATGCACTTGCCGTTCACAAGGTGTTCCGTTGCTTTTGATAT CATCTGATCTTCCCAACCAGGGCTTATTT[A/C]TGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTG TGAAGTGAAATGATTTGCTTGCACAAGGTCATATGGGCTTGGGACGAG

WI-2573d	129	T	C	...	TGGGATTAAAACCCTGTTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTGTTGTGCTAGAAAATTAACA TTAACAGCAGTAAAAATAGTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTT[T/C]TGA TATCATCTGATCTTCCCAACCAGGGCTTATTTATGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165	A	C	...	TGGGATTAAAACCCTGTTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTGTTGTGCTAGAAAATTAACA TTAACAGCAGTAAAAATAGTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTTTTGATAT CATCTGATCTTCCCAACCAGGGCTTATTT[A/C]TGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTG TGAAGTGAAATGATTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573b	165	A	C	...	TGGGATTAAAACCCTGTTTTCTTCCTTCCCAGTTCAGTGTGCCTTAATGTTGTTGTGCTAGAAAATTAACA TTAACAGCAGTAAAAATAGTCTTAAAAATGCACTTGCCGTTCACAAGGTGTTTCCGTGCTTT[T/C]TGA TATCATCTGATCTTCCCAACCAGGGCTTATTT[A/C]TGCCTAGGTAAGGGGTAAGCAAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGCACAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573a	129	T	C	...	GACTTCATGCTCATGAACAAGCATTGTCTTAATTACAGACATTAAGAACAAGCTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAACGCTTTCCCAATGATGCAGCCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAAACAGCTGAAAAATGAAAATATCGATATAC
WI-2868b	60	A	G	...	GACTTCATGCTCATGAACAAGCATTGTCTTAATTACAGACATTAAGAACAAGCTTCC[A/G]CTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCAACTACTCTATTAACGCTTTCCCAATGATGCAGCCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAAACAGCTGAAAAATGAAAATATCGATATAC
WI-2868	60	A	G	...	CATGCTGTGTAACCTCTGTGCTGCTTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCATTTAAATTATATCACAGCTTATGTCCACTTCCTGTCCTGCCATCAC TGGGCTTTTTACAAAGGAGGGCTTT
WI-2870b	131	T	C	...	CATGCTGTGTAACCTCTGTGCTGCTTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCATTTAAATTATATCACAGCTTATGTCCACTTCCTGTCCTGCCATCAC TGGGCTTTTTACAAAGGAGGGCTTT
WI-2870	131	T	C	...	

ID	No.				Sequence
WI-2954c	49	T	A	---	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAAGGCATAAAAAA[T/A]CAGCACCTGGGGCACAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCAATGAGTCCTTTGAGTCCTTGGAAAGACTCTATTCCCTGGGCAACCCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCAGAG
WI-2954b	41	A	G	---	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAAGGC[A/G]TAAAAAATCAGCACCTGGGGCACAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCAATGAGTCCTTTGAGTCCTTGGAAAGACTCTATTCCCTGGGCAACCCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCAGAG
WI-2954a	38	G	T	---	TTAGCACACATATCTGTTGTGGGACTTAACTGAGACAA[G/T]GCATAAAAAATCAGCACCTGGGGCACAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCAATGAGTCCTTTGAGTCCTTGGAAAGACTCTATTCCCTGGGCAACCCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCAGAG
WI-2971b	62	T	C	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTTCTAAGA[T/C]GCTGCCAGCACCAATAAAGCTTCTTCTTCAAAACAATTTGTGTAACCTCCTCCTTAATAAACCTAACATTTCCTTGTTCCCCTGACATTCTGAAAGAAAACCTTTTACTTAGGGATTTGTCTAGTTCTTAATGTTATTCTGAAAGAAAACCTTTTACTTAGGGATTTGTCT
WI-2971	62	T	C	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTTCTAAGA[T/C]GCTGCCAGCACCAATAAGCTTCTTCTTCAAAACAATTTGTGTAACCTCCTCCTTAATAAACCTAACATTTCCTTGTTCCCCTGACATTCTGAAAGAAAACCTTTTACTTAGGGATTTGTCTAGTTCTTAATGTTATTCTGAAAGAAAACCTTTTACTTAGGGATTTGTCT
WI-2995d	133	A	T	---	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCCTCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTT[A/T]AAATCTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151	G	C	---	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGTAACATCTTTGCCTCCAGTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNAAATCTTCTTTCTGGT[G/C]TTTAAGGAAGTTATCTGAAAACCCACTGTATCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A	T	---	TTCCTGGGAAAGAAAAGATGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCCTCCAGTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTT[A/T]AAATCTTCTTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT

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WI-2995c	151	G	C	TTCCTGGGAAAGAAAAAGATGGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAAACATCTTTGCCTCCAGTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNAAATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A	T	TTCCTGGGAAAGAAAAAGATGGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAAACATCTTTGCCTCCAGTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTT[A/T]AAATCTTTCTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151	G	C	TTCCTGGGAAAGAAAAAGATGGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAAACATCTTTGCCTCCAGTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNAAATCTTTCTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151	G	C	TTCCTGGGAAAGAAAAAGATGGGGGGTTTTTNTTGTTCTCTGACTACAATCCAGAGATAAACATCTTTGCCTCCAGTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTT[A/T]AAATCTTTCTTCTGGTGTTTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAGAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133	A	T	GTGGTGCAGTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCACATCTCACTTAGCTCCTT[C/T]CCTGCCATATCCTGTTTCCTTACCTCCTCCTGAGACTTCTTCCTGAATGAATTACATCGCACTCAAATCCAATCCCTGCCTCTCTGCTTTNAGGGAACTTGACCTAAGACAGAAATCTTAGTACCAAATACTTTGCAAGG
WI-3147	85	C	T	ATTCGTAATGTTTCACTGCTTCCAGTAAAATTCTTTATTGAGGTCCATGTCCATTACCCTCTACTTA[T/C]GACAAGCAAGAACAACAACAGAAAAGCCTCGTTGCAATCTGGCCTCTTATAAATACTTTCTGTATATTTAAACAAGTACTGTGAGTNATGAATCATTACATCTTAATAAGCATATCAAAATTTTACTCAGTAATTCAGAAGACAGAAAGGACAATGAAGTGTACTTATTTNATATCTTAT
WI-3234b	68	T	C	ATTTCGTAATGTTTTCACTGCTTCCAGTAAAATTCTTTATTGAGGTCCATGTCCATTACCCTCTACTTA[T/C]GACAAGCAAGAACAACAACAGAAAAGCCTCGTTGCAATCTGGCCTCTTATAAAGCATATCAAAATTTTACTCAGTAATTCAGAAGAGAGAAAGGACAATGAAGTGAATGGAAGAAAGGA
WI-3234	68	T	C	TCAGTAATTCAGAAGAGAGAAAGGACAATGAAGTGTACTTATTTNATATCTTAT

WI-3292b	106	G	A	...	GTTTTGCTAGACTAGGAGTTCAGCTTCATCATCCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCCGTCCCAAGCCTATGCT[G/A]TGGTATTGGATTGGGATGGATTACTT GCCATGAATATTTCCATTGTTTCTCATTAATGTATTAATTAAGTAAAATATTATTTNCCATGA GACACAATGGAAAAATGGAAAACATTCATGGAAAAAACCCATTTCAATC
WI-3292	106	G	A	...	GTTTTGCTAGACTAGGAGTTCAGCTTCATCATCCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCCGTCCCAAGCCTATGCT[G/A]TGGTATTGGATTGGGATGGATTACTT GCCATGAATATTTCCATTGTTTCTCATTAATGTATTAATTAAGTAAAATATTATTTNCCATGA GACACAATGGAAAAATGGAAAACATTCATGGAAAAAACCCATTTCAATC
WI-3355	19	G	C	...	CCATGAACCATGGGCTACA[G/C]ATATTCCTAAACTTCAGAGTCCTCCTTACTGGAGAGGGATCCA CTTTTTAAAATATGATTTCTTGAAGTGGCTGCATACTATTCCTTCCAAGCACTAAAACTCATCAGAA AAAAAAATCATCAAAAGTCGAAGTTAGTTTNATTACCTTCACCTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	G	A	...	CCATGAAGAATGAGTTCCTCCCCCTGGGTCACGTCTAAGAATAGCACACCCTTGAGAATTNACT TAGCACGTGGCATTGTAATGCGTGGATTTCCTCCCGTCTAAGACACACCTTTATGCTTTCNAAGCTTT CTGGAATTGGGATGAATCTNACATTCAAATGTGCACCCTTCGTGTGGGATCACTTCTCC[G/A]TGCCCC ATCTCTGGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAATCAGG
WI-3505b	131	G	A	...	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCCATTTGTCATCAGTGCACTAAAAAATTATTT GAAAAATTGCCATTTTTAATATCTTTGGAACTTCCTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAAANANGGAAAAAAATGTTGATGATACCT GTTTAATTGGGAAATATGTTTGCATAT
WI-3505	131	G	A	...	TAACTTATGCCTCATCTGGCTTACTGCTTAGTTCCCATTTGTCATCAGTGCACTAAAAAATTATTT GAAAAATTGCCATTTTTAATATCTTTGGAACTTCCTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAAANANGGAAAAAAATGTTGATGATACCT GTTTAATTGGGAAATATGTTTGCATAT
WI-3564b	177	C	T	...	GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGAGTCACTAAATGTTTGAGAAAATAAAAGT GAAAATCAATGTGTCTTCCCAGTGTATTCACAGTGGCACAGTGTCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTCACCTTCCTTCACAAAACAAA AGTGTCACACACATGCTACCTTCCTTCACAAAACAAA
WI-3564	177	C	T	...	GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGAGTCACTAAATGTTTGAGAAAATAAAAGT GAAAATCAATGTGTCTTCCCAGTGTATTCACAGTGGCACAGTGTCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTCACCTTCCTTCACAAAACAAA AGTGTCACACACATGCTACCTTCCTTCACAAAACAAA

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WI-3649	64	A	G	AATGTCCATGCTGCTGTGCTGACCTGACCTGTCTAACACCTTCCTAGTATTCCTTAGTGGAAGAATTCAC[A/G]AGACCAGTTTGCCTTCACTTAGTAGGCCAATGACGTTTTAGTGTGCTACCACAAGGGGTACCTGCACAGCCACATCATATGTCACAGTATGGTTGCAAAGGACCTGTCTAGACTCTTCTGCCTGGTCTTCCTGTTTTACCCATATTAATGATGACACATGCAAACCTCAGAGCCTTTA
WI-3674b	133	G	C	ACAGTACACACATGGCCCCATATGGAAACAATCATCTGACTTATGTTACCTGAGAAGTTCCCTCTCTAAATTTAACTACCAGGCGGAGTGCTTTATAGTAATTAAAATATGTTTATTAGAAAATAACAAAAT[G/C]AAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACTTGGTCAAATGATTGTTAATTCTTAATTAATTGTGTTTATGTTTNATTACTGCCAATCACAGCCAAG
WI-3674	133	G	C	ACAGTACACACATGGCCCCATTATGGAAACAATCATCTGACTTATGTTACCTGAGAAGTTCCCTCTCTAAATTTAACTACCAGGCGGAGTGCTTTATAGTAATTAAAATATGTTTATTAGAAAATAACAAAAT[G/C]AAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACTTGGTCAAATGATTGTTAATTCTTAATTAATTGTGTTTATGTTTNATTACTGCCAATCACAGCCAAG
WI-3682	137	G	A	CAATATAGACCAAATGACTGCCACAAAGAGAAATTAGTGGATCTACATTTAGAAACCACACATGTTTTATTGGCTCTCTCTCTCTTTTAAGTCTCTCCAACACCAATTCACTTATTCTTTCAA T[G/A]AGCATTTGTCCAATTTAAAGTCAATGAAAAAATAATGTACATTTTCAACAAGTATACATTAAGCCCCTGCAAAGTGCTTATATGCTAT
WI-3854b	194	G	A	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGACAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTCTACCTGCTTCTGATTAATAACTCTGGTTCAGGAAGGCAAGGGCAGTTATGACCACTTACAACTGAGGAAATCAAAGCAAC[G/A]AGAAGTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-3854	194	G	A	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGACAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTCTACCTGCTTCTGATTAATAACTCTGGTTCAGGAAGGCAAGGGCAGTTATGACCACTTACAACTGAGGAAATCAAAGCAAC[G/A]AGAAGTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-4039	210	G	A	AGCCAGCCACCATCATGTTGAGTCCTGCTCATTCTTCCATCTTCTCTATTTCTCTCTACTGCCTTCACCTTCCATTAACAGAACTCTTGTGATTACATTGTATGTTTGGTTACACTACAGAATCCAAGATGACCTCCCCATCTCAACTCTCAAATTAACCTTAATTGTCAATCTATTTGTCATTACCATAACATATTCATGG[G/A]TTCTGGGATAAGGGGTAGACATTTTATGGGAGGCATTA
WI-4110b	130	T	C	GAAAAATGATGTTTTTGATTTTGATTCTTCCCTTCCTATCTTCAGATTATTGGAGTGTCATTAGAAAACTGATAGTAACCTTTATTGATGAAACTCTGTCTATAATTAAACCTTCCTGCTTTATTTGCC[T/C]ACAGTTTAGGTAATAAAAGATGCCCAAGAATTCAGTATTCAGATTCCAAGAATTCAAGTACAGTAAAAGTAGCAACCATGGGTAGGGACAAGTNCAGAAAAAGGGAGGAGGTNGGGGGGTTTTCTGGGAAGA

ID	Pos			Sequence
WI-4110	130	T	C	GAAAAATGATGTTTTGATTCCCTCCTATCTTCAGATTATTGGAGTGTCATTAGAAAACTGATAGT AACCTTTATTGATGAAACTCTGTCTATAATTAAACCTTCCTCTTCCTGCTTATTTGCC[T/C]ACA GTTTAGGTAAATAAAAGATGCCCAAGAATTCAGTATTCAAGTACAGTAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGGAGGAGGTNGGGGGTTTCTGGGAAGA
WI-4119b	168	G	A	ACCTCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAAATAG AATGGAAGGAGTAAATAAAGGTAACTACGGGGAAGAACACAGGACAAGAACAGAGACAGAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTGTTTTTCTTTCA TGAGACCGTCTGCATTCTTTGTTTTTTAAAGGGCTCTGTTGATCATCTTCA
WI-4119	168	G	A	ACCTCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAAATAG AATGGAAGGAGTAAATAAAGGTAACTACGGGGAAGAACACAGGACAAGAACAGAGACAGAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTGTTTTTCTTTCA TGAGACCGTCTGCATTCTTTGTTTTTTAAAGGGCTCTGTTGATCATCTTCA
WI-4123b	51	T	G	CAAAGTCAGATTTGATTATTCAGGATAACAATTTGAAAAATAGAAAAGTG[T/G]TTAAACTATTT CAAATAAACAATAAAGAAAAACATGATGAAATTCTTCGTTACATAATTGTATAGAATTAGTGGGG TTCTTCCATGACATTGGCTTGTTCTTCTCCAACAGTGGGTGGTTTGGATGTTTCCTATGCTTCTC AGGCACAACAAACAACAGTGAAGAAACCTTTAGCAACATTCTGCTGAATGTGTG
WI-4123	51	T	G	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTGAAAATAGAAAAGTG[T/G]TTAAACTATTT CAAATAAACAATAAAGAAAAACATGATGAAATTCTTCGTTACATAATTGTATAGAATTAGTGGGG TTCTTCCATGACATTGGCTTGTTCTTCTCCAACAGTGGGTGGTTTGGATGTTTCCTATGCTTCTC AGGCACAACAAACAACAGTGAAGAAACCTTTAGCAACATTCTGCTGAATGTGTG
WI-4149b	145	G	C	TTGTACATGTTCATTCATCCCCTCCCCATTCTTTCTGTCTTATAAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTCCATCAAAGCTTTCTCAGCATCTCTATATACT GTGCTGT[G/C]CCTTGTGAAGAAGCCAGAGCCGAGCCATACCAACATGATCTTTGCTTGAACTGTAGT AGGAGAGACAAGACAAGACAGATGTGCGGGGTCCCCATGATATAAGGTAATTG
WI-4149a	137	T	C	TTGTACATGTTCATTCATCCCCTCCCCATTCTTTCTGTCTTATAAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTCCATCAAAGCTTTCTCAGCATCTCTATATAC[T/C]GTGCTGTGCCTTGTGAAGAAGCCAGAGCCGAGCCATACCAACATGATCTTTGCTTGAACTGTAG TAGGAGAGACAAGACAAGACAGATGTGCGGGGTCCCCATGATATAAGGTAATTG
WI-4182	188	G	A	TAACACACTTTCATTGGTTCCTATTACTGCAGTTAAAGGACCATCCATTATTACAATTCCCTC AGTTCTATGCTTTAGAGTNCTATTATAGGACTACTGTAAAATTTCAGAGGGAATTACCTCCTTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTGCAGGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCCCTTCCCAAGTTCTTAAATTCCTAG

Clone	Pos	Variant		Sequence
WI-4230	93	T	...	AGAGACGTTGAATGGGGGACATCTTTCTATTCGATTTAGTTTAACATTGATAAGAATTGATGAAAGTTGTCACATTCCAGATTTATCTTATAGCAGCAGAAGTCTGGCAAATAATAACAGCACACTGACTTTCCATGGTAAAAGAAGTTAGAGAAAAACAGCCTATTTTTCTTAAATGTAATTCTGAATACATTTAAATGGAGGAGAATGAATAGTGACCTTGAAATTTATGG
WI-4241	118	C T	...	GAAAATTCCATTGAAGTTTGACCTTGACTCTCATTAATACTTTNCTTGTAGTGGTTGTATTCATTTTTGACAACAGACGAAAATTTCCACTTAAAATTAAATTCTC[C/T]AAGTATCTATGATTTAGCACTGTTAGCACCAGAAACTGTGAAATTTATCTCCTAGATATTCTTCAGAATCTAGGATGGAAGAA
WI-4271b	151	A	...	CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTCAGCATCAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAATAAGAGCCTCAGGGGACTGAATCCAACGGGGAATATTAGAGTNCTACAGGGAGCCCCAACCCTCCCCCCTTTGTCTCAGGCTCTTAGAAGGTCCAGTCAGGGGC
WI-4271	151	A	...	CAGGGCTTTTGGGAAGATCAGTTAAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTCAGCATCAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAAATAAGAGCCTCAGGGGACTGAATCCAACGGGGAATATTAGAGTNCTACAGGGAGCCCCAACCCTCCCCCCTTTGTCTCAGGCTCTTAGAAGGTCCAGTCAGGGGC
WI-4389b	156	G A	...	AATCGAAACATTGATTTTTTGTAAAGGAACCACATTATTATGATATTGTGCCCAGTTTAGCATATGAAATTTGAAAGGGATGAACCTGGAGGAAGAGAATAGAAAGGATATTATTGCATAAACCTTTGGAAGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAGTGAACAGACATGATTGACTTAAGAGGTATTGTAGGAACTGGAAGCGGTAA
WI-4389	156	G A	...	AATCGAAACATTGATTTTTTGTAAAGGAACCACATTATTATGATATTGTGCCCAGTTTAGCATATGAAATTTGAAAGGGATGAACCTGGAGGAAGAGAATAGAAAGGATATTATTGCATAAACCTTTGGAAGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAGTGAACAGACATGATTGACTTAAGAGGTATTGTAGGAACTGGAAGCGGTAA
WI-4488	31	A G	...	GATGACAATTATTGTGTATTGGCATTTAAA[A/G]GTACCATTCCATTTCTTCTGGCTTTCGTGTGTTTGTTGTTGAGAAGTCAGGGGTTAGTGCGTATTGCGTCCTTTTCTAGTTCTTCTCAGTAGGAAGACTGATCCTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTAAAGAACATAAATCAAATTGTATTATCCTATGCTTAAAATGCTCAG
WI-4491	145	G C	...	ACCATCAATGTATCACCTTCTAAAATTTATTAGATGATTAACTGGCTCTGTTAAAAAATAAAAACCTGTCTTGGACATTGAAAATAAAACATTACTATTGGTCATTTCTGCTACTTACAAAGGTACTGCACTAAACAAGTTAAG[G/C]GTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAAATTTCTACCACTGTCATTTCTTGTCCCATAAATAAATTTTACATGCCT

ID	Pos.			Sequence
WI-4584	144	A	G	TTGGTTGGCATTTAGCCTCATAAACAACTATTTACAAATCATAATTGTTACTCTTTATTTTACAAAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTCTTAGTCGCAGAGCCAAGATTTGAACCCAGGAATCCATT CACCGGTAC[A/G]TGCTACCTGGGTAAAAATGTTAATTAACTCTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTGAAATAGGTGTGCTTAATTGTTATCAGTATGC
WI-4639	185	C	T	TTTCTGCATTTGAAATGTGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCCTATTATCAGAGAGAGATCTCAGTTTAACTTCCAATTCCACCATTTAC TGACCATATGACTGGGGAACATTATCTCACCTACTATCATTGTGAGTCTGTATCC[C/T]CATCTTTAAATTGTA AATTTTAAGGACACCTATCATCATAGTAATATTGTGAGGATAAAATGAAATAA
WI-5327	63	A		AAATGAATCCGCTTTAGAGCAAATACCAGTAAGGGCTGGTGCAGGATGGTGGTGGCTGAGAGA[A/--]GATTACTACTCTATAAAAGCATATTAATTTTATAAAATATGGAAAATTAACTAGATAATTAAAATGTGAAT TGAGTTTGAAGGTTGCATGAGAGTAGGGAGGAGGAGTAGTTCTACTTATATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCGGATGACAATGATGAACTGTTCTAAGCAGACAG
WI-5390	87	C	T	GCTTTTGAGAATGAAAAGGGGAGCCTGGACCATTGCAGGGCTTCTTCATCTCTGATTATTTGTGTAT TTATTGTTCACTTATTTATTC[C/T]GTCTGTCTCCCTTGGTATGCTTGTGTCATGAAACAATGAATC CCCAGTGCCTGGCCGATTCGTGGCCGATTCGTGGCGCTCCTGGAACCTGTGAATCTATGGAAGACAAACGAAT ACGAATGGGTTCAGAATTGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	C	T	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAAGCAGT GCAAAACATTATTTTAATT[G/A]AAAGAAACTTGTTTCTGAACTTTGTACTCTTGTAGTNAAATTG AATCTTTCCTTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTTCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTTAGAGTTTCATAACAA
WI-5404	87	G	A	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAAGCAGT GCAAAACATTATTTTAATT[G/A]AAAGAAACTTGTTTCTGAACTTTGTACTCTTGTAGTNAAATTG AATCTTTCCTTCTCAGCAGTTCCATGGTCGTGAATCCACCCCATCTCTTTTCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTTAGAGTTTCATAACAA
WI-5545b	77	A	C	TAGGAAAGGGGATGGGATGGTGATGGCCTCTGAGACATTAAATCTATTCTTTCACCACTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTTCTGTTTCTGACAGCCAAGTTTGGCTGGCTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAAGATTTGGCTGACTTTGGCTGACAACTGCTACAAAAGANTC GAGATACACCATGAATTTTATTTCATTTCA
WI-5545	77	A	C	TAGGAAAGGGGATGGGATGGTGATGGCCTCTGAGACATTAAATCTATTCTTTCACCACTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTTCTGTTTCTGACAGCCAAGTTTGGCTGGCTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAAGATTTGGCTGACTTTGGCTGACAACTGCTACAAAAGANTC GAGATACACCATGAATTTTATTTCATTTCA

WI-5860b	134	A	G	---	ACTCAAGTTGGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTGCTAAGATTTTATTGTTCTTTTTATATAAATTATGGATTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACTAC[A/G]TTATACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTAAGGGAATCAATTTCCAAATCATCAACTTCTGTAT
WI-5860	134	A	G	---	ACTCAAGTTGGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTGCTAAGATTTTATTGTTCTTTTTATATAAATTATGGATTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACTAC[A/G]TTATACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTAAGGGAATCAATTTCCAAATCATCAACTTCTGTAT
WI-6106	208	C	G	---	GCAAACAACCTATTATACCTGATTCCAACCCAGGTCTACTAACATTAATCAACCTAACCACAATACTATATTGTCCTGTTCTGAATTATTTCATTTAGAATCTGATGAGATTTAGCATGGGATAAGTAGTGCAGTGCAGAGATAGTAAACACTGCTCTCTTTTGCTTCCAGGAGTCTCAATGTGAAGTATATTCTTACAGAGTAATT[C/G]ATAGTAGGTCACCACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T	C	---	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAAATGTACATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAAAACCCTATATTTNCTGTCTTGTGCATACTTAAAATGTATAATGTGGGAGAAGGAATTTTGATGTGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109c	147	T	C	---	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAAATGTACATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAAACCCTATATTTNCTG[T/C]CTTGTGCATACTTAAAATGTATAATGTGGGAGAAGGAATTTTGATGTGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109b	147	T	C	---	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAAATGTACATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAATGTGTATAATGTGGGAGAGAGGAATTTTGATGACCCTATATT[T/C]CTTGTGCATACTTAAAATTTATACCATGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109a	129	T	C	---	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAAATGTACATTGAGTCTTCCTTCTCTGTCATATTTGATTGATTCATAACTGCTTATTGTTTAGCACCTGTCTTCCAACACATGCTGTTTGTTCAATGA[T/C]GCATATCCCAAGTGCCTTAGACAATGCCTCCCATACAGTGAACAGTATTTGACTAAAACATACTTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG
WI-6112	96	T	C	---	GAAC

WI-6244	103	T	C	TAATTGCACAACTTACACATATCAGGGTTTCTGATTGAAAGGAAGGAGAGAATATTCCTTCTTTCTTTAGTGATT GCTTAATTAATTCATAATAAGTGCACCATCTCT[T/C]GCTCCTTATAAATGTGTTTAGAAGAAAGG AAATTGAGTGTTGGGAATTAAGCAACCAGGAGACATTTTATATACTCCTACAGTGGGGGAAGACTT CCTATTTTCTTTCCCAAGGATGGATACATTCTAC
WI-6268	124	C	T	CTGGCCTATAATCCAAGTTTAGGATTAATCTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTTCCTCCTCCTAGTAGGGCTTTGGGGTGTTGGCACCGTTTGGCTCATTC[C/T]ACTCTCCCT GGGGTCTTATTGACTTTCAGGGAGGAGCTAGAAGAGAGCTAGGACAAAACCTGCTCTTTGCAGAAAGAGTCG GGGGTTCCAAAGATTTCGTTACGATTTTTTA
WI-6336b	234	C	T	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCCC ATATATTCCCCCTTTACATGTTTTCTTTATAAGACATACAGTTTAATCAATTAACAAACTAAACAGCTT ATATACTGGCAATAATATTACAGATGGGTTTATGTCAGAGTAATACATCACATGAAATGGACCATGTG GTACCCCAGTGCATTATGTCTTGGTAGAGCC[C/T]TTGAGGACACTGACAGT
WI-6336	234	C	T	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCCC ATATATTCCCCCTTTACATGTTTTCTTTATAAGACATACAGTTTAATCAATTAACAAACTAAACAGCTT ATATACTGGCAATAATATTACAGATGGGTTTATGTCAGAGTAATACATCACATGAAATGGACCATGTG GTACCCCAGTGCATTATGTCTTGGTAGAGCC[C/T]TTGAGGACACTGACAGT
WI-6381	92	C	A	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGGNTTCATGTTTAACAA[C/A]GTATTTTAAAAGCTCAAACATTTTAAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGCGTTTGAATGTCCCACTCCCAACTTCACAATCAAAATC TACAGANGCGGGCAAAAGAATCAGAGTTCAG
WI-6436	198	C	G	GGTTGAGGGCATTGGGAAAGGCAGAAATTGAGGCAGTAGAAAATGGACACATTTTAGGAAAAGAGAAGT TCAGAGGCAAAGTCATGACACAGCGAAATACAAGGCTTAGGAAGAGACAGTAGTCTCTGTGGTTGAA ATTTTGGTGTCATAATAAGAAGTTAGACTTGGTGGTGTAGTAGTGTAGTAGGCGTT[C/ G]ATTGGGTGTATTCCACAGACAAGGTGATGTTCTAAGATTGATATTATTGT
WI-6449	186	C	T	GAGGCCCTCTTGCTTTCCTCAGTCAAGGCTGTATCCAGGGTGTATCAGGGTCTATATGCCCATATGT GTATGGCTAGTGTTGTTCTGATTGGTTGGTGCTCACACTGCCCCAGATTGTTAAATATTTGAAAATC GTATCTGGTTCTATTCATCTGCATTCTCTGATCTTATGTCTGGTCTATT[C/T]ATCCCTATTCTCTGA TCTTATGTCAGAACCTGAAGTTCCTCTAATTTTTCTGTGTGGTGTATTTATA
WI-6449	186	C	T	GAGGCCCTCTTGCTTTCCTCAGTCAAGGCTGTATCCAGGGTGTATCAGGGTCTATATGCCCATATGT GTATGGCTAGTGTTGTTCTGATTGGTTGGTGCTCACACTGCCCCAGATTGTTAAATATTTGAAAATC GTATCTGGTTCTATTCATCTGCATTCTCTGATCTTATGTCTGGTCTATT[C/T]ATCCCTATTCTCTGA TCTTATGTCAGAACCTGAAGTTCCTCTAATTTTTCTGTGTGGTGTATTTATA

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WI-6463	72	T	C	---	GCTGGAGAGAGAAAGACCTCCAAAAGAAGAAGAAACTAAATCAGAGTCTCTTGAGCAAGAGAGGAATTGAAA AGAACA[T/C]TGAAAAAAATTAAAGTAGAACTCAAAGAGCCAAAAGTCCCAATTGTGTCCATTA TAAGAAATATTTTGAATGGAAATCTTAAGAATGATTTATTGATCAGTTAAATGTTCTTCCTCTCCTC CAGTCCCATTTATATGACATTCCGCATGCTG
WI-6474b	76	C	T	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAGTAGGGATTTTGAAAGGCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACTAAAGTATAAAAGAGTGAGCACTTAGGGTACCATAA
WI-6474	76	C	T	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAAATGTTATAGAAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAGTAGGGATTTTGAAAGGCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACTAAAGTATAAAAGAGTGAGCACTTAGGGTACCATAA
WI-6478b	175	T	A	---	GAACTCAATTAACTTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGCCACGCTTCGAGGCCTGCTATATGCTTTATTTTTGTGA CACTGTCTATTTACCCTCCCCAATAGTGGAGAATCAGAG[T/A]GCTCCTTGTCAGTGTTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACTG
WI-6478	175	T	A	---	GAACTCAATTAACTTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGCCACGCTTCGAGGCCTGCTATATGCTTTATTTTTGTGA CACTGTCTATTTACCCTCCCCAATAGTGGAGAATCAGAG[T/A]GCTCCTTGTCAGTGTTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACTG
WI-6559	149	G	A	---	CACATTTTGAATGCAACTGAGAAANTGGTTTTNTAGGCCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCAAACATGCAAAACATAAGGCCAACAATTCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA[G/A]TCAAATTTTAAAAGAGAACAGGAGAAATAAGGAGAAGCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54	G	A	---	TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACACTCACATATGTCTGTGTCCTGAAAATCTCAATTAATTTCTCCTNCCTTTTCCAT GCTCTGCCTCATTTNCTCAGAAATTGAAGGCATTGATTATNATTTTTGTTTGGGTCTGTGTAAAG GTTCCTTGGCAGGAGAACATGCATATGACTTTAAAATAAAGACCAACA
WI-6564	54	G	A	---	TTCTTTATTGGTCCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACACTCACATATGTCTGTGTCCTGAAAATCTCAATTAATTTCTCCTNCCTTTTCCAT GCTCTGCCTCATTTNCTCAGAAATTGAAGGCATTGATTATNATTTTTGTTTGGGTCTGTGTAAAG GTTCCTTGGCAGGAGAACATGCATATGACTTTAAAATAAAGACCAACA

ID	Pos			Sequence
WI-6608b	46	C	-	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGTIC/- JAGTTCAGGCAGCTAAAGGGAGGGGGATTTCCTCCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTGAACTCCCAGCACTAG GTAAAACTGCAAAAGAAAAAACACCTGTGCCCAGGCCACTAGCTACAAGGCCACCAGAAAAGGAA AGC
WI-6608	46	C		CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGTIC/- JAGTTCAGGCAGCTAAAGGGAGGGGGATTTCCTCCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTGAACTCCCAGCACTAG GTAAAACTGCAAAAGAAAAAACACCTGTGCCCAGGCCACTAGCTACAAGGCCACCAGAAAAGGAA AGC
WI-6666	68	C	A	GTTAGACAGTATCCAGCAAAAAGGTTATTTATACCCTCACTTTTCCAAAACGAGGAAACCTCCCC A[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGTCTTCTTACTCTGTTGGTTCATGTAA ATGTTTGGGGTGACTCATTCCGCCTCTCTNTTCTCAAGTTCCAGGCTCTTGGGTAGACCAAAACTA ATACACAATGTTAGAGCACAAGAGA
WI-6670b	120	A	G	AGATTAACACATAATTATACTGGGGCCATTGTAGGGTTNGGGGAGGAGTGTTTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTCAGGGCCGGAGTCAGGGTTGTGGGGCTCAGGGAATTGTAACACAGACACAGAATCTTAGAAGGGAT AAAAAAAGAAATACAGAATTGTAACACAGACACAGAATCTTAGAAGGGAT
WI-6670	120	A	G	AGATTAACACATAATTATACTGGGGCCATTGTAGGGTTNGGGGAGGAGTGTTTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTCAGGGCCGGAGTCAGGGTTGTGGGGCTCAGGGAATTGTAACACAGACACAGAATCTTAGAAGGGAT AAAAAAAGAAATACAGAAATGTAACACAGACACAGAATCTTAGAAGGGAT
WI-6704c	33	T	C	TTTGAAAATAAATTCATGCACCAATGTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAAT/AAGTTTTCATGACACACGGNCA CTATTGCTCTCTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33	T	C	TTTGAAAATAAATTCATGCACCAATGTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTCATGACACACGGNCA CTATTGCTCTCTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28	T	C	TTTGAAAATAAATTCATGCACCAATGTT[T/C]TAACTCACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTCATGACACACGGNCA CTATTGCTCTCTTAAATATGGTTGTACATGTCATCATTAATCGATTCATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106	G A	CCATGGACAGTTTAATTAGGAAGCTTCGACTTGTTAGAATAACAGAGGAAGTCCCAGTTATCTACCT ATTCCTTAAAACACATTTGTCAGCCTGGAATGATTCCC[G/A]TAGTAGAAAACTCAACATCCACACCT GCATAAACATCGCCTCCCAAGTGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC ATCTCCAGTCCAATGGA
WI-6766b	148	G C	AAAACAAATGGTGCATTGCATAATATTTGTGGTCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATACCTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAAN[G/C]AAAGTCAACGTTTCTCTTCTAGGGNTCTGCACACATATTTATCACTGA GAATTGGTCAAACAGTGGAGGNGAACTTACCCAAATCCCAGTTCCCTTCTTC
WI-6766	148	G C	AAAACAAATGGTGCATTGCATAATATTTGTGGTCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATACCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAAN[G/C]AAAGTCAACGTTTCTCTTCTAGGGNTCTGCACACATATTTATCACTGA GAATTGGTCAAACAGTGGAGGNGAACTTACCCAAATCCCAGTTCCCTTCTTC
WI-6787b	97	A G	ACAGATAAAAGTCTTTATTCCCCTGTATGTTTACATAAGAAAGTTCTTTACAGACTTTTTTTTATACA ATACTTGTCAGCAATGTTCAAATTTCAC[A/G]TTTTTACTGCATAAGATATCTTCATGTACAACTGT ATGCTTTGTCTCTTCTGGGAAGGACGCGTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTGCAATAGGGCAGAGTAGANTACTCACAGAAAAGAGTAAATTCAGGT
WI-6793	105	C G	GAACCCACCAGGTCCTGTTATTTATTAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGGTCTTCAAATCAGTCAACCCC[C/G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTGGCTGTGTGAGGAAGTAGGGTTAATGCCCTGCTAATCCCGGAAAGGGGCAGAGCTGAAGCCA GAGCCAGANTCCTGGCAATTCCACCAGTTTCTCATCACAGGTAAAAAGGCAAC
WI-6810b	37	T C	CACAATAATAAAATCACTCCCTACCTTGAAAACTTTA[T/C]AGAAGCATTTTAATTTTACAACACA AAGCTCAAACGNACCTACAATAAGTCTAGTAGTCTGTTTACGNGCCAAGGGATAAGGCTGAACAATA AATTAACCCTTTAAAAATGTCTATGNACAAGTACAATTTCTTTTGAGTTCTGCGAGAGCAATGACC ACTAAGNAATATTTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6810	37	T C	CACAATAATAAAATCACTCCCTACCTTGAAAACTTTA[T/C]AGAAGCATTTTAATTTTACAACACA AAGCTCAAACGNACCTACAATAAGTCTAGTAGTCTGTTTACGNGCCAAGGGATAAGGCTGAACAATA AATTAACCCTTTAAAAATGTCTATGNACAAGTACAATTTCTTTTGAGTTCTGCGAGAGCAATGACC ACTAAGNAATATTTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145	C A	GCATGATTAAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTTGTAATCCAGTTAAGACCATCAGCATATACAACATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C/A]TGTGGAATACCCTGTGTGCTCTACTNGCCTCCAAAGGCATTCAGGGGATCATCA AAGAGTGTTGGACACCCTTGTTGTTCAAATCTTGGTTCAGGTGCGGCCTGTGCAG

			Sequence
WI-6817	145	C A	GCATGATTAAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTTGTAATCCAGTTAAGACCATTAAGACTACCCTGTGTCTCACTNGCCTCCAAAGGCATTCAGCGGGATCATCA GCAGGGTAAC[C/A]TGTGGACACCTGGTTCAAATCTTGGTTCAGGTGCGGCCTGTGCAG AAGATGTTGGACACCTGGTTCAAATCTTGGTTCAGGTGCGGCCTGTGCAG
WI-6819b	221	C	GATGGAAAGCCATTTATTTTCTCTAAATTTAAAATAGAAGACTTTAATGGAAAACATTTAGTAGTAC CATCATGTCACCCTGAATGCCAGCAATACCTCGACTTTACACACGCAGGAAGCCTAGTAAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCCTTCAACAGTTTGCATATACAAAATTTTCTGCTATTTG CTTTAGCAAACAGCAATAACTTTGTGTTCCTATATGACACCTAATATCCAG
WI-6819a	175	G T	GATGGAAAGCCATTTATTTTCTCTAAATTTTAAAATAGAAGACTTTAATGGAAAACATTTAGTAC CATCATGTCACCCTGAATGCCAGCAATACCTCGACTTTACACACGCAGGAAGCCTAGTAAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATT TTGCTTTAGCAAACAGCAATAACTTTGTGTTCCTATATGACACCTAATAT
WI-6826b	154	A G	GCAAAAAGCTTTATTGGCTCCAACAAATATCCCTTTAAAACTCCTCTCTTCTCTGTCTCAGTG GAACAACACATTTGAATTTGCAGTTTATAGCCATTTTTTCCCTAAGAACCATATAAATAC ATGCAAAAACCTTGTACAT[A/G]GAGCTTAAATAATCAAAATGCAAATGATTGGGTGCACTGT TAAGCTGAATTGCAAATTATGGCAACACACTGGACTGGGGTATACGTTG
WI-6826	154	A G	GCAAAAAGCTTTATTGGCTCCAACAAATATCCCTTTAAAACTCCTCTCTTCTCTGTCTCAGTG GAACAACACATTTGAATTTGCAGTTTATAGCCATTTTTTCCCTAAGAACCATATAAATAC ATGCAAAAACCTTGTACAT[A/G]GAGCTTAAATAATCAAAATGCAAATGATTGGGTGCACTGT TAAGCTGAATTGCAAATTATGGCAACACACTGGACTGGGGTATACGTTG
WI-6857a	122	T C	AGTGCAAACTATTTTGAACAAAAGTAAACATAGTGAGTCAACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAACAATATTCACTCAAGTAAAAATACAGCAGATGAGTGTCTCTCACATGTA[T/C]ATTTAAT TATTCATGCTTTTCATCAAGTATGTCTTTCAGTCAACTTTCAGTGTAATTTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAAGTTGGCAACTGTTTGGGCTAATT
WI-6865	153	G A	TTATAGAATACTTATGGGGCATACGNGTAAATGAACCTTAAAATCTAAACAACAAACAGCTTG TTTGTGGTTCGTCCTGAAATCCTCCCGCCCAGTAAATCCAGCTACTNGGTTTTCTAAAAGACGTA ATTTTGCAGGCAGGCAAACTTC[G/A]TAGAGCCATTCTGTGCAGAAGAGGGGAGAAGCTGTTTGTT TTACCTGTAGTAGTGAAGAATTCTTTGGCGTGTTAGAGAACTGAGCTCATTAA
WI-6909	73	C T	ATTGAAAACTGGTTAGCAACAGATAAATTACAATAGAGCCTGGATATAAAAATGAGAGAAGAATGC AGACTTA[C/T]AAGCTTTATAGAGAAAGGAGCAAGTTTTGAAATCAGATTTTATGATAC GGAAAAAAAATTTCCTTTTTGCCAACAAATATTCCACAATATTTGCCTATTTTACACATATC AAACACCATTTCCACAATATTCCACAATATTTGCCTATTTTACACATATC

ID	Pos			Sequence
WI-6910b	163	G	T	CACTCAAAACCTTTATTCATTGATTTACAAACTGTACAATATTTACAAAGTTTAGGCATTAATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAATTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCCGACCTTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144	A		GCTTGTTTTTGTTTTTGTTTTTGTTTTTAAGTGACACCTTGGCCTTCTTCACTTATCTTACCC AAAAGTGCCTTTGGGCCCAGCCACTGACTGATTTAAAACCCAGAAATGTGGTTTAAACAATGTGGT CGTGGTGAATTCAGGTGATTTNATTTCTATTGGTAGTATTTTCAGATTTTCCCACAAAGAACAATG TATTGTCTTTGTAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175	T	C	CAATCAAAAAGTTCCAAGTTTCAAAGCTGGGATGAAAAGCCAGGTCTTCTGCACTCTGTCAC ACTGGATTTNCCTCTGATCCAGCTGCGTGTCCCATAAGAAGTTCACTCTTAATTTCATGTCCCATG CTTTGTCTTGGTCCCGTGTGAGGAAAGGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCCTCTGAAATAGTAAAGGTGACCTTAGAAGTTA
WI-6928	175	T	C	CAATCAAAAAGTTCCAAGTTTCAAAGCTGGGATGAAAAGCCAGGTCTTCTGCACTCTGTCAC ACTGGATTTNCCTCTGATCCAGCTGCGCAGCCCCCATAGAAGTTCACTCTTAATTTCATGTCCCATG CTTTGTCTTGGTCCCGTGTGAGGAAAGGGGTCAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCCTCTGAAATAGTAAAGGTGACCTTAGAAGTTA
WI-6955b	79	G	A	TTTTTATGAAACATTTCAGATTCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCATCGAGGTAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAAACTATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955	79	G	A	TTTTTATGAAACATTTCAGATTCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCATCCAGGTAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAAACTATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6957	47	C	G	AAACTAAAAACCCTTATTGTCTCCAAGTGTGTGGCAAAATAGAAAAT[C/G]TTTCAATTACATTAGG AAATCGGGTGGATAACGGAGGTAGTTATTCCACTTAAGAAGCATTCCAGTCAAATAATCACAAAA ACAAATTCAGATTGCTTGGATCTTATTATGGCTTGAAGAACTGGATTTGAAAACCACTTTAGG CTAAAATAAATGTATATGTATATGAATAATGCATACAGACTGTGTATCTCAGAAAATCATGC
WI-6996c	242	G	T	ACTTCTAGTGCCTCTGGCCTGGCGTGCCCTCTGTTACCACCACCCTCTAATGCCTCTGGTCGCCGCCCGACCCCTGGTCGCCGCCGAGAGGCCT TAAATCTGCCTGCCTGGCCTGGCGTCCCCTCCCTCTGTCTTCAGCACCCAGGTCCTCAGTTCCCTG CAGGAGGAGAGAGGGGGCCCTGGTGGGCCCCTGTGCTGCTGCTCCTGCTGCTCCTCTTCCTTCC[G/T]GTCGGATC CTCTCCTGATGGTGGGCCCTCTGTTGCTGCTGCTCCTGCTGCTCCTCTTCCTTCCTTCC[G/T]GTCGGATC

Marker	Pos	Alleles	Sequence
WI-6996b	242	G T	ACTTCTAGTGCCTCTGTTACCACCACCTCTAATGCCTCTGTCGCCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCCTCCCCTCTGTCTTCAGCACCCAGTTCCTCAGGAGAGAGGCGGCAGTTCCCTG CAGGAGAGAGGAGGGGCTGCTGGACCCAAGGCTCAGTCCCTCTGCTCCTCTCTCC[G/T]GTCGGATC
WI-6996	228	T G	ACTTCTAGTGCCTCTGTTACCACCACCTCTAATGCCTCTGTCGCCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCCTCCCCTCTGTCTTCAGCACCCAGGAGAGAGGAGGCGGCAGTTCCCTGCTGACT CAGGAGAGAGGAGGGGCTGCTGGACCCAAGGCTCAGTCCCTCTGCTCCTCTCTCC[T/G]GCTCTTCTCTCTCCGGTCGGATC
WI-7021b	112	G A	TGGGGAGGACAGGGGAGGAGATGCTGCAGTTCCAAAAGAGAAGGTTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCCTGAAAGCCACAGACAATATGTCCCAAAT[G/A]CCCGACTGCCACCTTCTGTG CTTCAGCTCTTCTTGACATCCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAATTAATCAAACC ACTGTATTAACAGATAATAGCAACTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G	TGGGGAGGACAGGGGAGGAGATGCTGCAGTTCCAAAAGAGAAGGTTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCCTGAAAGCCACAGACAATATGTCCC[A/G]AATGCCCGACTGCCACCTTCTGTG CTTCAGCTCTTCTTGACATCCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAATTAATCAAACC ACTGTATTAACAGATAATAGCAACTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T	GGCAGTAGGACCACCAGTGTGGGGTTCTGCTGGGGACCTTGGAGAGCCTGCATCCCAGGATGCGGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACGCGCTAAACGTTGGTGA[C/T]GGTTGGGGAGCCTCT GGGGCGTGTTGAAGTCACCTTGTGTGTTCCAAGTTCCAAACAACAGAAAGTCATTCCTTCTTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7056b	118	C T	GGCAGTAGGACCACCAGTGTGGGGTTCTGCTGGGGACCTTGGAGAGCCTGCATCCCAGGATGCGGGGTGG CCCTGCAGCCTCCTCCACCTCGTGTTGTTCCAAGTCACCTTGTGTGTTCCAAGTTCCAAACAACAGAAAGTCATTCCTTCTTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACAGATGCCACACATAAGGGGTTTGCCATTTGATA
WI-7091b	153	A C	AATTCGCTGAAAAAGGAACTACCTATCCTTACATTCACCTACTAATGTCTCTTCTTCTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTTATACTGCTCTATAAATAGTATTCCAATCACTACTGTG CTTAATTTAAATAGCATT[A/C]TCTTATCATTTATCAGCCTTTATGTATTTCCAAGTAAAATATTA ACATATTATTTCATTGGTCTCTTTTTTATCTGGTTCTATATGAATGCTAT
WI-7091	153	A C	AATTCGCTGAAAAAGGAACTACCTATCCTTACATTCACCTACTAATGTCTCTTCTTCTTCTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTTATACTGCTCTATAAATAGTATTCCAATCACTACTGTG CTTAATTTAAATAGCATT[A/C]TCTTATCATTTATCAGCCTTTATGTATTTCCAAGTAAAATATTA ACATATTATTTCATTGGTCTCTTTTTTATCTGGTTCTATATGAATGCTAT

				Sequence
WI-7136	58	T	C	TGTGAAGCCACATTTTCCAACATGAGCCTCATGAAGCCAACTAAGTGTTATTGAACTGT[T/C]AATTC TCTCAATAACTCAGTGTAGCACTTTAAAGTCTGAAGGACCAACATGAAAGAGCATATCAATGTG GTGGAGAAAGGGAAGGGGTTGGCTTTTAATTTATTTCTTCATCTTTATAACAAGAAAGNNNNNN NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTAGCTTTCTATATATG
WI-7146c	210	A	G	GGGACGCCTGTTGTTTGGCTCAATTGGGTTTGTTGGTCACATGGAGCTCTTCCATTTCGTTTAGCTG AATAATGAGTTGTTCCTAGAGGAGACAGCGTCTGTCTCCTGTTGCCCCCAAAGCCCATGCCCTGCCG TGGTGCAGCTGGGGCTGTGGATGGGAGGGGTCCCAACATGGATGTGTTGCCCCTCCTCCGCATGCC AACGC[A/G]GTTCATGTACAAGGCCCCTCTGCAACTGGAGAGAAAATTA
WI-7146b	210	A	G	GGGACGCCTGTTGTTTGGCTCAATTTGGGTTTGTTGGTCACATGGAGCTCTTCCATTTCGTTTAGCTG AATAATGAGTTGTTCCTAGAGGAGACAGCGTCTGTCTCCTGTTGCCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGTGGATGGGAGGGGTCCCAACATGGATGTGTTGCCCCCTCCTCCGCATGCC AACGC[A/G]GTTCATGTACAAGGCCCCTCTGCAACTGGAGAGAAAATTA
WI-7146	202	G	A	GGGACGCCTGTTGTTTGGCTCAATTTGGGTTTGTTGGTCACATGGAGCTCTTCCATTTCGTTTAGCTG AATAATGAGTTGTTCCTAGAGGAGACAGCGTCTGTCTCCTGTTGCCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGGCTGTGGATGGGAGGGGTCCCAACATGATGTGTTGCCCCTCCTCCGCAT[G/A]]CCAACGCAGTCATGTACAAGGCCCCTCTGCAACTGGAGAGAAAATTA
WI-7153	161	A	T	ATATTACAACTTGCTTTTAGCTGATCTTCCATCCTCAAATGACTCTCTTTTTCTTTATATGTTAAACATA TATAAAATGGCAACTGATAGTCAATTTGATTTTATTCAGGAACTATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAAACNNNNNNNNN[A/T]AAAAAAGTTATTTAACAGTAATCTATTTACTAATTAT AGTACCTATCTCTTTAAAGTATAGTACACATTTACACATATGTAAATGGTATGTT
WI-7155	156	T	G	TAGAATAGATGCGGTCATATTCTTCTTTGGCTTCGTTCTTCCAGCCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAACACCAGCTGGCCCTACCCCTATAATGATCCTGTGTCCTAAATTAATATACAC CAGTGGTTCCTCCTCCCTG[T/G]TAAAGACTAATGCTCAGATGCTGTTTACGGATATTTATATCTAG TCTCACTCTCTGTCCCACCCTCTCTCTCTCCCCCAACTCCAG
WI-7169b	161	A	G	AGCTCCACCAGAATGCAGATTTGTGTTTGTGTTTGTTATCCATGTACCAGAGCTTATAACATGTAT GCTTTCAGAATACAGTGTCTAGCCAAGCCATCAAGTGTCTGAAATTCAATATTGGTTATGCAAAT ACAGCAAAACTTTATTTAAGTAGAT[A/G]GGGAGAATATGTTAAAATATTAGGAATCCTAGACCATA TTTTCAAGTCATCTTAGCAGCTAGGGATTCTCAAATGGAAGTGTTATATATA
WI-7175b	194	C	T	CTCCTAGACTAGACTAGTGCTTACCTTTATTAATGAACTGTGACAGCAGGAGGCCCAAGGCAGTGTTCCTCACCA ATAACTTCAGAGAAGTCAGTTGGAGAAAAATGAAGAAAAAGGCTGGCTGAAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAAATGTTTACTGCTGTCATTGTCCATGCCTA[C/T]AGAT AATTTATTTGTATTTTTGAATAAAAAACATTTGTACATTCCTGATACTGGG

WI-7175	194	C	T	CTCCTAGACTAGTGCTTACCTTTATTAATGAACTGTGACAGGAGGAGCCCAAGGCAGTGTTCCTCACCA ATAACTTCAGAGAAGTCAGTTGGAGAAAAAGGCTGGCTGAAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGCTGTTCCATGTCCATGCCTA[C/T]AGAT AATTTATTTTGTATTTTTGAATAAAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273	G	A	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTTCCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGCTGGCTGGCTGCTCAGGGGAACAGACCAGTGAACAAAGCATAACACCA ATCCCAGGGGCTGGCTCTGCACTAAGAGAAAATTGCACTAAGAATCTCGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGGACTGTTCCAAAGCCAGTGAAATGTGAAGGAA
WI-7178	273	G	A	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTTCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGTCACTGGCTGGCTGCTCAGGGGAACAGACCAGTGAACAAAGCATAACACCA ATCCCAGGGGCTGGCTCTGCACTAAGAGAAAATTGCACTAAGAATCTCGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGGACTGTTCCAAAGCCAGTGAAATGTGAAGGAA
WI-7182b	116	A	C	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAATTTATTCACCAGTTCCTCTGCAACCCACTCTGAGCCT[A/C]TCTCTCCTCCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCTGAAGCCTAGTACCCAATT
WI-7182	106	C	A	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAATTTATTCACCAGTTCCTCTGCAACCCA[C/A]TCTGAGCCTATCTCTCCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCTGAAGCCTAGTACCCAATT
WI-7191b	273	T	A	ATAATTGCTTGTTTCTAGCCTGGCAAGATATTTCATAAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAAATATTTTAGATAAAATGCACAGCACCACATCTAAGCATTAGTGATGGGTAGC TGATGTCAGCTTCATGTGGATTTTAAGCACTCTAGAAACAATGAAGCTTCTTGGCATATTTTAAGGAG CTCCCAAAATGTGTTACCTATTAAAATTGTAACTCAGCAAGTAGAAGACCATTT
WI-7199c	112	T	C	CCCAGTGGTGAACAGAACCTCCAAATTTGAGTTGCACCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCCTGTCAGCTCCTGACCTATGAGC[T/C]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAAGCATTCCTAATGTTTGTTTGGTGCTCTGAATTTCTTCTTTATTAT AGTCCTATAGTTTTACTCCTCAGTTCCTCACCATCATCTTGTCTAA
WI-7199b	112	T	C	CCCAGTGGTGAACAGAACCTCCAAATTTGAGTTGCACCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCCTGTCAGCTCCTGACCTATGAGC[T/C]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTAATGTTTGTTTGGTGCTCTGAATTTCTTCTTTATTAT AGTCCTATAGTTTTACTCCTCAGTTCCTCACCATCATCTTGTCTAA

ID	Pos	Allele			Sequence
WI-7216c	237	T	C	...	TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTCTCCCCAAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAGATTCCCCTCCACCTAAAATTGACTGTACTGTTTAATTAAAAACCCTTCCTGCTATACATAGGAAAAGACACACAGTTTGTTTT[T/C]CTTGTAATCACTT
WI-7216b	237	T	C	...	TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCCTTCTCCCCAAGGACAAAATGTGAGAAAGATGTGAGATAACTTACTCAGATTCCCCTCCACCTAAAATTGACTGTACTGTTTAATTAAAAACCCTTCCTGCTATACATAGGAAAAGACACACAGTTTGTTTT[T/C]CTTGTAATCACTT
WI-7220b	147	A	T	...	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTATTTGTCTCTTAAGCTGGCAAACCCATCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCAGTGGCACTAGAA[A/T]AATCTTGAGCACAGTGAATGACCTATCCTGCAAACATCTAATGGATCTCTAAAGGGTAACAAACCCTATAAATTCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7220	140	A	T	...	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTATTTGTCTCTTAAGCTGGCAAACCCATCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCAGTGGC[A/T]CTAGAAAAATCTTGAGCACAGTGAATGACCTATCCTGCAAACATCTAATGGATCTCTAAAGGGTAACAAACCCTATAAATTCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7226	232	C		...	GATCGAATTTTCAGATGATTCGGAAATTTTCATTCAGGTATTGTAATAGTGACATATATATGTATATACATATCACCTCCTATTCTCTTAATTTTGTTAAAATGTTAAACTGGCAGTAAGTCTTTTTGATCATTCCCTTTTCCATATAGGAAACATAATTTGAAGGTGGCCAGATGAGTTTATCATGTCAGTGAAAAATAATTACCCACAAAATGCCACCAGTAACTTAACGATTCTTCACTCTTGGGGTTT
WI-7228b	254	C		...	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAAATGCATACCAGTAATTGGCTCCAATTCATAATATGTTCACCAGGAGATTACAAATTTTTGCTCTTCTTGTCTTTAGTTGATTTATTAGTTGATTTAATTACTTTCTGAATAACGGAAGGGATCAGAAGATATCTTTGTGCCTAGATTGCAAAATCTCCAATCCACACATATTGTTTAAAATAAGAATGTTATCCAACTATTAAGATATCTCAATGT[
WI-7228a	163	G	A	...	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAAATGCATACCAGTAATTGGCTCCAATTCATAATATGTTCACCAGGAGATTACAAATTTTTGCTCTTCTTGTCTTTAGTTGATTTATTAGTTGATTTAATTACTTTCTGAATAACGGAAGGGATCAGAA[G/A]ATATCTTTGTGCCTAGATTGCAAAATCTCCAATCCACACATATTGTTTTAAAATAAGAATGTTATCCAACTATTAAGATATCTCAA
WI-7233c	213	C	T	...	CGATCGTACTGCCAGTAGCATTGCTTGTCGTCTGTTGTTGTACATTCCATTTCAATTGTTACAGATGTGAACTTTATTCCTTGTCACTAATTATTTCTAGGAAGTCAAAAAATATAATAAAGGGTTGAGCCCCTCTACTTTCTTCTTGCCACCTTTTGTGGCAATATTAAAGTGAACTGCTAATAGTGTAAGTA[C/T]GTGCACAAAACCACTGCCAGATAACCAGAGGGGCCTG

ID	Pos	Alleles	Sequence
WI-7233b	213	C T	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCCGGTCTTGTTGTTGTACATTCCATTTCAATTGTTACA GATGTGAACTTTATTCCTTGTCACTAATTATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTGAGCCCTCTACTTTCTTCTTGCCACCTTTTTGTGCAATATAAAGTGAACTGCTAATA GTGTAAGTA[C/T]GTGCACAAAACCACTGCCAGATAACCAGAGGGCCTG
WI-7233	211	T C	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCCGGTCTTGTTGTTGTACATTCCATTTCAATTGTTACA GATGTGAACTTTATTCCTTGTCACTAATTATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTGAGCCCTCTACTTTCTTCTTGCCACCTTTTTGTGCAATATAAAGTGAACTGCTAATA GTGTAAGT[T/C]ACGTGCACAAAACCACTGCCAGATAACCAGAGGGCCTG
WI-7238	128	T C	GGGTCTACAGAGACAGCTCACCATTTTGTCCTGTATCTGTAAACACTTTTGTTCTTAGTCTTTTTCTTG TAAAATTGATGTTCTTTAAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGTTT[T/C]CCGTT CTGTTTAAACAGAAAATAAAAGGAGTGTAAGCTCCTTTCTCATTTCAAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAGAAGAAACATTCAGTAGAAACATTTTATTGCCTA
WI-7252f	520	T C	CCACCAGGATCCCAGCCCAAGCGGCCCCCTTCCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCGGCGCGCCCCCGGCCAGCCCGGCCGGCCTGGAGGCTGCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCCTAGAGCCTGCCTGGAGGCGTTTCTAGCAAGTCAGTCAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252e	552	T C	CCACCAGGATCCCAGCCCAAGCGGCCCCCTTCCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCGGCGCGCCCCCGGCCAGCCCGGCCGGCCTGGAGGCTGCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCCTAGAGCCTGGAGGCGTTTCTAGCAAGTCAGTCAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252d	540	T C	CCACCAGGATCCCAGCCCAAGCGGCCCCCTTCCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCGGCGCGCCCCCGGCCAGCCCGGCCGGCCTGGAGGCTGCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCCTAGAGCCTGGAGGCTGTTCTAGCAAGTCAGTCAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252c	552	T C	CCACCAGGATCCCAGCCCAAGCGGCCCCCTTCCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCGGCGCGCCCCCGGCCAGCCCGGCCGGCCTGGAGGCTGCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCCTAGAGCCTGGAGGCTGTTCTAGCAAGTCAGTCAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA
WI-7252b	540	T C	CCACCAGGATCCCAGCCCAAGCGGCCCCCTTCCCACTCGCAGCAGACGCCGGGGACAGAG GCCTGCCCGGCGCGCCCCCGGCCAGCCCGGCCGGCCTGGAGGCTGCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCAGCCCCTAGAGCCTGGAGGCTGTTCTAGCAAGTCAGTCAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCTCCA

WI-7252a	520	T	C	CCACCAGGATCCCAGCCCAAGCGGCCCCTCCCGCCCCCTTCCCACTCGCGCAGCAGACGCCGGGGGACCAGAG GCCTGCGGGGCGGCCGGCCGGGGGGGCCCCTGGGCTCGCGAGGCCTGGGCGTTCAGCCGTTGAGAGAGATGGGAG GACACTCCTAGAGAACGCAGCCCTAGAGCCTGCCTGGGAACTCAGTCATTAGACTCCTCCTCCA ———— CTCCTCTCCTGGAGGATGCCAGTTCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAATAAAAAAGGCATGCTATGTGTTACGTGTT TTTCCAGTATGTGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATTGTAAAATATAACGATCTT AAAAATACCACAGTTTGTATTTTTCTT[T/A]AAGGAGTAAAGATTTGCCT[T/
WI-7265l	231	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAATAAAAAAGGCATGCTATGTGTTACGTGTT TTTCCAGTATGTGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATTGTAAAATATAACGATCTT AAAAATACCACAGTTTGTATTTTTCTT[T/A]AAGGAGTAAAGATTTGCCT
WI-7265k	121	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAATAAAAAAGGCATGCTATGTGTTACGTGTT TTTCCAGTATGTGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTT[T/G]GGTTCATTGTA TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTT[T/A]TATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265j	174	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAATAAAAAAGGCATGCTATGTGTTACGTGTT TTTCCAGTATGTGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTT[T/A]TATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265i	227	T	C	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAATAAAAAAGGCATGCTATGTGTTACGTGTT TTTCCAGTATGTGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATTATGTAAAATATAACGATCTT AAAAATACCACAGTTTGTATTTT[T/C]CTTTAAGGAGTAAAGATTTGCCT
WI-7265h	80	T	A	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAATAAAAAAGGCATGCTATGTGTTACGTGTT TTTCCAGTATGTGTT[T/A]TATTTGCCACCATTCTGTGGTTCATTGTA GTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTGTTTATATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265g	170	T	G	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAATAAAAAAGGCATGCTATGTGTTACGTGTT TTTCCAGTATGTGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTT[T/G]GTGTTTATTATGTAAAATATAACGATCT CTTAAAAATACCACAGTTTGTATTTTTCTTTAAGGAGTAAAGATTTGCCT

					Sequence
WI-7265f	231	T	A	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTCATTTGTTTGTTTATATTATGTAAAATATAACGATCTCTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTTTCTT[T/A]AAGGAGTAAAGATTTGCCT AAAAATACCACCAGTTTGTATTTTTCTT[T/A]AAGGAGTAAAGATTTGCCT
WI-7265e	227	T	C	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATTAGTGATTTTGTTTATATTATGTAAAATATAACGATCTCTT AAAAATACCACCAGTTTGTATTTTT[T/C]CTTTAAGGAGTAAAGATTTGCCT
WI-7265d	174	T	A	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATTAGTGATTTGT[T/A]TATATTATGTAAAATATAACGATCT CTTAAAAATACCACCAGTTTGTATTTTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265c	170	T	G	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATTAGTGATT[T/G]TGTTTATTATTATGTAAAATATAACGATCT CTTAAAAATACCACCAGTTTGTATTTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265b	121	T	G	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCCATTCACCCATTCTGTGTTACGTGTTT TTTCCAGTATGTGTTTATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGT[T/G]GGTTCATTGTA GTTTAAGGAAACCAAGCATATAGTCATTTTGTTTATTATTATGTAAAATATAACGATCT CTTAAAAATACCACCAGTTTGTATTTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7265a	80	T	A	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCCAGTATGT[T/A]TATTTGCCACCAAAAAGTAAATGCATTTCACCCATTCTGTGGTTCATTGTA GTTTAAGGAAACCAAGCATATAGATGCATTTGTTTATTATTATGTAAAATATAACGATCT CTTAAAAATACCACCAGTTTGTATTTTTCTTTAAGGAGTAAAGATTTGCCT
WI-7281b	183	C	---		GATCACCCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCCAGCTTGGAGCAGAGAGCCAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAGTCTGGCCCTGCCAGGTCTCCCATGAAGGCCA CCCCATGGTCTCGATGGGCATGAAGCATCTCAGACTCCTTGGCCAAAAACGGAGTCCGCAGGCCGCAG GTGTTGTTGAAGACCACTCGTTCTGTGGTTGGGGTCCTGCAAGAGGCCTCCTC
WI-7281	171	C	A	---	GATCACCCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCCAGCTTGGAGCAGAGAGCCAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAGTCTGGCCCTGCCAGGTCTCCCATGAAGGCCA CCCCATGGTCTCGATGGGCATGAAGCATCTCAGACTC[C/A]TTGGCCAAAAACGGAGTCCGCGAGGCCG CAGGTGTTGTGAAGACCACTCGTTCTGTGGTTGGGGTCCTGCAAGAAGGCCT

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WI-7282b	159	G	C	TGTCACCTGGCACATTCATTTCTCAGTTGAAGAAGAGAAATTTGAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGTGAGTGTTTCCACTCAAAAATATGTCAACTTNNNNNNNNT AGGCCCTTCATAAAAACCAAACT[G/C]TAGCAAGATGCAAATCATGGCAAATCTGTCGGTCTCCA GTTGGTTATCTGAATAGTGTCACCAATTCCACCAAGACAGTGCTGAGATTGG
WI-7292	92	T	C	CTTGATTACTTCCCACTGAGGTGGGAGCATCTCCAGTGCTCCCAATTATATCTCCCACTCCACTAC TCTCTCCTCCACTTCATTTTCC[T/C]TTGTCCTTCTTCTCTCTCAATTCAGTGTTTTGGAGGCCTGACTTG GGGACAACGTATTATTATTGTCTGTTTCCTTCTTCCCAATAGAAGAATAAGTCATGGAGCC TGAAGGGTGCCTAGTTACTGACACAAAGGCCTCTAGTTGGGCTGA
WI-7301f	133	A	G	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGGCGGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTG[A/G]CGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAAATTATGGACACATGAAAGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG
WI-7301e	94	T	G	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGGCGGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCCGGTG[T/G]TGGAGGATATAATGATTTTGGAAATTACAGTGGACAACAGCAA TGACGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG
WI-7301d	138	A	G	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGGCGGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGT[A/G]GTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG
WI-7301c	211	A	C	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGGCGGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC[A/C]CATGAAAGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG
WI-7301b	182	C	T	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGAGGCGGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTA[C/T]AGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG
WI-7301	88	G	T	AACTATGGCAGTGGTCCTGGTTATAGTAGTAGAGGCGGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTG[G/T]CGGTGTTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TGACGGTAGTAACTATGGTGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGCAGTTTTGGTGGAAGAAGCTCGGGCAG

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WI-7301	205	A	C	AACTATGGCAGTGGTCCTCGGTTATAGTAGTAGAGAGGCGGGGTATGGTGGTGGTGGTGGTGGACCAGGAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAGTAACTATGGTGGTGTGGGAACTATAGTGATTTTGGAAATTACAGTGGACAACAGCAATCA AATT[A/C]TGGACACATGAAACTCGGGCAG
WI-7314c	49	G	A	CTCTCCTTTTTCTTCAGATCTGCTCCTGGGTTTAATTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCCTTTGCAGCAGTGTAATAAAGTCAATTAAAAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCACCATGTGGGTCCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAAATGTGTAGTCTACCTTTATTTTTATTAACAAACTTGTTTTTT
WI-7314b	49	G	A	CTCTCCTTTTTCTTCAGATCTGCTCCTGGGTTTAATTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCCTTTGCAGCAGTGTAATAAAGTCAATTAAAAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCACCATGTGGGTCCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAAATGTGTAGTCTACCTTTATTTTTATTAACAAACTTGTTTTTT
WI-7314	36	A	G	CTCTCCTTTTTCTTCAGATCTGCTCCTGGGTTTA[A/G]TTGGGAGGTCAGTTGTTCTACCTCACTG AGAGGGAACAGAAGGATATTGCTTCCTTTGCAGCAGTGTAATAAAGTCAATTAAAAACTTCCCAGG ATTTCTTTGGACCCAGGAAACAGCCACCATGTGGGTCCTTTATTTTTATTAACAAACTTGTTTTTT CAGAAAATGTGTAGTCTACCTTTATTTTTATTAACAAACTTGTTTTTT
WI-7321b	199	C	T	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGGTGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCCTGACAGTCAAGGGACTGCTTTGGCACTGGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACCACATCAAAGNNNNNNNNNAGGTGGCACCACCATC[C /T]GTTTGCTGGGGTGTGGCAGCACATGGGAGCAGGCTGGCCA
WI-7321	199	C	T	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGGTGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCCTGACAGTCAAGGGACTGCTTTGGCACTGGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACCACATCAAAGNNNNNNNNNAGGTGGCACCACCATC[C /T]GTTTGCTGGGGTGTGGCAGCACATGGGAGCAGGCTGGCCA
WI-7336b	248	A	C	AGACAATTCTCGCTTCCCTGAAAGACTGAAGAAGAAAGTGTAGTGCATGGGAACCCACGAAACTGCCCTGGC TCCAGTGAAACTTGGGCACATGCCAATGATGATGTCCAGAAGTCCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAAAATTCTGAATTTGGGGATTTCAAAGATAATATTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA[A/C]CA
WI-7338c	221	A	G	CTCTTTCTCAGCACATTGATGGCAACTAGAATTACAGCAGTTCAAACTCTACCATGGATAATGCA AACAACCGAAGCTACATGCCAATGATGATGTGCAAAGATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAAAACAAAAGAAACAGAATCAATATAATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTTCTTTTACACAC[A/G]TATACACAGACACATCAGAAAATTCTGTT

ID	Pos			Sequence
WI-7338b	125	A	C	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAAGAAACATACCACAGACATCAGAAAATTCTGTT CTAGTGTGTTCTTCTTTACACAC
WI-7338	125	A	C	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAAGAAACATACCACAGACATCAGAAAATTCTGTT CTAGTGTGTTCTTCTTTACACAC
WI-7338	221	A	G	CTCTTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAAGAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAAGAAACATACCACAGACATCAGAAAATTCTGTT GTGTGTTCTTCTTTACACAC[A/G]TATACACAGACATCAGAAAATTCTGTT
WI-7384c	146	T	A	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTAAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAAATACCATTAAAATACATTGTATTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTT[T/A]AAAATTCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384b	146	T	A	CCTATGTCAATGAAATGCTAGGGGGCCAGGGAAACAAAATTTAAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAAATACCATTAAAATACATTGTATTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTT[T/A]AAAATTCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384	145	T	A	TGAAATCCTGGGTCTCTTGGCCTGTCCTGTAGCTGGTTTATTTTTACTTTGCCCCTCCCCACTTTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/T]TAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTGTCTGTCCAAGAACTTTCCCCCAAGATGTGTATAGTTATTGG
WI-7388c	106	A	T	TGAAATCCTGGGTCTCTTGGCCTGTCCTGTAGCTGGTTTATTTTTACTTTGCCCCTCCCCACTTTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/T]TAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTGTCTGTCCAAGAACTTTCCCCCAAGATGTGTATAGTTATTGG
WI-7388b	106	A	T	TGAAATCCTGGGTCTCTTGGCCTGTCCTGTAGCTGGTTTATTTTTACTTTGCCCCTCCCCACTTTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/T]TAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTGTCTGTCCAAGAACTTTCCCCCAAGATGTGTATAGTTATTGG

Marker	Position			Sequence
WI-7388	94	T	A	TGAAATCCTGGGTCTCTTGGCCTGTCCTGTCTGTAGCTGGTTTATTTTTTACTTTGCCCCCTCCCCACTTTTTT TGAGATCCATCCTTATCAGAAGAG[T/A]CTGAAGCGACTATAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTTACCTCTATTTGCCAAGCGTCTCGGGATTGTGTTGA CTTGTGTCTGTCCAAGAACTTTCCCCCAAAGATGTGTATAGTTATTGG
WI-7438	64	A	G	TTAGATTTTAATTGGCAACCAGCAACTCACTGCCACCATTCCACTGCAGATCTNCTATTCCTGG[A/G] GTTGATATGACAAGGAAAACCCTATTGGAACCAAGTCTTCAGATTGTNCCATGTGCAGACAGGCTCCT TGTCTGTAGGTGTAGTAGCATGTACACTGTACACTGTTCACTGTAACACATAGTTTGTNCTGGTATTTGTTA TTGGAAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152	T	C	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCAAACC CAGTACAAACTGAGAATGAGAGAACCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCTT/C]TGTTGTTTAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAATGTTTTGACA
WI-7454	152	T	C	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCAAACC CAGTACAAACTGAGAATGAGAGAACCCTGATAGCACTGTCTGAATTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTTCTT/C]TGTTGTTTAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAATGTTTTGACA
WI-7464c	177	G	C	AATTTGAAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACTCAGTCCATCTTAACCATGTACAATGCACTAAATTACTATTTATAATTCCTATGTA CAACAGAGCCACAGCCACAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7464b	168	C	A	AATTTGAAAAATCTGAAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCACTCAGTCCATCTTAACCATGTACAATGCACTAAATTACTATTTATAATTCCTATGTA CAACAGAGCCACAGCCACAGCCGTGGGCATAAG[C/A]AGTTGCCAGCCAGAAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7464a	103	C	A	AATTTGAAAAATCTGAAAATCTGAGTCCAGTCCATCTTAACCATGTACAATG[C/A]ACTAAATTACTATTTATAATTCCTAT GTACAACAGAGCCACAGCCACAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAAGCAACGTTCACCAACAATTAT
WI-7499b	134	T	G	CAATTCTCAATCCAACCTAGTCTGTNTGCCTAAACCATTCCAGACAAACTTCCACTTCGAAGGTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTGAATGCTTCA[T /G]TATAGTCCTCTTCATTAGCAATCAGTGAGGCAATACACTGGCATCATGGAAATGAGTGATGA ACTCTGTACAAATTCCCTTTGAAAATATAAATTTTGGAAATGAGTGATGA

ID	Pos				Sequence
WI-7499a	33	A	G	---	CAATTCTCAATCCAACCTAGTCTGTNTGCCTAA[A/G]CCATTCCAGACAACAACTTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTC ATTATAGTCCCTCTCTTCATTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTAGGAA CTCTGTACAAAAATTCCCTTTGAAAATATAAATTTGGAAATGAGTGATGA
WI-7506b	118	A	C	---	TGGGAATAGTAAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAAAGTAGTCCTGGTGCTGATTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGAATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAAATATTTGGACCACTCTGTTCTCTACCATCCCTACCCACT
WI-7506	118	A	C	---	TGGGAATAGTAAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAAAGTAGTCCTGGTGCTGATTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGAATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAAATATTTGGACCACTCTGTTCTCTACCATCCCTACCCACT
WI-7534b	143	C	T	---	TGTGAATTCTTAGCTCTGGAAGGTGTTTATGCCTTGCGGGGTTTCTTGATGTGTTCGCAGTGTCACCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATTCCCGGGTGATAGAATTGCT AAATTGT[C/T]GTGAAATAGGTTAGAATTTTCTTAAATTATGGTTTTCTTATTCGTGAAAATTCGG AGAGTGCTGCTAAAAATTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135	T	C	---	TGTGAATTCTTAGCTCTGGAAGGTGTTTATGCCTTGCGCAGTGTGTTCGCAGTGTCACCCA AGAGTCAGAACTGTACAACATCCCAAAATTGGTGGCCGTGGAACACATTCCCGGGTGATAGAATTGC[T /C]AAATTGTCGTGAAATAGGTTAGAATTTTCTTAAATTATGGTTTTCTTATTCGTGAGTTGTAATTT AGAGTGCTGCTAAAAATTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162	G	A	---	GGGAAAGAATAAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAACTTGAAGACC AGTCCTGTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGTGACTTGAAC TAGATTGCATGCTTCCTTGCTCTT[G/A]GGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCCCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162	G	A	---	GGGAAAGAATAAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGTGACTTGAAC TAGATTGCATGCTTCCTCTCTTGCTCTT[G/A]GGAAGACCAGCTTGCAGTGAGTGGGGTT CTCTGCAGCCCTCAGATTATTTTCCCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60	T	C	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGG[T/C]CTA AAAGAAAGTGGTATGTGTGATGATCAGCACTAAGTCCTGCTCATTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGGAAGTAAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATAGTTTTCATTTGATGTGTGCAATTTCAG

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WI-7555b	60	T C	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGG[T/C]TCTA AAAAGAAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTCCTGTTAAAGCCACTTGGGTC ATAAGAGGGGAAGTAAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTCATTTGATGTGCATTTGAATTTCAG
WI-7555	60	T C	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCCTCAAAATTTGTAGAGG[T/C]TCTA AAAAGAAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTCCTGTTAAAGCCACTTGGGTC ATAAGAGGGGAAGTAAAAAATGAAGTCTGACTAGAAATTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTCATTTGATGTGCATTTGAATTTCAG TGAGCCATCACTAGAAGAAAAGCCCATTTCAACTGCTTGAAACTTGCTCGGGTCTGAGCATGAT GGGAATAGGGAGGAGACAGGGTAGGAAAGGGCGCCTACTCTTCAGGGTCTAAAGATCAAGTGGGCCTTGG ATCGCTAAGCTAAAGATCAAGTGGGCCTCTGTTGATGCTATTTATGCAAGTTAGGGTCTATGTATTTAGGATGCGCCTAC TCTTCAGGGTCTAAAGATCAAGTGGGATCGGTCTGGCTCTGTT
WI-7567b	290	G T	AATGTATCCCCTTTCGGTCCAACAACAGGAAACCTGACTGGGCAGTGGGCAGTGAAGGAAGGGATGGCA[T/C] AGCGTTATGTGTAAAAAACAAGTATCTGTATGACAACCCGGATCGTTTGCAAGTAACTGAATCCAT TGCGACAATTGTGAAGGCTAAATGGGAAATAGCGTTGTATCGGTTATCGCCCTTGGGTTTAAATT ATTTGATGAGTTCCACTTGTATCATGCCCTACCCGAGGAGAAGAGGAGTTTG
WI-7569b	63	T C	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTCCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCTGCCCCCTTAATCCCCTTCTACAGTGAGTCCACTACCCTCACTGAAAATCATTTG TACCACTTACATTTAGGCTGGGGCAAGCAGCCCTGACCCTGAAGGAGAATGAGTGGACAGTTCTTG ATAGCCCAGGGC[A/G]TCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574c	216	A G	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTCCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCTGCCCCCTTAATCCCCTTCTACAGTGAGTCCACTACCCTCACTGAAAATCATTTG TACCACTTACATTTAGGCTGGGGCAAGCAGCCCTGACCCTGAAGGAGAATGAGTGGACAGTTCTTG ATAGCCCAGGGC[A/G]TCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574b	216	A G	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTCCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTCTGCCCCCTTAATCCCCTTCTACAGTGAGTCCACTACCCTCACTGAAAATCATTTG TACCACTTACATTTAGGCTGGGGCAAGCAGCCCTGACCCTGAAGGAGAATGAGTGGACAGTTCTTG ATAGCCCAGGGC[A/G]TCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574	216	A G	AATGATGATAATGATGATGACGACGACGACAACGATGATGCTTGTAACAAGAAAAACATAAGAGAGC CTTGGTTCATCAGTGTTAAAAAATTTTGAAAAGGCGGTACTAGTTCAGACACTTTCAGCACTTTGTGT TCTGTTTGTTAAAACTGGCATCTGACACACAAAAAA[A/T]GTTGAAGGCCTTATTCTACATTTCACCTAC TTTGTAAGTGAGAGAGACAGAAGAAGCAAGAGCAAANNNNNNNNNAAGAAAAAATAAAC
WI-7576c	168	A T	

WI-7576b	168	A	T	AATGATGATAATGATGACGACGACAACGATGATGCTTGTGTAACAAGAAAACATAAGAGAGC CTTGGGTTCATCAGTGTTAAAAAATTTTGAAAAGGCGTACTAGTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTTAAAACTGGCATCTGACACAAAAAAA[A/T]GTTGAAGGCCTATTCTACATTCACCTAC TTTGTAAGTGGAGAGACAAGAGACAAGACAAANNNNNNNNAAAGAAAAATAAAC
WI-7577g	77	T	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTGCTTTCCTTAA AAATATGCA[T/C]CAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50	G	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAA[G/C]TGTTTGCTTTCCTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTTACAC[G/A]TAGGAAAGAAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACAT[A/G]AGTGTTTGCTTTCCTT TAAAAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48	A	G	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTGCTTTCCTTAA AAATATGCATCAAATC[G/A]TCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCAT[T/C]ACTTTCTCTGAGGGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93	T	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTTA[C/A]CGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154	C	A	

WI-7577j	117	A	G	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTTAGTA[A/G]ACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACTGTATTTC
WI-7577i	77	T	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCA[T/C]CAAATCGTCTCTCATTACTTTCTCTGAGGGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACTGTATTTC
WI-7577h	50	G	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAA[G/C]TGTTTGCTTTCCTT TAAAAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACTGTATTTC
WI-7577g	157	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTTAGTAAACAGTAGGAGTTAATAACT AGAAGTTCATTTGGTTTACACAC[G/A]TAGGAAAGAAGAAGCATCAAAGTCAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACTCTTCTGAATTGACTGTATTTC
WI-7577f	48	A	G	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACAT[A/G]AGTGTTTGCTTTCCTT TAAAAATATGCATCAAATGTCTCTCTCATTACTTTCTCTGAGGGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACTCTTCTGAATTGACTGTATTTC
WI-7577e	84	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATC[G/A]TCTCTCATTACTTTCTCTGAGGGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACTCTTCTGAATTGACTGTATTTC
WI-7577d	93	T	C	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATGTCTCTCATT[T/C]ACTTTCTCTGAGGGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCATTTGGTTTACACGTAGGAAAGAAGAAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACTCTTCTGAATTGACTGTATTTC
WI-7577c	154	C	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTTGCTTTCCTTTAA AAATATGCATCAAATCGTCTCTCATTACTTTCTCTGAGGGTTTTAGTAAACAGTAGGAGTTAATAA AGAAGTTCATTTGGTTTA[C/A]ACGTAGGAAAGAGAAGCATCAAAGTGGAGATCAAGTGACTGTATTTC ATTGTATATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

Marker	Pos			Sequence
WI-7577b	117	A	G	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTGCTTTCCTTTAAAAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTTAGTA[A/G]ACAGTAGGAGTTAATAAGAAGTTCATTTGGTTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACTCTCTGAATTGACTGTATTTC
WI-7577	107	G	A	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCAACATAAGTGTTGCTTTCCTTTAAAAATATGCATCAAATCGTCTCTCATTACTTTTCTCTGAG[G/A]GTTTAGTAAACAGTAGGAGTTAATAAGAAGTTCATTTGGTTTACACGTAGGAAAGAAGCATCAAAGTGGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACTCTCTGAATTGACTGTATTTC
WI-7619q	106	C	G	ACAAGGGCGACTTGAAGAGGAGGACGGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGACAGAGAAGGGGCCAATGGGGTCATCCCCTAACGAGACT[C/G]TCGTGTGCTGGGGGTGCTAATTACATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCTCTCGCTTTCTTTCTTCTTACACAGAAAACATACCGAGAAACCTATTTC
WI-7619p	150	T	C	ACAAGGGCGACTTGAAGAGGAGGACGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGACAGAGAAGGGGCCAATGGGGTCATCCCCTAACGAGACTCTCTGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCCAGGAAGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCCT[T/C]CTAACAGAAAACATACCGAGAAACCTATTTCTCTCGCTTTCTTTCTTCTTACACAGAAAACATACCGAGAAACCTATTTC
WI-7619o	228	A	G	ACAAGGGCGACTTGAAGAGGAGGACGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGACAGAGAAGGGGCCAATGGGGTCATCCCCTAACGAGACTCTCTGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCTCAGGAAGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCATACCTACCGAGAGGACACAGACCGCTTTCTTTCTTCTTACACAGAAACAT[A/G]CACATACCGAGAAACCTATTTC
WI-7619n	237	G	C	ACAAGGGCGACTTGAAGAGGAGGACGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGACAGAGAAGGGGCCAATGGGGTCATCCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTACATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCTCGCTTTCTTTCTTCTTACACAGAAAACATACC[G/C]AGAAACCTATTTC
WI-7619m	99	C	T	ACAAGGGCGACTTGAAGAGGAGGACGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGACAGAGAAGGGGCCAATGGGGTCATCCCCTAA[C/T]GAGACTCTCTGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCTGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCATCTTTTTCCTCTCTCGCTTTCTTTCTTCTTACACAGAAACATACCGAGAAACCTATTTC
WI-7619l	189	T	A	ACAAGGGCGACTTGAAGAGGAGGACGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGACAGAGAAGGGGCCAATGGGGTCATCCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTACATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGGTCTGTCTCTCCCTTTTTCCAT[T/A]CTTTTTCCTCTCTCGCTTTCTTTCTTCTTACACAGAAAACATACCGAGAAACCTATTTC

WI-7619k	90	C	G	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTCTCTCCCTTTTTCCATCTTTTTCCT ATGGCAGGAAGAATGGGCCTCTAAGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTTCTTTACACAGAAACATACCGAGAAACCTATTTC
WI-7619j	206	T	G	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAACGAGACTCTCTGTCTCTCCCTTTTTCCATCTTTTTCCT CAGGAAGAATGGGCCTCTAAGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCTCT CGGC[T/G]TCTTTCTTTACACAGAAACATACCGAGAAACCTATTTC
WI-7619i	106	C	G	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAACGAGACT[C/G]TCTGTGTCTCTCCCTTTTTCCATCTTTTTCCT ATGGCAGGAAGAATGGGCCTCTAAGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTTCTTTACACAGAAACATACCGAGAAACCTATTTC
WI-7619h	150	T	C	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAACGAGACTCTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCT CAGGAAGAATGGGCCTCTAAGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCTCT TCTCGCTTTCTTTCTTTACACAGAAACATACCGAGAAACCTATTTC
WI-7619g	228	A	G	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAACGAGACTCTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCT CAGGAAGAATGGGCCTCTAAGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCT CGCTTTCTTTCTTTACACAGAAACAT[A/G]CACATACCGAGAAACCTATTTC
WI-7619f	237	G	C	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAA[C/T]GAGACTCTCTGTCTCTCCCTTTTTCCATCTTTTTCCT CAGGAAGAATGGGCCTCTAAGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCT CGCTTTCTTTCTTTACACAGAAACATACCGAGAAACCTATTTC[G/C]AGAAACCTATTTC
WI-7619e	99	C	T	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAACGAGACTCTCTGTCTCTCCCTTTTTCCATCTTTTTCCT TGGCAGGAAGAATGGGCCTCTAAGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCTCT TCTCGCTTTCTTTCTTTACACAGAAACATACCGAGAAACCTATTTC
WI-7619d	189	T	A	ACAAGGCGACTTGAAGAGGACGCGCAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGTCATCCCCTCCCTAACGAGACTCTCTGTGTCTCTCCCTTTTTCCATCTTTTTCCT CAGGAAGAATGGGCCTCTAAGGGAGTGTGGGGTCTGTGTCTCTCCCTTTTTCCA[T/A]CTTTTCCTC TCTCGCTTTCTTTCTTTACACAGAAACATACCGAGAAACCTATTTC

WI-7619c	90	C	G	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTCTAAGGGAGTGTGGGGTCTGTCTCCCTTTTTCCATCTTTTTCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206	T	G	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATCCCCTCCCTAACGAGACTCTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCCTCTAAGGGGAGTGTGGGGTCTGTCTCCCTTTTTCCATCTTTTTCCTCTCT CGC[T/G][T/C]TTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189	T	A	ACAAGGCGACTTGAAGAGGACGCAGGCTTCCAGAGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCAATGGGGTCATCCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCCTCTAAGGGGAGTGTGGGGTCTGTCTCCCTTTTTCCA[T/A]CTTTTTCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105	A	G	CCTTTGTATGTGGAAGTATACCTGGCTTTTTAAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGGATCTGTCTGGC[A/G]TTAAACCACATCATGGACCAAATGTG CCATACTAATGATGAGCATTTAGCACAAATTGAGACTGAAATTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGCTGTATTTATAGTAACCATTTTCCTTTGGACTGTTCA
WI-7626c	155	C	T	CCTTTGTATGTGGAAGTATACCTGGCTTTTTAAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGGATCTGTCTGGC[C/T]TTAAACCACATCATGGACCAAATGTGCCA TACTAATGAGCATTTAG[C/T]ACAATTTGAGACTGAAATTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCTTTGGACTGTTCA
WI-7626b	28	T	A	CCTTTGTATGTGGAAGTATACCTGGCT[T/A]TTAAAATATATGTATTTAAAAACAAAAAGCAACAG TAATCTATGTGTTTCTGTAACAAATTGGGGATCTGTCTGGCATTAAACCACATCATGGACCAAATGTG CCATACTAATGATGAGCATTTAGCACAAATTGAGACTGAAATTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCTTTGGACTGTTCA
WI-7626	144	T	C	CCTTTGTATGTGGAAGTATACCTGGCTTTTTAAAATATATGTATTTAAAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAACAAATTGGGGATCTGTCTGGCATTAAACCACATCATGGACCAAATGTGCCA TACTAATGA[T/C]GAGCATTTAGCACAAATTGAGACTGAAATTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCTTTGGACTGTTCA
WI-7689c	134	A	G	TCCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCCAGTGGCTGCTGCCCAGGCCCAGACCTTCTAGGACGCGCACCCAGCAAAATTGCAGACTGTGTAACAAAT[A /G]TAAGGGCAGAGTCACACTGGGCGCAGCTGATACAAATTGCAGACTGTGTAACAAATAAAATGGA GATAATATTGTGGTGTGCCACAAATAAAAATGGATTTATTAGAATTTCATATGAC

				TCCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCCAGTGGCTGCTGCCCAGGCCCAGCACCTTCTAGGACGCCACCCAGCACAAATTGTTCCTAAA[A /G]TAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTGATTATTAGAATTTCATATGAC
WI-7689b	134	A	G	··· GATAATATTGTGGTGCCACAAATAAAATGGATTTATTAGAATTTCATATGAC
				TCCCATAACCGCTGATTCTCAGGGTCTCTGCTGCCGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCCAGTGGCTGCTGCCCAGACCTTCTAGGACGCCACCCAGCACAAA[G/A]GTTGTTCCTAA AATAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAAGAGAGCTTAAT
WI-7689	121	G	A	··· GATAATATTGTGGTGCCACAAATAAAATGGATTTATTAGAATTTCATATGAC
				TGGAGAACATTCAATCTTGCCGTCACTATTCATCAATGAAGATTA[G/A]CACTGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTCACCAGCACATGGTAGTGGCAAAGAGAGAGGTCCAGAGTCCTGGCCCTTGAT GCCCAGCTCAGTGCCCACAAAGCTCAGTGGAGGGGGATGTTCCAGTGGATGAGGGCCACCAGGAAGCAC
WI-7690	45	G	A	··· AGGTCCAAGGCTGTGTCCCACACTTATCAGCAGCAACAACTGTCAGTTCATCC
				ACAGAAAAGTTGAAATTTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAATTGGTTTTCACATTGGAAAACAAGTCAGTCATTCAGATATGATTCAA TGTCTATAAACCAAACTGATGTAAGTAAA[T/C]GGTCTCTCTCACTTGTTTATTTATTTAACCTCTAAATTCT
WI-7703b	164	T	C	··· TTCATTTTAGGGGTAGCATTGTGTTGTTGAAGAGGTTTTAAAGCTTCCATTGT
				ACAGAAAAGTTGAAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAATTGGTTTTCACATTGGAAAACAAGTCAGTCATTCAGATATGATTCAAA TGTCTATAAACCAAACTGATGT[T/C]AAGTAAATGGTCTCTCTACTTGTTTATTTAACCTCTAAATTCT
WI-7703	156	T	C	··· TTCATTTTAGGGGTAGCATTGTGTTGTTGAAGAGGTTTTAAAGCTTCCATTGT
				TTAAATGAGTGTGTTTGTCACCGTTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGAGCCTCGGAGGCAGGGGTCAGGA
WI-7743e	106	C	A	··· GAGGGGCAGAACAGCCCGGCTCCTGGTCTGCCAGCAACAGCCCAGCCTCTCAGCC
				TTAAATGAGTGTGTTTGTCACCGTTGGGGAATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAATTCTGCTACCTCACTGGGGTCCTGGAGCCTCGGAGGCAGGGGTCAGGGATCAGGCAACG
WI-7743d	275	C	T	··· GGGCAGCAGAACAGCCGGCTCCTGTCTGCCAGCAACAGCCCAGCCTCTCAGCC
				TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGAGCCTCATCCGGACCAACG
WI-7743e	106	C	A	··· GAGGGGCAGAACAGCCGGCTCCTGTCTGCCAGCAGCAGCCCAGCCTCTCAGCC

				Sequence
WI-7743d	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGGCCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGCCTCCGGAGCCTCATCCGGAGCCAGGGTCAGGAGAG TACAGAATTCTGCTACCTCACTGGGGTCTGCCCAGCCAGCCAGCCTCTCAGCCAACG GGGCAGAACAGCGCGCTCCTGTCTGCCCAGCCAGCCAGCCTCTCAGCC
WI-7743e	106	C	A	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGGCCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGCCTCCGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGGGGTCCTCATCCGAGGCAGGGTCAGGA GAGGGGCAGAACAGCGCGCTCCTGTCTGCCCAGCCAGCCAGCTCTCAGCC
WI-7743d	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGGCCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGCCTCCGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCTGCCCAGCCAGCCAGCTCTCAGCC GGGCAGAACAGCGCGCTCCTGTCTGCCCAGCCAGCCAGCTCTCAGCCAACG
WI-7743c	106	C	A	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGGCCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGCCTCCGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCTGCCCAGCCAGCCAGCTCTCAGCC GGGCAGAACAGCGCGCTCCTGTCTGCCCAGCCAGCCAGCTCTCAGCC
WI-7743b	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGGCCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAATTCTGCTACCTCACTGGGGTCTGCCCAGCCAGCCAGCTCTCAGCC GGGCAGAACAGCGCGCTCCTGTCTGCCCAGCCAGCCAGCTCTCAGCC
WI-7743	106	C	A	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGGCCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGCCTCCGGTAATAAGTACTGTG GTGTACAGAATTCTGCTACCTCACTGGGGTCCTGGGGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCGCGCTCCTGTCTGCCCAGCCAGCCAGCTCTCAGCC
WI-7743	275	C	T	TTAAATGAGTGTGTTTGTCACCGTTGGGGATTGGGGAAGACTGTGGCTGGCCACTTGGAGCCAAGG GTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAGGAGCCTCCGGTAATAAGTACTGTG TACAGAATTCTGCTACCTCACTGGGGTCCTGTGTCTGCCCAGCCAGCCAGCTCTCAGCC GGGCAGAACAGCGCGCTCCTGTCTGCCCAGCCAGCCAGCTCTCAGCCAACG
WI-7758	144	A	G	TGACATTTATTCAAAGTTAAAAGCAAACACTTACAGAATTATGAAGAGGTATCTGTTAACATTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAAGGAACAGAGTGAGAACATCATCAAGTG GAGAGAAATC[A/G]TAGTTTAAACTGCATTATAAATTTATAACAGAATTAAAGTAGATTTTAAAA GATAAAATGTGTAATTTTGTTTATATTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126	G	C	ACAGGGGCCTTTGGCAGGTGCAGCCCCCACTGCCTTTGACCTGCTGCTCCCTTCATGCATGGAAATTCCCT TCATCTGGAACCATCAGAAACACCCTGACCACTGGGGACTTGCAAAAGGGTCAGTATGG[G/C]TTAGG GAAAACATTCCATCCTTGAGTCAAAAAATCTCAATTCTTCCCTATCTTTGCCACCCTCATGCTGTGTG ACTCAAACCAAATCACTGAACTTTGCTGAGCCTGTAAAATAAAAGGTCGGA
WI-7773b	237	C	G	TTAATTTACTGATTCCAGCAGCAGACCAAATCATTGTATCGAGATTATTTTAAGTTTTATCCGTAGTTTT GATAAAAGATTTTCCTATTCCTTGGTTCTGTCTCAGAGAACCTAATAAGTGCTACTTTGCCATTAAGGCA GACTAGGGGTTCATGTCTTTTACCCTTTNNNNNNNNNTTGTAAAAGTCTAGTTACCTACTTTTCTTT GATTTTCGACGTTTGACTAGCCATCTCAAGCAA[C/G]TTTCGACGTTTGA
WI-7774b	170	T	C	TGCAACCTCTTTCGTGATGGGCAGCCTGCTGGTCAGCACTCCAGTAGCGAGGACGGCACCCAGAAT CAGATCCCAGCTTCGGCATTTGATCAGACCAAACAGTGCTGTTCCCGGGGAGGGAAAACACTTTTTAA TTACCCTTTTGCAGGCACCACCTTAATCTGTTT[T/C]ATACCTTGCTTATTAAATGAGCGACTTAAA ATGATTGAAAATAATGCTGTCCTTAGTAGCAAGTAAAATGTGTCTTGCT
WI-7785c	165		G	GCAGAGACCTTCCAAGGACACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGTCTGTAAATACTGTAAATGCATTGGAATAAAAACTGTCTCCCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNNNGCCAAGGCTAATCCAATTATTATTATCACATTTACCA TAATTTATTTGTCCATTGATGTATTTATTTGTAAATGTATCTTGGTGCTGC
WI-7785b	165		G	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGTCTGTAAATACTGTAAATGCATTGGAATAAAAACTGTCTCTCCCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNNNGCCAAGGCTAATCCAATTATTATTATCACATTTACCA TAATTTATTTGTCCATTGATGTATTTATTTGTAAATGTATCTTGGTGCTGC
WI-7785	156		T	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGTCTGTAAATACTGTAAATGCATTGGAATAAAAACTGTCTCTCCCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANN[- /T]NNNNNNNNNGCCAAGGCTAATCCAATTATTATTATCACATTTACCATAATTTATTTTGTCCATTGA TGTATTTATTTGTAAATGTATCTTGGTG
WI-7789c	84	G	A	TCTCCCCCTCATCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCGCTCCCTAGGATAT GCCCTCCTGGTGGGGCTGTCTCAGACGACTAGCCCAGGACCCATCT
WI-7789b	84	G	A	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCGCTCCCTAGGATAT GCCCTCCTGGTGGGGCTGTCTCAGACGACTAGCCCAGGACCCATCT

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WI-7789	73	G A	TCTCCCCTCATCCAACTCTCGAAAGTCTGAATCTCCCAGGAGGGGCACCATCTTACAGAGACTCTCCTGACG[G/A]TGGAATTTAAGTTTAGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGACCCAAAATGTGAATGAAGCTAATGTGAGTGAGCTCCCTCAGCGCCCGCTGCCCTAGGATATGCCCTCCTGGTGACTCGGGGGCGTGTCTCAGACGACCCCATCT
WI-7790b	190	C T	AATTGTCAGTCACTTCTTCAAAACCTTACAGTCTCCTTCCTAAGGTTACTCTTCATGAGATTCATCCATTACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTGTAGCTTTTACTTTTATGGTGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGAACTC[C/T]TTCTATACTTTAAGATACTCTATTTTAAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190	C T	AATTGTCAGTCACTTCTTCAAAACCTTACAGTCTCCTTCCTAAGGTTACTCTTCATGAGATTCATCCATTACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTGTAGCTTTTACTTTTATGGTGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTTCTTGAACTC[C/T]TTCTATACTTTAAGATACTCTATTTTAAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81	C A	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTTGGCTCATATTCTTTTCTTTTCTTTCTCATCTTGATGATGAT[C/A]GTCATCATCAAGAATTAATGATTAAAATAGCATGCCTTTCTCCTTCTTTCTCTTAATAAGCCCACATATAAATGTACTTTTCTTCCAGAAAAAATTCTCCTTGAGGAAAAATGTCCAAAATAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7795	81	C A	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTTGGCTCATATTCTTTTCTTTTCTTTCTCATCTTGATGATGAT[C/A]GTCATCATCAAGAATTAATGATTAAAATAGCATGCCTTTCTCCTTCTTTCTCTTAATAAGCCCACATATAAATGTACTTTTCTTCCAGAAAAAATTCTCCTTGAGGAAAAATGTCCAAAATAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7814c	41	G A	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCC[G/A]TTTCATTTAGTCATGTGACCACTCTGTCTTGTGTTTCCACAGCCTCAAGAATCTTCAGTCCAGGATGCTAACATCTAAAAATACTTAAATCTCATTGCTTACAAGCCTAAGAATATTGTATATTTTAAGAAATAACAGAA
WI-7814b	41	G A	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCC[G/A]TTTCATTTAGTCATGTGACCACTCTGTCTTGTGTTTCCACAGCCTCAAGAATCTTCAGTCCAGGATGCTAACATCTAAAAATACTTAAATCTCATTGCTTACAAGCCTAAGAATATTGTATATTTTAAGAAATAACAGAA
WI-7814	28	G A	TTCTCTCTCATTTTATCCCTCACCTGTA[G/A]CATGCCAGTCCCGTTTCATTTAGTCATGTGACCACTCTGTCTTGTGTTTCCACAGCCTCAAGAATCTTCAGTCCAGGATGCTAACATCTAAAAATACTTAAATCTCATTGCTTACAAGCCTAAGAATATTGTATATTTTAAGAAATAACAGAA

WI-7830d	150	C T	GCAGGAAATAGTCACTCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTTCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAAACTTTAGT[C/T]TAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTTCCTTTG AGGTTGATCGTTGTGTGTTTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7830c	54	G A	GCAGGAAATAGTCACTCACTCCATCCCACATAAGGGGTTTAGTAAGAGAAGTCT[G/A]TCTGTCTGA TGATGGATAGGGGGCAAATCTTTTCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTTCCTTTG AGGTTGATCGTTGTGTGTTTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7830b	134	G A	GCAGGAAATAGTCACTCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC[G/A]ATCCATAAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTTCCTTTG AGGTTGATCGTTGTGTGTTTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7830	44	A G	GCAGGAAATAGTCACTCACTCCACTCCACATAAGGGGTTTAGTA[A/G]GAGAAGTCTGTCTGTCTGA TGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTTGTTGTTTCCTTTG AGGTTGATCGTTGTGTGTTTTGCTGCACTTTTTACTTTTTGCGTGTGGA
WI-7865e	25	C T	CCACTTCCTATCTGATTTTTCCCAG[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865d	191	C T	CCACTTCCTATCTGATTTTTCCCAGCAAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGGT ATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAA
WI-7865c	25	C T	CCACTTCCTATCTGATTTTTCCCAG[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865b	191	C T	CCACTTCCTATCTGATTTTTCCCAGCAAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGGT ATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTCACCCAGTAAACCCAAA

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WI-7865	25	C	T	CCACTTCCTATCTGATTTTCCCAG[C/T]AAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCACATGCCTATGTAAGGAAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865	191	C	T	CCACTTCCTATCTGATTTTCCCAGCAATGAGGCAGGCAATTCTAGTCTTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGGT ATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAGTA[C/T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7867c	92	A	C	TTCAAACACCTGTCTTCCACCCTCCCACCATCTGTGCAATCACTTCACCCTTCAGCCTCACTAGTCCCC CTAACAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGGTTTAATATGGC CTGTTGAGTTAATGTTAATGTTCTTAAGTAACCATTCTGTTCTTGCTATAAATCTATGT CTATATGTCTATGCTTAATTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92	A	C	TTCAAACACCTGTCTTCCACCCTCGTGCAATCATCTGTGCAATCACTTCACCCTTCAGCCTCACTAGTCCCC CTAACAATTACCCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTTAATGTGGGTTTAATATGGC CTGTTGAGTTAATGTTAATGTTCTTAAGTAACCATTCTGTTCTTGCTATAAATCTATGT CTATATGTCTATGCTTAATTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173	C	T	TTGATCGATCTTTTCCCACCCTGTCACTCAACGTGGTCCCTAGAACAAGAGAGGCTTAAAACCGGGCTTT CACCCAACCTGCTCCCTCTGATCCTCCATCTTCCCACGTCTCCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAA[C/T]TAGAGGCCAGAAAATGGGCAAATTAT CACTAACAGGTCTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868b	173	C	T	TTGATCGATCTTTTCCCACCCTGTCACTCAACGTGGTCCCTAGAACAAGAGAGGCTTAAAACCGGGCTTT CACCCAACCTGCTCCCTCTGATCCTCCATCTTCCCACGTCTCCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAA[C/T]TAGAGGCCAGAAAATGGGCAAATTAT CACTAACAGGTCTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868	66	T	C	TTGATCGATCTTTTCCCACCCTGTCACTCAACGTGGTCCCTAGAACAAGAGAGGCTTAAAACCGGGCTTT /C]TCACCCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTTCCCATCTCAGTACAC AATCATTTAATATTTCCCTGTCTTACCCCTATTCACCCCTATTCAAGCAACTAGAGGCCAGAAAATGGGCAAATTAT CACTAACAGGTCTTTGACTCAGGTTCATTCTCAATGCCTAGAT
WI-7870b	85	T	C	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAATACTCTGCAGTGATTAGAAGGG GTGGGGTGGCGGGAAATCC[T/C]ATTTATCAGACTCTGTAATTGAATATAAATGTTTTACTCAGAGGA GCTGCAAATTGCCTGCAAAAATGAAATCAATTACAAGCTGTGTAGACCTAATTACCATTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTGTAGACCACCTAATATCAATTTG

WI-7870	76	C/T	ATCTTTGCTCCCTGCAAGAAATCAGCCATTAATACTCTGCAGTGATTAGAAGGGGTGGGGTGG[C/T]GGGAATCCTATTATCAGACTCTGTAATTGAATATAAATGTTTACTCAGAGGAGCTGCAAATTGCCTGCAAAAATGAAATCCAATTACAAGCTGTAGACCACCTAATATCAATTTGTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54	C	TTAGGTCTCATGCCCACTCCCCAGGAGCAGCAGCAGCGCTGACGAGCTCTCTCCCCCTGCAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGGCCGGGCCCAGGGCCTCTGGCTTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGGAATTGAAATGGGGGCGCTGGACACCTACAGCAGCACGCATGTCCCTCCCAGGCTGTGTCTTCTCCCAGAGCACAAGAAG
WI-7889b	54	C	TTAGGTCTCATGCCCACTCCCCAGGAGCAGCAGCAGCGCTGACGAGCGCGCTCTCCCCCTGCAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGGCCGGGCCCAGGGGCTCTGGCTTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGGAATTGAAATGGGGGCGCTGGACACCTACAGCAGCACGCATGTCCCTCCCAGGCTGTGTCTTCTCCCAGAGCACAAGAAG
WI-7894c	142	A/G	AGCCCACCCCCAAATATAAACTGTTATCCAGAAGCTGTTATGTCCTGTTCCATACATGTTTTTGTACTTTTACTATATCTACACACATCAATTAAACTTATGTCCTATTGTTTGTGAATTTATATTTGCGTATACATTATC[A/G]TATGTAAAATTTGCATTTTTATTGAAAATTATGTTTCTTGAGATTTATCCACATTGAAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATTCCATA
WI-7894b	142	A/G	AGCCCACCCCCAAATATAAACTGTTATCCAGAAGCTGTTATGTCCTGTTCCATACATGTTTTTGTACTTTTACTATATCTACACACATCAATTAAACTTATGTCCTATTGTTTGTGAATTTATATTTGCGTATACATTATC[A/G]TATGTAAAATTTGCATTTTTATTGAAAATTATGTTTCTTGAGATTTATCCACATTGAAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATTCCATA
WI-7900e	84	C/T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGCCACAGTAAAACAAGTGACCTTCAGAGCAGCTGCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACAAAAATGCATTGATCATGAATAGGAGCCCATGCCATGAAGTACATTCTCTCAGATTTGAACCAGTGAAATATGATGTATTTCTGAGCTAAAACTCAACTATCAAACTATAGAAGACATTAAAAGAAATC
WI-7900d	128	C/T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGCCACAGTAAAACAAGTGACCTTCAGAGCAGCTGCCACAACTGGCCATGCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGAC[A/C]CAAAAATGCATTGATCATGAATAGGAGCCCATGCCATGAAGTACATTCTCTCAGATTTGAACCAGTGAAATATGATGTATTTCTGAGCTAAAACTCAACTATCAAACTATAGAAGACATTAAAAGAAATC
WI-7900e	84	C/T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGCCACAGTAAAACAAGTGACCTTCAGAGCAGCTGCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACAAAAATGCATTGATCATGAATAGGAGCCCATGCCATGAAGTACATTCTCTCAGATTTGAACCAGTGAAATATGATGTATTTCTGAGCTAAAACTCAACTATCAAACTATAGAAGACATTAAAAGAAATC

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WI-7900d	128	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATGCCCTGCCATTGAAACAGTTGATCAAGCCATGGTGA[C/T]ACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900e	84	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900d	128	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900c	84	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGAAATC
WI-7900b	128	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900	84	C	T	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAAACAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAGTGAAA TATGATGTATTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7901c	33	C	T	AGACTTAGGTACAATTGCTCCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTATAAAACATGGTAAGAC CCTTTTAAAACAAACTCCAGGCCCTTGGTTGCGGGGTCGCTGGGTTATTGGGGCAGCGCGGGTGGTCGT CACTCAGTCGCTCTGCATGCTCTCTGTCATACAGACACAGGTAACCTAGTTCT
WI-7901b	33	C	T	AGACTTAGGTACAATTGCTCCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTGCATCTATTTCCATATAGTCATCAAGAGACCATTTATAAAACATGGTAAGAC CCTTTTAAAACAAACTCCAGGCCCTTGGTTGCGGGGTCGCTGGGTTATTGGGGCAGCGCGGGTGGTCGT CACTCAGTCGCTCTGCATGCTCTCTGTCATACAGACACAGGTAACCTAGTTCT

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WI-7901	33	C	T	...	AGACTTAGGTACAATTGCTCCCCTTTTTATATA[C/T]AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTGCATCTCATTTTCCATATAGTCATCAAGAGACCATTTATAAAACATGGTAAGAC CCTTTTAAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCGCTCATACAGACAGGTAACCTAGTTCGT CACTCAGTCGCTCTGCATGCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901	271	T	G	...	AGACTTAGGTACAATTGCTCCCCTTTTTATATACAGACACACACAGGACACATATATTAAACAGATT GTTTCATCATTGCATCTCATTTTCCATATAGTCATCAAGAGACCATTTATAAAACATGGTAAGACCCT TTTAAAACAAACTCCAGGCCCTTGGTTGCGGGTCGCGCTCATACAGACAGGTAACCTAGTTCGTCAC TCAGTCGCTCTGCATGCTCTGTCATACAGACAGGTAACCTAGTTCTGTGT
WI-7926c	150	C	A	...	CATTCCGCCATCTGTCAACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACTTA[C/A]ATTTTAATACTCTTGTAGGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28	A	T	...	CATTCCGCCATCTGTCAACCAGGACAGAA[A/T]GCATGGACAAGGGATGAGCTTTACAAAGATGATGC ACTTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGAATGATGAATGTA ATTTTACAAATGCAATACTTACATTTTAATACTCTTGTAGGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150	C	A	...	CATTCCGCCATCTGTCAACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAAATTCATATTTAATACTCTTGTAGGGAGAAAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCTTCATT TACAATGCAATACTTA[C/A]ATTTTAATACTCTTGTAGGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7947b	203	G	T	...	AAGAGCCAGCAGGTCAAAAAGGCCAACAACCATAAGCAGCCAGCCGAGGCCACAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAACACCAGCCGAGGCCACAGAATCCCATCCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCAGCAGACTATGGGCAGCCCAGTGCTGCCACCACA GA[G/T]TCTCTCCCTGGAGCAGCAGGTCAGCCCAGTGCTGCCACCTG
WI-7947	203	G	T	...	AAGAGCCAGCAGGTCAAAAAGGCCAACAACCATAAGCAGCCAGCCGAGGCCACAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAACACCAGCCGAGGCACAGAATCCCATCCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCAGCAGACTATGGGCAGCCCAGTGCTGCCACCTG GA[G/T]TCTCTCCCTGGAGCAGCAGGTCAGCCCAGTGCTGCCACCTG
WI-7963b	145	T	C	...	CATGTGCTGCGATGAAGAGCTAATTTAAAAAAGCAAAGTAAGACTAATTATTTAAAATAAAAAATGCC ACAAATTTCATTTTCTCCTTCTAAGTATTACAATGGAGTTTATTCTGCCTAAAAAGTGGAAGAAAT TGAGTGAATGA[T/C]AATTTGTAATTTAGGATAAGATCCAAGTTATTTCCCAACTCTTGTTTCCC CCATAAAGTTAGGCATGAGGAGGAGCACTCATTAAAGGCAGAGACGGAAAA

Clone	Pos			Sequence
WI-7972c	268	T	G	GGAGTTCTGGTTCCTACTGGGGGCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTCACAGTTCTCT CCTTCTTCCCCCCGCTGTCAGCCATTCCTGTTCCGGCTTCCTGTGTGGAAGAGCTCCTTGATATCCT GTAGAGCGGAGAAAGGAAGGCAGCAACAAAAGAGGCTATGTGAGCACAAAGGTA CTTTGAGTGAAGCTGGG ---
WI-7972b	268	T	G	GGAGTTCTGGTTCCTACTGGGGGCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTCACAGTTCTCT CCTTCTTCCCCCCGCTGTCAGCCATTCCTGTTCCGGCTTCCTGTGTGGAAGAGCTCCTTGATATCCT GTAGAGCGGAGAAAGGAAGGCAGCAACAAAAGAGGCTATGTGAGCACAAAGGTA CTTTGAGTGAAGCTGGG ---
WI-7972	268	T	G	GGAGTTCTGGTTCCTACTGGGGGCAACCCTGGTGACCAGCACCATCTCTCCTCCTTTCACAGTTCTCT CCTTCTTCCCCCCGCTGTCAGCCATTCCTGTTCCGGCTTCCTGTGTGGAAGAGCTCCTTGATATCCT GTAGAGCGGAGAAAGGAAGGCAGCAACAAAAGAGGCTATGTGAGCACAAAGGTA CTTTGAGTGAAGCTGGG ---
WI-7981	261	T	G	AACCCCTGAAATCGGAAGGGACTTCCTCTTCTCTCCCTGTTTAAATTATAAGATGTCAT CCCCTTGTGTCATCTCAGAGACAGACCCCTTGGCTTTGCTTGGCTGAGCCCACTGGACTGGGTTTG TCTCTGCATCTCATTGTAGAGCTTGGTGGCTGAGCCCATTAAGATAAAATAAAATAGAGTTCCAAATA AGGATTTGTTCACGTCACATGCATCATAACCATTCCCATTGGTTCTCCTAAAACAT ---
WI-7992b	62	A	G	GAGCTTCCACAGTGAAGATGGAGAAGGTGAACTGCTTGAATATNCCAGATTTGCTTGGTC[A/G]T GCGTATGGCAGTGAGCAGGTATGTGTTTCTTCTTCACGAAAATTAAATTGCTATCAAGAGCAAAC TATGAACATTATATTCAAGATGTCTCCAGAGTGAAGATGCCGAGGATGAACTTGCATTGAACATTCC AGATGTGTGAGATCATGTGTATTGCAGTGGGCAGGTATTTGCTTGC ---
WI-7992	62	A	G	GAGCTTCCACAGTGAAGATGGAGAAGGTGAACTGCTTGAATATNCCAGATTTGTTTGGTC[A/G]T GCGTATGGCAGTGAGCAGGTATGTGTTTCTTCTTCACGAAAATTAAATTGCTATCAAGAGCAAAC TATGAACATTATATTCAAGATGTCTCCAGAGTGAAGATGCCGAGGATGAACTTGCATTGAACATTCC AGATGTGTGAGATCATGTGTATTGCAGTGGGCAGGTATTTGCTTGC ---
WI-8004b	183	C	T	ACTAAGAGAAATATTTATTGGTGGCCTATAAAACTCTGTTCAGTCTTTACTTGCTAATGATTTATTTT CATTAAAGTAAATGATCATCTTGGGGAGGCATTTTATAAAAACATATTAGGAGAGAAATTCTTTGA TTTATGCTATAAGGTAAATGTTGCATAATTCTTGCCTATGTGAATTG[C/T]AGGTTCCACTTTGAG AGAATTCTCAATCTAATAATAAAGACCAAGGGCCAGAAACACTAAGATA ---
WI-8021c	57	C	T	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATTCTCATCTGGAAA[C/T]GATCCC ACGTCTTAGAAACCTTCACCACCAGGAGTTTTCTTGTAGTGATTCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCTTTCACTTTGAGATTCTTTTCTTTGCGCCCTCTATCAAGTCAGCACACCTTTCCAAG GATTTTACGTTGCGGCCTTGTTAGGGGTGAATTCGGTGAATTGCCA ---

WI-8021b	57	C	T	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATTCTCATCTGGAAA[C/T]GATCCC ACGTCTTAGAACCTTCACCACAAGGAGTTTTCTTGTAGTGATTCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCTTTCACTTGAGATTCTTTCTTTGCGCCTCTATCAAGTCAGCACACCTTTTCCAAG GATTTTACGTTGCGGCCTTGTTAGGGGTGATTCGGTGAATTGCCA
WI-8021	57	C	T	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATTCTCATCTGGAAA[C/T]GATCCC ACGTCTTAGAACCTTCACCACAAGGAGTTTTCTTGTAGTGATTCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCTTTCACTTGAGATTCTTTCTTTGCGCCTCTATCAAGTCAGCACACCTTTTCCAAG GATTTTACGTTGCGGCCTTGTTAGGGGTGATTCGGTGAATTGCCA
WI-8024c	206	A	G	CTGAAAAATTTACTATGTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGTATTCAGGAGGACAGAGGCAGAGGGGATCCCAGTGGCCACTTCCCAGTGGGAAGACAGAAGAGAGT GGGCCCCAGAGATGGAAGGAACCCCAGTGTCATCACCAAACAACCATTTCAGCCGCCTCTAA TTCCC[A/G]CTCTAGAAACAGCTGGCCCTGGTCCGTCGTCAGTACACAAGGAAAGAGC
WI-8024b	206	A	G	CTGAAAAATTTACTATGTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGTATTCAGGAGGACAGGGCAGAGGGATCCCAGTGGCCACTTCCCAGTGGGAAGACAGAAGAGAGT GGGCCCCAGAGATGGAAGGACCCCAGTGTCATCACCAAACAACCATTTCAGCCGCGGCTCTAGCCCTCTAA TTCCC[A/G]CTCTAGAAACAGCTGGCCCTGGTCCGTCGTCAGTACACAAGGAAAGAGC
WI-8077	167	A	G	GAATGAGCCTTCCTAGCGCCGAGGGACCTGCTGCTTGTGTTGGCCTGCACATGCATTCTATGGAATGC TTTTTGGCCAAGCGGGGGCCACTGAGGACTAAGCTCTGANNNNNNNNATCTCGCCCAAACTCCTTTCT AAGGAGTCTGGGGTGTCATGCCCTACAAACC[A/G]TAAATTCTCATCAGATGGATTTTATTTAACGTT GTGTATTGTGACTTACTTTCCAATCTGACTCTGGCATAACAAGGGAAAAA
WI-8118f	114	G	C	TCTAGGTTTAATCAAAGCAATTTGCANTTGGATTTGGAATGACCACTCCCTTGCCTAAGGAAGCTAT GTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTT[G/C]TTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCCTCCTATTCCTTCCT AAAAATCAGAACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A	G	TCTAGGTTTAATCAAAGCAATTTGCANTTGGATTTGGA[A/G]TGACCACTCCCTTGTTTCTTAGCCTTGAAGA TATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCCTCCTATTCCTTCCT AAAAATCAGAACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T	G	TCTAGGTTTAATCAAAGCAATTTGCANTTGGATTTGGAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTTGTTT[T/G]CTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTCCCTGCCTCCTATTCCTTCCT AAAAATCAGAACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

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WI-8118c	44	C	T	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAATGA[C/T]CACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAAACTGGCAAATACAGAATGTAGCTTGTTTGTTTCTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTTCTGATTTCCCTGCTCCTCCTATTCCTTCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88	T	C	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAAC[T/C]GGCAAATACAGAATGTAGCTTGTTTGTTTCTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTTCTGATTTCCCTGCTCCTCCTATTCCTTCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299	C	T	TTTTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGAACAGGAAAGGAGACCCTCTTGGCACACA TTTATGGAGGGTTGTCCCTGAAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTCACGGCA ACCAGTGGGCAAAGAGCACAATGAAGAGAGCACAATCACGGCA
WI-8171c	46	A	G	TTTTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAC[A/G]TGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGAACAGGAAAGGAGACCCTCTTGGCAC ACATTTATGGAGGGTTGTCCCTGAAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAAGAGCACAATGAAGAGAGCACAATGATGATAAAAACAATCAC
WI-8171a	46	A	G	TTTTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAAC[A/G]TGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGAACAGGAAAGGAGACCCTCTTGGCAC ACATTTATGGAGGGTTGTCCCTGAAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAGTGGGCAAAGAGCACAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298	T	C	TTTTCTCCTTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCAGCATTCTCTGTAGAGGAAGAACAGGAAAGGAGACCCTCTTGGCACACA TTTATGGAGGGTTGTCCCTGAAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAGGC ACCAGTGGGCAAAGAGCACAATGAAGAGAGATGATGATAAAAACAATCACGGCA
WI-8314b	85	G	C	GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTCTAAGGG[G/C]AGTCTCAAAAATCCCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAGTGCTCTGTAGTCTTATGATGCTCTTATGATCTTAGAAGAGCACTGTCCAATAGAACTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATCATAGGGGTAACCACT
WI-8314	78	C	G	GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCT[C/G]TAAGGGGAGTCTCAAAAATCCCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAGTGCTCTGTAGTCTTATGATGCTCTTATGATCTTAGAAGAGCACTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT

WI-8321	178	G A	TTTTTAAATATGCCCGTTTAGAGAGCAGACAGCAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAGTATGGTTCAGAAT[G/A]AGTATCTTAGTATTCTTCTA TCCCCTTAGATAATAGCTGCCACTTTCAACCTACTTTATTAGCTGAACTGTTGGC
WI-8321	178	G A	TTTTTAAATATGCCCGTTTAGAGAGCAGACAGCAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCGTGTATACTGAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTCAGTATGGTTCAGAAT[G/A]AGTATCTTAGTATTCTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTATTAGCTGAACTGTTGGC
WI-8332b	123	A C	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGGCGGGATATA AATTACCTCTAGATTGTCCAAAGCCCAGTCTCTTCCCTTCCCTGTGC[A/C]GCCTTAGAAACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTCCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACTAG AGGTGGAGGGGNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGGCGGGATATA AATTACCTCTAGATTGTCCAAAGCCCAGTCTCTTCCCTTCCCTGTGC[A/C]GCCTTAGAAACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTCCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACTAG AGGTGGAGGGGNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAAGAAAGAGAAGGGAGAAGTCTACACACTTTT AAACAACCAGATCTCATGAGANTTCCATGGGAGAGAGCAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCINTCACCAGGCCCCTCCTCCAACACGTGGGG
WI-8378	308	T C	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAAGAAAGAGAAGGGAGAAGTCTACACTTT AAACAACCAGATCTCATGAGANTTCCATGGGAGAGCAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCINTCACCAGGCCCCTCCTCCAACACGTGGGG
WI-8426	184	T G	TTTAGCACATATTTAGCATTAAGCCTCAAACGATACAGCAATATGTTACATTCTCTTGTGAAAACAG TTGTTGTAGACTGTTAANNNNNNNNNAAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNTTAA GAGGNTTCTTTGCTGTGGANGGGNCCGGGGCCCTTGGCNATNGNATNGNATTCAGTGAG AGGCTGGGAGTATGGANGGNCCCGGGGCCCTTGGCNATNGNATTCAGTGAG
WI-8450h	61	C A	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTACAGCACCCTTCTACATACACTT[C/A]JCA TCTTCTCTATCTTAGTTCCAAGTTTAGTTTCAATCCAATTATACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAAACTATGATTTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGAGGATGGGAGTGTAATATGAGCAGTACAGAGTACTTAATGCAATTCAT

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WI-8450g	55	T	C	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTTAACAGCCCTTCTACA[T/C]ACACTCCAT CTTCTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTATACCATTCCATTGTTATTTTAAGA AAAAACCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450f	108	T	A	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTA[T/A]ACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450e	125	T	C	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTATACCATTCCATTGTTA[T/C]TTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450d	125	T	C	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTATACCATTCCATTGTTA[T/C]TTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450c	108	T	A	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTA[T/A]ACCAATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450b	61	C	A	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACATACACT[C/A]CA TCTTCTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTATACCATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450a	55	T	C	TTGAGCCTCCACAAATAATGCAACCAAGTTTTACATTTTAACAGCCCTTCTACA[T/C]ACACTCCAT CTTCTCTATCTTAGTTCCAAGTTTTAGTTTTCAATCCCAATTATACCATTCCATTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8458b	60	A	G	CAAGGAAAGCTGTCAGTCTTCATAAACTTTCAAAGAGTTACAAAAATACGTATTTTTAA[A/G]CTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATCGTCACACACCATACAACCTTCAC ACCTGGCTACAGCAATGTTGACTTACGTCACATCACCATTGTTTATACTTGTGAAAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTTCTCA

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WI-8461c	105	A	T	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAAATCATTTTTT[A/T]NNNNNNNNCCTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38	T	C	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACACAA[T/C]ATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAAATCATTTTTTNNNNNNNNNCCTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38	T	C	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAA[T/C]ATAACTACAACCTTACAAATGCCAATTA TTAGACAAAGAGANTAAATGATATAATATAAATCATTTTTTNNNNNNNNNCCTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105	A	T	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAAATCATTTTT[A/T]NNNNNNNNNCCTGTCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTAACAACATTACAANTTNTTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77	A	G	AATAACATGTTATGAAACAAGCTGGTTACAAGTAGTAGGTAGATGACTTAATTTTGATAAAAAAT TAAAAAGCAT[A/G]AACATGCATATAAAAATTAGATTATGTACAAAATACCAACAGTATTACTTC TGCTCAGTAATTAAATATTCTTCCCTTGTTTTGTCTTTTAAAAAACATTATTTCTGAAAAAAAA ATCAGAAAAACATGATCGTGGAGAATTATTA
WI-9439b	101	C	T	ACAGAAATTGACCTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAATCCCAGTCTGTCAGCTACCTGT[C/T]TGTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACTTAGAAAACAGCCCCTACCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAAACTTGTACCTGTAAAACAAAG
WI-9439a	76	C	T	ACAGAAATTGACCTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAT[C/T]CCAGTCTGTCAGCTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACTTAGAAAACAGCCCCTACCCCAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAAACTTGTACCTGTAAAACAAAG
WI-9446b	75	T	C	GAAGGCTTGATTAAGGGAGGNTTTATTTGATGTNAACTTACCATTCCATAGACTATAAAGANCATTA TAAAAAA[T/C]CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTCATATGTGTTTGTNCCCTACTNTTATCACTGTGTCTTTATCACTGTGTCTTTATCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT

Marker	Pos	Allele 1	Allele 2	Sequence
WI-9446	75	T	C	GAAGGCTTGATTAAGGGAGGNTTTATTTGATGTNAACTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAA[T/C]CCTCTAAAGNGACACATGCCCAAATGACCANGNCATAAGCAAACCTTTAAAT TACTCATCTTTCATATGTGTTGTNCCCTACTNTTATCACTGTGTCTTCTGTCTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185	A		ATTAAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTCTAGATTCCAGGCTTTCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTAATTAATCAAAGTATGTTAATGTCACTT GGAATTCTACACTGACATGGAAAAGCCAACAAAAATAAACTAAAACTTGACTAATGAAG
WI-9497	185	A		ATTAAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTCTAGATTCCAGGCTTTCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTAATTAATCAAAGTATGTTAATGTCACTT GGAATTCTACACTGACATGGAAAAGCCAACAAAAATAAACTAAAACTTGACTAATGAAG
WI-9523b	193	C	A	GTGAAAAAGTTTCTATTCATTCCATCATCACAATAGATTGTGCTAAGGATCATTTGGAAGAATGTG CAGCATTCAGAGAAGTTGTATCTCATCATGCAGCCATGACATTTATCTAAAAGTACGTGCACA GACTCAGACACAATTACAAACTATTTCAGCCATGTGATTTCCACACATTGTACAGTGA AAAGCTCTTCAGCTTGGAACAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9523a	47	G	A	GTGAAAAAGTTTCTATTCATTCCATCATCACAATAGATTGTGCTAAG[G/A]TCATTTGGAAGAAT GTGCAGCATTCAGAGAAGTTGTATCTCATCATGCAGCCATTTATCTAAAAGTACGTGCA CAGACTCAGACAATTACAAACTATTTCAGCCATGTGATTTCCACACATTGTACAGTGA AAGCTCTTCAGCTTGGAACAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9554	202	T	C	AAAAACACAAGTTTCATACATCACAAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGTACTGCCTTTNCTAGTTGTTATTGTACAATGCTGTGAGATAATGCAGCCCATG CAATACACCCAAGAACACTAGAGTCCTACACCCAAGTACAATATGTGAAAGCAGCCCTCTGCAAGTG G[T/C]GCTGGATACCACCACTAAGAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97	G	A	CCAAAAGCCAAACCATTCATATGTATGGATTTCATAAACATTTATTGATCCTTTTTGAGGTAAGTAT AAATACCTTTACATGGCTAAAC[G/A]CTTGAAAAATCAATTTCAAGGGACTCTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAAATACAGGTAAGTATTCAG GGNTAAAATGGTACAAAAAAAGGCTGTAACTCTTTNCTTCACATTGATCACA
WI-9625b	172	A	T	TTGAACATTTAATGAATGACAAAGAACATAACATCCTCTGAAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCCATATATTTGTATCTNCTCNCCTGGGAAAACTTGGAAAAAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCT[A/T]GTTTACCAATTTTTATATTGACATAA AGTAGCACAGACGAGTAGTTATTTCATTTCATATTAAAAAACACACTGACAAATCTTTTC

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WI-9625	172	A T	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAACTTTGGAAAAAAAACACGCACA TAAGTATCATAACTGAGGGGTTGTGGACAAGTTACTTCT[A/T]GTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAAACACACTGACAAATCTTTTC
WI-9647	144	C T	TTTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTATGTCTACTATACCTTTTTTTCATCCTTTCA ACATCTTTTGTCACATTTAGGTGATGCTCTTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAGCT TACAAACT[C/T]GTCCTTTACCTGATACATTTATTCCATTTCATTTACTTTCATTTGGATTTTTAAAAATGTA ACTTAATACGTCTCTTTCAGATGTCCCTGCTTTTTTAGTTAATTGTGTTT
WI-9676n	114	A G	GGGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA[A/G]GATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTGTTT
WI-9676m	184	G T	GGGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGC[G/T]CATGAAATAACTTGA GGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTGTTT
WI-9676l	84	A C	GGGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTG[A/C]GTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTGTTT
WI-9676k	202	C T	GGGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG[C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTGTTT
WI-9676j	92	C T	GGGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTA[C/T]GGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTGTTT
WI-9676i	173	T C	GGGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCT[T/C]CCTCTGTGCGCATGAAATAACTTGA GGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAATCCTATGCATTGTGTTT

WI-9676h	134	C	A	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC[C/A]ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTT
WI-9676g	202	C	T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG[C/T]CAGGGTCTCTCAGCTTTAAAGCCTTT
WI-9676f	184	G	T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCC ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTT[T/C]CCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTT
WI-9676e	173	T	C	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGAGCAAGATGTGGCTTTCCTGCCCC[C/A]ATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTAAAGCCTTTAAAGCCTATGCCTATGCATTGTTTGTTT AGGCCAGGGTCTCTCAGCTTTAAAGCCTTT
WI-9676d	134	C	A	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA[A/G]GATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTT
WI-9676c	114	A	G	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTA[C/T]GGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTT
WI-9676b	92	C	T	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTT
WI-9676a	84	A	C	GGCCACTGTCCAAAGTCTGTCACAGTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTA GGGGTACCAAGGNTCTG[A/C]GTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTT

WI-9738b	40	C	A	TGGACCAAACACAGACAGATGTATTCCTGGTGCCTGTGTA[C/A]ATTACAACTCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGTAAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTCACCTGCCTGGTGGGGCACATGTCTGTATTGCTGTCC TCTTTTATTTCTGTCCCCTTATGTTGGTGGGCACATGTCTGTATTGCTGTCC
WI-9738	40	C	A	TGGACCAAACACAGACAGATGTATTCCTGGTGCCTGTGTA[C/A]ATTACAACTCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGTAAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTCACCTGCCTGGTGGGGCACATGTCTGTATTGCTGTCC TCTTTTATTTCTGTCCCCTTATGTTGGTGGGCACATGTCTGTATTGCTGTCC
WI-9756	47	A		ACTGAAATGTAAATGGCCAAGGCACCCAGGACCTTAAAAATCATAAGAAGTTAATCTGTGGGAAAA GAGTAACTACAAAAGCATCTAAACAGAGCAGGATGTGATGTAATGTGTCCCCTTATCACTTTAGTC AGTAAAGATAAGAAAGCCCTGGTAGTATCCACTTCCACAAACACACAGAATATACACTTTTGGAAG ATTTCCACTTAACCACTTGATTCTTCACTTTTTATGATTTAAAACTCTCCGTGG
WI-9758	135	A	G	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAAACTGGGAGAATTCAATTCAAAGAAGAAATTCTTGTTCGCAAGGTCAATTTTTATACTATTA A[A/G]TAAAATAACTCTGGTAGGTTCTATAGCAAATGCTAAGTAAAGTAACCGCTGGTTTCTAAATT ATTACG
WI-9778	127	G	A	ATTTAAATCCAGGCAGCAGCGGGGGAAAATGGATACTTTCATATGTCTGTACCCAACTATAAACTTTTG GTTCTCATGCACCATTTCATTTGCCTTCTCACTCCAAGTACCACTGATTTTACCAATT[G/A]CTCTC ATAATTGACTTTGCTACTGGAAGAAACTCTTAGAATGTTGGAATTCTCTATTACACACTTGCCTCA AAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGAGCC
WI-9832	116	C	A	TCTCCCCTTTGCCTCCTCATGCCCACTCCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCGAGGACTTGCTGACAATGCAGTTTC[C/A]TGGGATCCCACCCAGGA CTCAAAAAACTAGGAATTGGGAGAAGAGGACCTGGAATCGGTGTTGCTGCTAGCAGCCCCCCAGGTGG TTTGTAAGTGGACTAAAGTTGAGGACCAGACCATGGAAGGTTGGCTTTGGC
WI-9841	101	A	G	TGGAAAAATAGCTTTATCAATCTCTGATATGTCTACATATGCTACATATAC[A/G]TGTGTATGTATAAACTTAACACTT TATGAAAATTCCATTTTGAATGAATAAAAACTGTAAGATAAACTAAGGTTCTATCAGTGGGAAATGAGA AGGATTATATACACACAATAAAAACAATAAAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGGATGGTACTTGACTTGACTTACTGATATGCTGTTG
WI-9880c	222	G	A	GAACTAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGTGGGGTTGAGTTTTTATGATATCTCCTGTTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAAATTATATTTTATATAAGCACATGAA AATGGAATGAAAATAATGA[G/A]TTGACATAGGAATTACCTACACATATTTTG

ID	Pos			Sequence
WI-9880b	157	C	A	GAACTAACACCTTCTTGCATGGATTTTTCTTGATTATTGGCAGTTAACAATAAAAATGTTATTAGATCACTGGTGCTTCTGTGTGGGGTTGAGTTTTTATGATATCTCCTGTTAGACCCATAAGGGAGGCTGTGAGTTGTTTTCTACATCCTTGGA[C/A]TATATAAGATCCTCTTTAAAATTATATTTATATAAGCACATGAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTG
WI-9880a	108	C	T	GAACTAACACCTTCTTGCATGGATTTTTCTTGATTATTGGCAGTTAACAATAAAAATGTTATTAGATCACTGGTGCTTCTGTGTGGGGTTGAGTTTTTATGATATC[C/T]CTGTTAGACCCATAAGGGAGGCTGTGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTAAAATTATATTTATATAAGCACATTGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTAAAATTATATTTATATAAGCACATGAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTG
WI-10183	127	C	T	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACTTCGGAATCAACTCAGGCATGCACAGCATCCCTGTCGTGGAGTTTATTTTAAAAAACAACGCCCCAGTTATCACAGTTTCTNTTTTGT[C/T]CACCATTTTCCATAACAAAAGAAGCTACACAAAATTNGGGGGGAGAANACTCTCTTGGAGAACTGACACATTTGCAGAGGGGGTCATGAATAATGATTCCAAA
FB25G10b	109	A	G	TCCCTCAATGACAGATGAACTAAATTTCTCTGGGTAAGAAATACTTTATGTCCATTGTGATTAAAAAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAA[A/G]TGATTTTAGATCCTCCCCCAGTGACAAGTAAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCTATTTGGATATCCCGGAC
FB25G10	109	A	G	TCCCTCAATGACAGATGAACTAAATTTCTCTTGGGTAAGAAGAAATACTTTATGTCCATTGTGATTAAAAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAA[A/G]TGATTTTAGATCCTCCCCCAGTGACAAGTAAACTGAACTGACCATATTTATACATAAAATGGAATGTAAGAACCTATTTGGATATCCCGGAC
IB3071	102	C	A	ACAACGCTGAACTTCCATAACAGTCAATGGTACAGTCAAACATCACATGTACAGAACACAATTAGATGAACTGAAATTATAAGNTATAAAATAAAATAAAAT[C/A]CAATTTCAGNAACAAAAATCAAAACATTAAGGNTCCCTGNNATATTCTTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGAGGCATTCACAATATGACCCTATTAACCCAGTCTAGGGATTCTG
NIB551	161	C	T	CGTCCTTCCTTTTTGAGATTGCAATTAAGTAAGTAGATAATATGAGAGAGGAACTGACAATTGGGTTGTCCCTACTGAGCTTGGGGCCAGGTGTGTACTTAGGAACCAATCCCACCCCACCCAGAAGAGAGACTCATCTATGTTAACACTCAAGGATGCCCTGGAGAGGAGGTC[C/T]TGACCACATACATGCGGCCATTGGTTGATTTCAGCTTTGCAAGCAGCGTAGTGAGTGAGAAAACCAAAAGCTTGTCC
S72904	51	G	T	AGCATAGAAAGTGATTTATATTTTTAATGGTTTTCAAGTGGAAGTTCCTTT[G/T]AATTGTCAGTTCATTCCTGGAAAATCTTTTGAGTTAAAATAAGGATCCTAAAATAAGGATCCTCGAACTACAGGCCCTAAAGAGAAATTGCCCTCAAACCACACAAGTGCTAACTTCCTCCTCCCCCTTTCTGTCAATTGGTTGGTTGTCTTTAAAATATTGCAAAAGTCCTGATGCTCAAAACAGTATTTGGGAGTGTTTCAGTGTCTGTA

ID	No.			Sequence
UTR-00481	115	C	T	TATTCTTTTATCCTGGGGCCACAGTTCTTGATTATTCCTCTGTGTGGTTAAAGACTGAATTTGTAAACC CATTCAGATAAATGGCAGTACTTAGGACACACAAACACACAGA[C/T]ACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTCAGATTGAGC
ESTC1	33			CCCTGTAGCAGTCTTCAGCCTCCTCCTACCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37			GCTACTACCACGGCTGCTTCGTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21			GCCATCAAAATTTCCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTCTTGCTCATCCC ACTTGAA
ESTC107	20			TGCTGGCTCACTTCCTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35			AAAACCAGGAAGGGCCCTGCCCCGGAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23			AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37			AAGGGACACAGTGTTGCTGACAAGGTGACACTGAACANAACAGTTTCCTTAATTGTAAAAGCGGG CATCG
ESTC117	24			AATTGGCTCTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAATTTACAAAAGC CTCCA
ESTC119	24			TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34			GACAATAAACAGCTAAGCTACTGACATAAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21			GAAGCCAGTATGTTGTGGCAANATTCGAGAAAACACACTGAAAAA
ESTC128	42			GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCAGGCCATCATNTTCCATGGGACCAGGCTGGCTCAA TGTGGAACTGG
ESTC129	20			AGTCACCATGCCCAGCCTAGNATGAGTTTAGTAAGATTTGGTTATGCTGGGGAG
ESTC13	46			GTGTATCTGGGCTTCATGGGATGCATAAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGGTCTGGA TCAGAAAA
ESTC130	49			GCCTGCTCACAAGGTAGAGACAAAAACATAAATCTTCAGGAAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	GGTAAAGTCTAAATTACTGCCTTAGCAAACNCTATGTTGTCAGGTTTTCTGCTGCA
ESTC137	21	CCAGTTTGGCTTCTGTCCTCANAGTCTCTCTCCCATGTGGCAAACA
ESTC139	45	AGGAGCACAGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGAGNGGGGGCTGGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	CCCATTGTGGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCATGGTTTAGAAAGC TTGCCCTGGTG
ESTC142	72	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGAGCGTAATAATCTATTTTATTCATTTTAAATC AAAGANACCATTCCATTACCTAACAAACA
ESTC143	29	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAAATTTGTGATTTCCTTTTG
ESTC144	26	AAATCCATATTTCTTGACATGAGGTNGCTTTTTAGCAGCATTTCGG
ESTC146	20	CATGTCCAGGATAAGGAGCANACACCAGGATTTATACGGTGGCAGCG
ESTC148	42	TCTTTGGTTGTCTCACACAGACACTTAAGTACTGTATCGCTGNATGCAGCGGCCTGTGGAGGCCCCTG GGGGTGGCCTGGGCCCTGTGTCCTGAG
ESTC149	28	TCAGTTCATTATTTGCTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	GGATTGTAATATTGCCAGCTTTGGTTAAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT CCCAGGAAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATATATCATATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC150	20	GAAGCTAAGGCCCCATTTTTTTCTTTTAATACAAATCTACTGGTGCTNAAAACTCAGAGCTTAGGA AACACAGCC
ESTC151	49	TTTTTAATTGACAACTCAATCTCTACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCATTTACA
ESTC155	37	GCAGCATTTGTGACAGGAGAGCGCAAAACAAANCCTGGCCTCGGGGATGGAGCGGGGCGGCCTCA CCACCACTGCAT
ESTC156	32	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGCACGGTCTGGTTCTGC AA
ESTC158	35	AGCTGGCAAGAGACTTCCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACGGTCGGTTCTGCA GCTTTGAAAGG
ESTC159	31	

ESTC16	23	⋮	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCCACAAGGACAGGTT
ESTC160	38	⋮	TTCTAGCATTGCTGGTGCAGTGGGGGGCCTGAGCTGGGGNGCAGTCGGCAGTGTCACTGGGGCCCGTTTG GGACTGGGGTTGA
ESTC162	36	⋮	CTCTTCGTCCGTTTGCAAGTTGCTGTGTTGTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	⋮	TCATTCTCCATAGAATATTGGTTTTTGTAACANCGAATACAATCCAATATATAAACAATCC GATACATACCA
ESTC169	22	⋮	GTCTCTGGTGTGCAGGGAATCANTTTGCTGGATTAGAGGAAAGGTGCCGCCGTCTGTTTCCATGACTT
ESTC176	23	⋮	CACCTCCTCCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	⋮	TGGGTGGCTCTTTAAATACCTTCCATTATATTTCAAATTTTNCTTTATTCTATTAAAATACCTTTTAT TCTCTTTATTCCCATAAAAAGGCAACCAA
ESTC18	29	⋮	TCAGACACTGCCGACATCAGCATTGTCTCNTGTACAGCTCCCTTCCCTGCAGGGGCGCCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	⋮	TAGGGATTCCAAGTTGCCTGGNTTTAATATAATACATATTCACAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	⋮	GCTTGACTAGCGGAGGCTACATCACACAATTTATAAAGTGCCAGATNAGTGCTAATTGTCATTCAGCTTG ATTTTTCACCTCA
ESTC187	24	⋮	ACCATGATTGCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	⋮	TCTATTAACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGTAAGCTCATCACTTGTCTTCCAT CTTGC
ESTC189	27	⋮	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	⋮	TCCTCAAATACCACTTTCCCCTAACTTATCCAGTCTAGTAAGCNTTTCAAAGGAGGAAATGGGTTAC CTTTCAGGGG
ESTC197	26	⋮	ATCTCCAGTGTCTGCTGCCTCCTCCCNGCAAAGTCTCCCACAAGCACA
ESTC20	33	⋮	AAGATTAGGACAGACACCGCGTATAGTAAGCTCTGNGGAACTCCAAGAATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	⋮	TTTGGTGAAAAATCCCAATATATGAGTTTAAAAAAAAAAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTGCCTGCAACAG

Clone	No.	Sequence
ESTC201	35	TCTTACTTGGGTAGTTTAGCAAACATTTTTAAAANCCACATCCAACAGATTGGTT
ESTC202	22	CTGCTGGAGGAGGAGGACAGAGACGGNCAGGCGGCCTGGGTGGCGCCTGGCGTGGGATGTTCGAGATGAGCC
ESTC203	27	ACACTTAACAGGTTAAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAATTTTATTTGTGCTACAAGACACGTTGCA
ESTC208	43	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAAGCCTAAGAGTGAAAA
ESTC210	29	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAAGTGAGTGACGGTGACCTGTG
ESTC212	27	GGGTAACCTGATGAGGAAGCTCTAGTGNGAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTC
ESTC214	21	CTCCAGAGTCCCTCCTCCTCANACCAGGGGCAGGAGGAGTTAGGGAAT
ESTC216	49	TGGCAAGAAATTTATTTACACTAACAAATTAAATTAATCACAGGTATTNTTAGATTGGTCAGAAAACAAAAGACCA
ESTC217	28	TTTTGTCAGTAAATGAGCAATACACTGANTGGAAATCTGCATGATTAAATAACATTAACAAGTTCATAAACACCCCA
ESTC219	32	GTACACATCCTGGGGGTGAGCACACAGCAAAANGGGGTGGGACGTGCAGAGAGGTATAGGGTAAAGGCAAAGGAAGC
ESTC22	41	TCATTGAAGAAAAATTATGGGTTTTATTCTATTCTAATTGNGAGAATGCTTAATGTCACAGGCTACATAAGGGCC
ESTC223	27	CTTCTGAAGCCCAAGAGAGGGGCAGAANGTAGTTCTTGATTAAAAAACAGAAAGGGGAGGAGGACTTCTGAAGCCC
ESTC224	37	CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAACACACACACACACACACACA
ESTC225	20	TGCACTGTTACTCCCCAGACNGAGACGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAGGAATGTGTAGGATCG
ESTC23	27	TTCTACTTTATTTCATATTCCCACCACNATAACGACTCCTTTAATTTAAACTAAAAACCATACAGGGTTCCTGAAAGGG
ESTC230	43	GCTTCCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAATTAAGA
ESTC231	24	CAAAAGGGTTAGTCATATTCCCCANCAACAGCATGATAAAATAATTCAAC

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ESTC28	23	GAAGAGCTGGGCACGCATCTGACNTTTCTTCCTCTATTCCTATAAAAATAAAAGGAAGCAGAAATCTGC
ESTC3	20	CAGACATGACCTACCGTCCCNGGCCCTCCAATCCATATTTTATTCTTGAGCCGCCTTGGTCAGGTTTGATTCGCACACTCC
ESTC31	32	ACAGCCCCACAGAACTATTGTAAAACAATATTNTCAGTCGGTGATCATTGTAATATACAATACAAAGCAATTTCCTCAGA
ESTC33	25	AGCACTTCCAGCTCCTTGACGTTGTNGGACCAGGGAACTTCCGGAA
ESTC39	26	AAGGAAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	CCACTGAATCACACAACATGGACNAATCTCAAATCATTATGCTGATGAAAGAAACCATT
ESTC40	22	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTAAAAATATTTGACTTGTTCCCCCTTCAC
ESTC45	37	TTTGGAGTTTGTGTCTCGGAGTTTGTTCTTTGTAACNTCTCTCATCATGAGGCTATATATTAA
ESTC50	56	CTGTCCGTGGTGAGCCCTGCCCGCTGTCCCATGGGCCCACTGGTGCGGANCCGGGCAGATGTTTACCCTGT
ESTC56	45	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGAGGGAAAGGACACCAAGT
ESTC57	20	AAGTGGGCCCTCCCAGTCCCNTCTCTGGGCACAGATCCCACCAGTCTGCTC
ESTC59	38	GAAACACAAAGTGTTGAGAAAAAACTTCTCAAAATTNGTTCCAGACTTCAGGAAAATGATTCCACATGGTAAGGCC
ESTC6	27	TCTGCAGCACTTCACTACCAAATGAGCNTTAGCTACTTTCAGAATTGAAGGAGAAAATGCATTATGTGGACTGAACCG
ESTC61	57	AGTGATTTTGGCTAGGCGTGGTTCTCATCTGTGAAATTCCACAGCGCAATGACAGCANCCTCTCTCCCACCCACTCAAG
ESTC63	20	ACAGACACAGCATCACACCANAGGGCCCACGGGGAGGGTCGGGGGAGACGACACTTTTTCCCTGGGAAAGGCAGCTCTAATC
ESTC69	20	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGTCACTTTCGCTAA
ESTC7	45	AGTTTCCCTAGAGCTGTGCGGCCAGATAGCTGTTCCTGAGTTGCANGCACGATGGAGATTTGGACACTG

ESTC72	37	⋯	GGGCTTCCAAAATGGGTATTGGGGCCAGGAGGCTGGCNTTTGGCGTGACGCGCCTAAAAAGTGTGACC AACAATTCACAGCTACAGGAAATCTAGAACAAATCAAATATTCATCACNTTGGGTTGAAAAGTTG
ESTC74	49	⋯	GAAGA
ESTC77	40	⋯	ATGACTTTCCTGTCCCATCGGAAACCAGAGTTTCCCCAGGNGAGCCCCTTCCTATCTGCGGTTA
ESTC81	20	⋯	GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG
ESTC82	25	⋯	TTTCAGATGATGGGGGTCTGAGATGTNTCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC83	53	⋯	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC85	28	⋯	TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTCGTGGTTGGGGAGGCTACAGCCTGACCACATTC TTTGC
ESTC89	22	⋯	ATTGCAAAGGAAGTGGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC90	33	⋯	CTGGTTCTTCTTCGTCTTGGCATTCGTCCTCCTCNGGCCAGTGCTCCACCCAAGTGTCCTTCCGATGAT
ESTC93	29	⋯	CTCCCCCTCCTCAGTTCACAGTGGGAGACTANGGAGATTCAGGGCAGGATCC
ESTC95	32	⋯	GCACGTTCTTGTTCTCCTCTTCCAGAAGTTGNAGACGTCTATTTAGTTTGATTATCTGTCG
DWU-100	127	C T ⋯	AAATGACTTGACGAAGCTCATAGAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTCA GTGGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCCTGACTGTTCTCCA[C/T]GCCAG AATTCTTATCAATGATCTTTCACCTAAGAAAACAGCAAAGATTCTGGCAAGCACACGATCTAGAGAGATAC ATCTTATTGGCGATTTTTCACAAAAATCAAAGAGAAGAAGAAGAGAAGGCTTAGCTG
DWU-177	77	A G ⋯	TTCCATCCTAGATATCTACTACTCAAAATAATTGAGACAACAAGTGTTCAAACAGAAGACGCTTGTGCTGAA TGTTCATGGC[A/G]GCCCTATTCACAGTAGCCAAACGATGAAAACAACCCCAAGCTACTATATTACCA GATGAAAGGATAAACAAAATGTGGTCCATCCATACAATGGTATTACACAGCCATAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-286	213	A C ⋯	CAAATACCTGGACTATCAACCTTGTTGCTTAATCCCTGCGCAGCATTCAAGGTTAATCCATCTAAGTGAC ATTTTGAAATTCCAGCGGTGCCACCCAATCATGCCCAGCTTCTCGTGTCATCATGAATGAGATATACATTT ATGTCTGACCTTCCCTCAAGACTGATTTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG[A/C]TGGGAAACCAGCCCTATCTGAGTCTTCGGCTCCCTCC

Name	Pos				Sequence
DWU-252	94	A	G	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACTTCATGTAAAGTGT CAGAAGGAGCTACAAAACCTACCCTCA[A/G]TGAGCATGTACTTGGCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTTCCTGTTGAATGACAAAGTATGTGGTTTTGTA AT
DWU-330	85	C	T	---	GAACATTCCTCTGCAGCACTTCACTACCAAATGAGCATTAGCTACTTTTCAGAATTGAAGGAGAAAA TGCATTATGTGGACTGAA[C/T]CGACTTTTCTAAAGCTCTGAACAAAAGCTTTCTTTTCCTTTTGCAA CAAGACAAAGCAAAGCCACATTTGCATTAGACAGATGACGGCTCGAAGAACAATGTCAGAAA CTCGATGAATGTGTTGATTGAGAAATTTACTGACAGAAATGCAATCTCCCT
DWU-370	231	A	G	---	GAAAATGTTAATTGGGCAGGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAAGAG AAGCATCATTTCCCAAACAGGGCAACTGTGAGAAGGCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAAAAGGTGAATGTTGAGGGCCCTCCACTTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTCCT[A/G]GCATCTATTCCTCTGTGC
DWU-1537b	89	A	G	---	CTCTTAACTTCAGTTCCCTCATCTATAAGAATAAGGGATTCAGTTGTGATCACATAGCTCAGGTAATC CAGGACCAGAAACCCAGGAGC[A/G]TGGGACCTGATCCACAGCTAGAGGATGGGGGACTCTGTAGCT ACAGCATTTTCCTGAACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52	C	T	---	CTCTTAACTTCAGTTCCCTCATCTATAAGAATAAGGGATTCAGTTGTGATCA[C/T]ATAGCTCAGGTA ATCCAGGACCAGAAACCCAGGAGCATGGGACCTGATCCACAGCTAGAGGATGGGGGACTCTGTAGCT ACAGCATTTTCCTGAACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196	C	G	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGCCCTGGGAATTCCAGGGTCACTGTTCCTTCCTGTCTCCGTGTGGGAAT CAAGCCAGCAGCTCCAGGCCAGAAGTGGGGACTGTGAGGACATGGAGTGGACTGTGAGGCCCTCGAGTCTTGTCCTC CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCGAGTCTTGTCCTC
ESTD-ADAa	184	G	A	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAACTGGGCAGGTCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGCCCTGGGAATTCCAGGGTCACTGTTCCTTCCTGTCTCCGTGTGGGAAT CAAGCCAGCAGCTCCAGGCCAGAAGTGGGGACTGTGAGGACATGGAGTGGACTG[G/A]CACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCGAGTCTTGTCCTC
ESTD-ANT1	160	T	C	---	TCTCCTGTCTCATTCCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGCAATTAACCAAGTAATTCA TGGACTGCCCAACTGCGAAACAAGAAGAGCCAGTGGAGCGCAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGC[T/C]GAGCTCAGATGATCCTGT
EST10398 2b	168	A	G	---	TGCCTGGGGTGGCAAGGCTGCAAACAAGGAGCAACCCAGGAGGCCTTTATGAAGCGGGGCCATGGTA AGATGCTGCCCACCTCTTATCTCACTGATGATGTTCACATTGGGCTTGACTTTCCAAACGGAGAAG CATTGTTTTCTTCGGCGCCAAGAAGGTATCTACC[A/G]ATAGTGTCTATTAGGCATTTG

ID	Position	Allele 1	Allele 2	Sequence
EST10398 2a	147	C	T	TGCCTGGGGTGGCAAGGCTGCAAACAAGGAGGCAACCCAGGAGGCTTTATGAAGCGGGCCATGGTAAGATGCTGCCACCTCTTATCTACTTGATGATGTTCACATTTGGGCGCTTGACTTTCCAACACGGAGAAGCATTGTTTTCTT[C/T]GGGCCAAGAGAAGTATCTACCAATAGTGTCTCATTAGGCATTTG
ESTD-C7	14	G	C	ATATCGTGGCCTTA[G/C]TTACCTAGAGCTGGACAATCCTGCTGA
ESTD-D4S95	90	T	C	CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAATTTGAGAAGAGCAAAACAACTTTCAAGGATAATGGGGCAATCACTTCTT[T/C]CTTCTTTAGAGTCTACCGG
ESTD-GPPK2L	38	G	A	AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACC[G/A]CCGAGAACTGCTCGATATC
ESTD-HRASb	82	A	G	CTGGGCTCGCCCCGCAGCAGCTGCTGGCACCTGGACGGCGGCGGCCGCCCAGGCTCACCTCTATAGTGGGTCGTATTCGTCCACAAA[A/G]TGCATCTGGATCAGCT
ESTD-HRASa	37	C	T	CTGGGCTCGCCCCGCAGCAGCTGCTGGCACCTGGACGG[C/T]GGCCGCCCAGGCTCACCTCTATAGTGGGGTCGTATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD-NRAMP	81	A	G	GGAGGCAGGAGGTGGGGAGGGGGTCTGTCTGCTCCAGGTCCCACAGACCAGGAAGCGGCCTCAGTGTATCCCCACCCCCA[A/G]TGTGGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18	A	G	GTGACCTTCTCACTTTAA[A/G]AAACTTTACCGGAGAAGAAATTAAATATATGCTATCAGCAGATCTGAAATTTAGGATAAAACAGAAAGGAGAGGTATGTAACA
EST36751 7	36	C	T	CCAAGTCGTTCAATTTTAGCTTGCAGGTTTAACT[C/T]GATTACTTTTCTATTCAAATCTCTGTAAAATTGAAATATGAACTTAGTTTTCTGATCTATGGTTCAAGTTAAACAG
EST40562	109	A	G	CACGTGGAAAGGAGCTATTTTTGGAGGCTTAAGAGTAAAGAATCTGTCCCCAAACTTGTGGCTGACTTTATGGCTAAGAAGTTTCACTGGATGCATTAATAACAAAT[A/G]TTTACCTTTTGAAAAAATAAATGAAGGATTTGACCTGCTTCGCTGCTGGAAAGAGTATCCGTACCGTTTTTGAAACAATACAGATGCCTTCCCCTTGTAGCAGTTTTCAGCCTCCTCTACCCTA
EST18288 3	121	C	T	GCTCTCTATACCCCTGTGGTCCTCCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAAGATTGACAGGTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA[C/T]GGGAGGCCAGTGTGGACAGCACACCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACCTCTCTGCTGGCTCTGGCCCCTAGGGACTTAGTATCC
ESTD-AK-168	31	C	T	GGGAGTGACAGCTAGAGCACCAAGGGGGGCTC[C/T]TACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTCATTCTGG
ESTD-ALB	180	A	G	AATCCCAGCACTTTAGGAGGCTGAGGCGCAGGCAGCATATCACCAGAGGTCAGGAGTTTGAGACCAGTCTGACCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGTCATGCGCCTGTAATCCCAGGAGGCTGAGGCAGGAGGAATCGCTTGAACCTGGGAGGCG[A/G]AGGTTGTGGTGAGCCGAGATCGGCACCATTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGTCTTC

ID	Pos.	Allele 1	Allele 2	Sequence
EST70523 3	182	G	T	TTCCGCGCAGCCCCCATCCTTGGCACCCTGGTCCCCCTCAGGGGCCACCCCGCGGCCACTCACCGCTCT CGCTCTCGGTAACATCCGGCGGGGCCGCGTCCTTGAGCACATAGCCTGCCGTTTCCGTATAGGAGG ACCGTGTAGGCCTTCCTGTCCCGGGCCTTGCCCAGGGGCCAGCCCT[G/T]CAGAGAGAGAGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCCACGTG
ESTD-APOA2	101	C	T	CCAGGTGTTGTGGCACGTGCCTGCCTGTAATCCCAGCTACTCGGGAGACTGAGGCATGAGAATCTTTGAAC CGGGGAGGCGGAGGTTGCAGTGAGCTGACATCG[C/T]GCCACTGCCACTGCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112	C	T	CAGTGTATCTGGAAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATTCCGAGAGAC[C/T]TAGAAGATACACGAGAC CGAATGTATCAAATGGACATTCAGCAGGAACTTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATA GCACACTTGTCACCTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCTT
EST74167 6	137	C		AGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGAGGAACAACTGACCCCGGTGGCCGAGG AGACGCGGGCACGGCGTGTCCAAGGAGCTGCAGGGGCGGCGAGGCGCTGGGCGGGACATGGAGGA CGTGCGCGGGCGGCGCCCTGGTGCAGTACGCGGGCGGAGGTGCAGGCCATGCTCGCGCCAGAGCACCGGAGGAGC TGCGGGGTGCGCCTCGCCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCCTC
EST43211 8	132	C		CGCCTGGTGCAGTACGCGGCGGAGGTGCAGGCCATGCTCGCGGCAGAGCTCGGGCGGGGTGCGG CCTCGCCTCCCACCTGCGCCAAGCTGCGTAAGCGGCTCCTCCGCGGATGACCTGCAGAAGCGGCC TGGCAGTGTACCAGGCGGCGGGCGGCGCCGGGCCGAGCCGCCCATCCGCGGAGCGCCGAAGCGCCCTG GGGCCCCTGGTGGAACAGGGCGGGTGCGGGGGCGGGCCACTGTGGGCTC
ESTD-ARSB	126	A		GGAAGAAAATGGAGCTGTGGGAAGAGGAGGTCCGAGGGGTGGGCTTTGTGGCAAGCCCCTTGCTGA AGCAGAAGGGCGTGAAGAAACCGGGAGCTCATCCACACTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAGCCTCTGACTGGCTGTGGAAAACCATCAGTGAA GGAAGCCCATCCCCCAGAATTGAGCGCTGCTGCATATATTGACCCAAAC
EST36770 4	144	C		TGTAGCCAAGTCACCTGCACATTGGCTGCTGCGGCAGGTTGCCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCCTCCCGATAGGGCTGGCCTGACCAAAAATATACTGGGTTTCCTGTTTCTTTCTGATCAT TCTTACAAGTTATACTCTTATTTGGAAGGCCCTAAAGAAGGCTTATG
EST26021 1	137	A		TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTTGAGGTTGAGTGACATGTTCGAAACCTGT CCATAAAGTAATTTTGTGAAAGAAGGAGCAAGAGAACATTCCTCTGCAGCACTTCACTACCAAATGA GCATTAGCTACTTTTCAGAATTGAAGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTTTCTTTGTCAACAAGACAAAGCAAAGCC
ESTD-BA511	29	A	G	GGGCAACATAGTGAAACCCCATCTCTACA[A/G]AAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGTGGGAGGATCCCTTGAAGTGGGAGGTTGCAGAGGCTG CAGTGAGCCAAGATGGTGCCACTGCA

Name	Pos	Allele		Sequence
ESTD-BCL2	116	A	G	AGCTGGATTATAACTCCTCTCTTTCTCTGGGGCCGGTGGGGGTGGGAGCTGGGCGAGAGGTGCCGTT GGCCCCCGTTGCTTTCCTCTGGGAAGGATGGCCACGCTGGGAGAAC[A/G]GGGTACGACAACCGGGG AGATAGTGAAGTACATCCATTATAAGCTGTCGCAGAGGGCTACGAGTGGGATGCGGGAGATGT GGGCGCGGCGCGGCGCCCGGGCGGGCGCCCGCCACCGGGCCATCTTCTCCTCCA
ESTD-BCR	69	C	T	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCATCTGCGCAAGA GA[C/T]CAAAGAGAGGTCAGCTTCGTGTTCCCGGGAAAGGAGGCAGGTGACAAGCTAACTCTGCTTC AAAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGGCACA
ESTD-BRCA1aa	119	C	T	AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAAGATCTCATGTTAA GTGGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCA[C/T]TGGTACCTGG TACTGATTATGGCACTCAGGAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACA GAACCAAATAAAT
ESTD-BRCA1bb	139	A	G	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGCTACCTGAAAGAGAA ATGGGAAATGAAGACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAG[A/G]AGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAATGAAA
ESTD-BRCA1cc	126	A	G	ATGCCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAAATAAAGGAAGATAC TAGTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAGCGTCCAGA[A/G]AGGA GAGCTTAGCAGGAGTCCTAGCCCTTCACCCATACACATTGGCTCAGGGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST512120	122	A	C	ATCCTGAGCTCGCCAATAAAGCTTCTTGGTTCTACTTCTCTCTCCACAAGCCCCAATTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCCTCAATACA[A/C]AAAGGCCCCT CTCTACATCT
ESTD-C1R	40	A	G	ACACAGGTGCTGGCCACTGGGCGTGGGGCTGGGGATCCTCCTCCCCT[A/G]ATTTGCTCCGGGAAGCACATTCAT CAA
ESTD-C1R	40	A	G	ACACAGGTGCTGGCCACTGGGCGTGGGGCTGGGGATCCTCCTCCCCT[A/G]ATTTGCTCCGGGAAGCACATTCAT CAA
ESTD-C6	31	A	C	CCCAGTCAGTTTGGGGGGACAGCGCCATGCGCACTG[A/C]GCCTCCTGTCTGTAGCCTTTCAACCATGCCATTCCATC TAAGCTCTGCAAAAT
EST201182	119	C		GTTCCGAATCCTCCTCCTGAAAGTGGCCGGGTTTAATCTGCTCATGACGCTGCGGGCTGTGGTCCAGCT GAGGTGAGGGCCTTGAAGCTGGGAGTGGGGTTTAGGGACGCGGGTCTCGTGCTCATCCTAAGCTCT GAGAGCAAACCTCCCTTGAAGCTGGGAGTGGGGTTTAGGGAGTCCGTGCATCCTCGTGCATCCTAAGCT CTGAGA
EST530186	67	A	G	ACAATCCAGGTCACACATTCCAGAAGAGAGGAGGGTGGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA [A/G]GGGATTCAGGAGGAGGGCCACGAGGATCGAAGTTAGTGAAGTC

ID	pos	allele		sequence
ESTD-CB22	119	C	T	GGCAAGTTTTATTGATAGAGAGGAAATCAAATAATGGCAATGAGGAGGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAATGGGCAGTGCCAACCCATAGGG[C/T]GGATACAAAAAG ACAGGCAAGGAAGGGGTAGAACCATCAAAGAGGAATAGGCTGGTGACCCAAAGCAAGGAGGACCT AGT[A/A]CATAATTGTGCTTCATTATGGTCCTTCCTGGCCCTTCTCTCTCACACAC
ESTD-CB23	136	C		TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAAGCAAGGACAGGACCTAGTAACATAATTGTGC TTCATTATGGTCCTTCCCGGCCCTTCTCTCTCACACATACACAGAGGAGACCCCTACCAGGACCAGCAGCT CTCAGAGCAACCCTAGCCCATTACCTCTTCCCTTTCCAGAGGACCTGAAAAACGTGTTCCCACCCGA GGTCGCTGTGTTTGAGCCATCAGAAGCAGAGGATCTCCACACCCAAAA
ESTD-CB24	145	A		ACCAGGACCAGACAGCTCTCAGAGAGCAACCCTAGCCCATTACCTCTTCCCTTTCCAGAGGACCTGAA AAACGTGTTCCCACCCGAGGTCGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAG GCCACACTGGTATGCCTGGCCACAGGCTTCTACCCCGACCACGTGGAGCTGGTGGGTGAATGG GAAGGAGGTGCACAGTGGGGTCAGCACAGACCCGCAGCCCCTCAAGGAG
ESTD-CB25	146	A	G	GTTTCTTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCCTTTTCTCTATCTTTCGCCGTC TCTGCTCTCGAAGCAGGCATGGAGAATCCACGGGACCACGGGGGAGGCCAGAGCCACCTG TGCACAGGT[A/G]CCTACACATGCTCTGTTCTTGTCAACAGAGTCTTACCAGCACAAGGGGTCCTGTCTGCC ACCATCCCTATGAGATCTTGCTAGGGAAGGCCACCTTGTATGCCGTG
ESTD-CB27	125	C	T	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGGCCTGGTTGCATTTCAGGAGTGTCTGTGGAGTTCTGCTCATCATCGAC[C/T]TATCTTC TGATTAGGGAAAGCAGCATCCCTTGGACATCGAAGTGACAGCCCTCTTCTCTCCACCCAATGCT GCTTTCTCCGTTCATCCTGATGGAAGTCCTCAAACACCATTCCATACC
ESTD-D4S338	59	A	T	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA[A/T]ATGTA TTTCTTAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGACTGCAGAATAAATGTTA TTTTAGCTGTCAGAAAAACAATACTAATCTTGCATATGTTCATCAGAGCCCTTGGGTGACCAGGTGTA TTGCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTCAATGCAGTAG
ESTD-CYP2D6	61	A	G	CAGGCCAGCGTGGTCGAGGTGGTCACCATCCCGGCAGAACAGGTCAGCCACCACTATGC[A/G]CA GGTTCTCATCATTGAAGCTGTCGCTCTCAGGGTTCCCCTGGCCCTGGACGAGGCGAGCATACTCGG
ESTD-D11S1873	40	A	C	AAAAAAACATTTTAACACCTTTCAATCATCATATACACCATA[A/C]ATTTCCATTTTCACATAAGTCA GTTGAGCTGAGTTTTCCAATTACTTGCAATCTAAAAATGTCATAAACTGATTAATGCAAGTTCAACAG ACAACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACACATATCTGGATTAAATTATGCCCA TATCTGCATGTC
ESTD-D17S33b	169	C	T	CATCCCCAAGCCCATCCATCCTCCTTAGCCACTGCCACTGGGGGCCCTACCCTTTGTAGTCCAG[C/T]GGGGCCTTTGGTTTCAGTTGCCACTATTGCGTT CATGCTGCACACATCCAGGGGGCGCCTACCCTTTGTAGTCCAG[C/T]GGGGCCTTTGGTTTCAGTTGCCACTATTGCGTT ATTGCAGATTGCTTGTCTTTGTCTTTCCACCTGAGGCGAGCCTC

ESTD-D17S33a	75	C	T	CATCCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTGCCGCCTCTGACAGATACACTCAGGGCCGT CATGCTG[C/T]ACACATCCAGGGGGCGCCCTACCCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCG GTGGGGGTTGTGTGTGCTATGTGGTCTTGTGTAGACGGGGGCTTTGGTTTCAGTTGCACTATTGCGTT ATTGCAGATTGCTTTGTCTTTGTCTTTCCCACCTGAGCGAGCCTC
ESTD-D18S8	133	A	G	TTTGAGACCACCCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGGTACATGCCTATCGTAATCCCAGCTACATCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCC[A /G]GGAGGCAGAGCTTGCAGTGAGCCAAGATCACACCACTGCACTCCAGCCTGGGTGACACAGTGGA GACTCTGTCTCAA
ESTD-D3S11	44	G	T	AACTGATTAGAACCTGAAAAATACATATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTTGCATCATTAAAAAAATCCAATAAAGTACAACTGTAATAAAAAATTAACAGAATATCATTGT TTATTCAAACTATTTATCACTTATTTATTGGTAAGCCATACTAAATTCTAAAGCATGTTTCTGAAAG TTTA
ESTD-D3S12	37	A	G	AGGTTCCACATTATTGCTGATGTTTGCTGATGTTTCC[A/G]GGAGCCTTGATGTCATTCTGTATCTCCT CAGGTATCCCACCTTGAGACGTACTTTCAAAAACTCTCTACAGCCGTTGTTGTTTATTAATTCAAGGT TGAACATAAAGTA
ESTD-D3S2b	247	C	T	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTCCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCTCACGATGG CAGGTATGAAATATAATAATCGTCCCTTTATTTGGAAGGATGC[C/T]TGGT
ESTD-D3S2a	248	G		GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCTCACGATGG CAGGTATGAAATATAATAATCGTCTCTTTATTTGGAAGGATGCCGGTATGT
ESTD-D7S399	83	A	G	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTGACACTTATCCATAGAT AACTGCTAGAGACCC[A/G]GTCTCCTACATCATCCTTCACAAACATTTCATCCCATGGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146	A	C	GTGGGGACACCGAGGCCTCCAGGCTGGGCGCTTGCACGTGTGGCCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGGCCTGGGACCTCACTGTCCCTGGGGAGGGAGGAGGAGGGAGTGGGAGGGAGGACA GAATGCTGATT[A/C]TCTGGTGGAGAACCAGAACTTCTGGCCTGTGGGTAGGGGCAGCTGCTTCCAAG ACCTCCTGATTTGAGGAAGGGGAGCGAAGAGAACAGAGT
ESTD-DMa	66	C	G	GTGGGGACACCGAGGCCTCCAGGCTGGGCGCTTGCACGTGTGGCCTCAAGCAGCTGCTCGGCCTCCA[C/ G]TTCCATGGGTGTGGGGCCTGGGACCTCACTGTCCCTGGGGAGGGAGGAGTGGGAGGGGAGGAGGA CAGAATGCTGATTATCTGGTGGAGAACCAGAACTTCTGGCCTGTGGGTAGGGGCAGCTGCTTCCAAGA CCTCCTGATTTGAGGAAGGGAGCGAAGAGAACAGAGT

			Sequence
ESTD-DRD1	154	C T	TCCCCAGCCCTATCGGTCATATTGGACTATGACACTGACGTCTCTCTGGGAGAAGATCCAACCCATCAC ACAAAACGGTCAGCACCAACCTGAAACTCGCAGATGAATCCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGGATTGCTCTGGGG[C/T]TCGCTATTAAGAAAACTAAGGTAC
ESTD-DRD2	144	C	TCTGCCCTTTGGTGCAGGAGGCTGCCCGCCGCAGCCCAGGAGCTGGAGGATGGAGATGCTCTCCAGCACCA GCCCACCGAGAGAGACCCGGTACAGCCCCATCCCAACCCCACCACCAGCCGCTGACTCGTCCCCGCCCCCG TCCCCACCACGGTCTCCCACAGCACTCCCGACAGCCCCAAACCAGAGAAGAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD-DRD3	109	C T	AAGAGACGATGGCCAGGATGAGCGCGCAGTAGGCGCGCCATAGTAGGCATGTGGGGGGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAGGTGGC[C/T]ACTCAGCTGGCTCAGAGATGCC ATAGCCCAGAGGGAGGTGCGTGATGCCAAGGGGCTTCCTGTGTGAGGAGA
ESTD-ERBB2	93	C T	TCTTTCAGGATCCGCATCTGCGCCTGGTTGGGCATGCCTAGGTGTCAGCGGCTCCACCAGCTGG GGTGAGGGGTGTGGGTCAGTGC[C/T]GGGGGGCCCGGTGCAGACCCCACGCGGGGCTGGGAGGACTTCA CCCCGCCCTCACCTCCGTTTCCTGCAGCAGTCTCCGCATCGTGTACT
ESTD-ETS2	43	A G	ACTCACAGTGCTTTTAAGTGAAAAATGGTCGAGAAAGAGGCACC[A/G]GGAAGCCGTCCTGCGCGCCTG GCAGTCCGTGGGACGGGATGGTTCTCGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGGTCGTGGACACA CACAGACTATTTTGAGATTTTCTTTTGCCTTTGCAACCAGGAACAGCAGCAAATGCAAAAACTCTTTGAG AGGGTAGGAGGGGTGGGAAGGAAACAACCATGTCATTTCAGAAGTTAGTTTG
ESTD-F9	111	A G	AGATCCTGATGATGATTTTTTTCCTATTTTTTTCTAAATGTTTTACAGTTTGAAGTTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTGTAAAGTATGATGTTTA[A/G]GTCAAACTTCATTTTTTTTCC ATAGGTATGTCCAATTTATCCAGCACAATTTGTTAAAACAAAAAC
EST687875	144	A	CTTCCTATGGGATTTGACTTTATTTTCTCCATTGTCTTACCTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCAGCTCATGACAATTTGAAAGCTGACAATTACACAGAAGGAAATAAATTCACAGTCAA AGAATCAAGCACACTTTCGAAACATTGAAAGTTGTTTTTGAACTTGGTGTCACCTTTAATTACAACCTAG CAGACGGAACTGAACTCAGGGTAAGAAT
ESTD-GCDH	200	C G	CGCAGACCGGTCAGTGTGGGGTCGGGAGTGTGGAGGGAAGGAGGGAAGGAACTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCGTCTGTCTGGTCGCACCGTGTTCTGCTGCCCCTGTTCAGCTGTCTGTCTGCCGAGT[C/ G]TGTAAGGGACCTGTGTCCCGGTCGCGGAAATTCCGAGAGCT
ESTD-GCK	88	A G	GTTTTATGCATGGCAGCTCTAATGACACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGA[A/G]CACAGTAAGCCCTGGCAGGAGAATCCCCACCCCACCACCTGGC TGGAGCAGGAAATGCCGGCGCGGCGCCTGAGCCCCAGGGAAGCAGGCTAGGAGTGTGAGAGACACAGTC ACCTGCAGCCTAATTACTCAAAGCTGTGTCCCCAGGTCACAG

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EST34088 2	62	A	T	...	GTGGGGGCAACAGTGGGAGAGAAGGGGCCCAGGGTATAAAAGGGGCCCACAAGAGAGACCGGCTC[A/T]AGGATCCCAAGGCCCAACTCCCGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTACAGGTAAG
ESTD-GNAT2	56	A	G	...	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCAC[A/G]GGCATCATTGAAACCAAGTTTTCCGTCAAAGACTTGAATTTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-HT2	154	G		...	GGGCTAAAATTTCCGAGCAACTTGCATAGACTTGTTTATTTGACTTGACAGGATTGCTAGAGATAGGCAGGGAGAGGAAGATGTGTACAGTTTGTCAGAGAGAATAAAAAGGATAAACCTGGGGTTTCTGTGCTTTGCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTTCAAAGAAACGGTATACAGGGACAGCAAAGCGCAGTCGTGAAGTTTTCAAACAAGACACCTT
ESTD-HT5	149	C		...	AACACACAAGCCCCAGCGAGAATTGAACTGCGACCCCTGGTTTACAAGACCAGTGCTCTAACCCCTGAGCTATGGAGCCCTCGTCTGCTGTTTTCTTCATCTTATAGATTGATGTTATGCTCCTAGCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAAATTCCAGGATATTCTCCTACAAAATGAAAACATTTTCGTGCTCTGTAAATCCCTCGAAAAGGTTCT
EST37382 5	124	A	G	...	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCCTCTTCTCTTCTCTCCCTTGGACTTTGAGTCAAATTGGCCTGGACTTGAGTCCCTGAACCAGCAAAGAGAAAAGAAGG[A/G]CCCCAGAAATCACAGGTGGGCACGTCGCGCTCTACGCGTCTCTACCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
ESTD-IGFBP1	43	C	T	...	ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGC[C/T]CTGGGAGAAGAAGGAAGATGTTCCAGGGCCACACATAGCTTAGTGGAGACTC
ESTD-IGHV4-6	120	C		...	TTTACTATTTCAATGGATACAGAATTGTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTTCAGTGTTAAGTAAGTGTTGCCTACATTGTGAGTGAGTGACGGGGCAGTGGTGATCCGAGAGTGTGGTGGGGTGCACGGACAAGTAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGGATACGAACTGAAAGTATGTAAAATACTTCACAAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	110	A	G	...	CAAAGTAAGCACCCAATAAAATGTTAGCTATTACTATCATTATTATTATTTATTTTATTTTTTG AGATGGAGTCTGGCTCTGTCACCCAGGCTGGAGTGCAG[A/G]CAATCTCGGCTCACTGCAAGCTCTGCCTCCTGGGTTCATGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCACCCGCCACTGTTCCCGGCTAATTTTTGTATTTTTAGTAGAGACGGGAGTTCACCGT
ESTD-IL1B	99	A	G	...	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCTC[A/G]GGAGCTCTCTGTCAATTGCAGG
EST74082	134	A	T	...	TCCAGGGTGGCTGGACCCCAGCTCTGCAGCAGGAGGACGTGGCTGGCGAAGCATGTGGGGGGTGAGCCCCAAGGCAGGGCCCAACTGGCCTTCAGCCCTTCAGCCTCCTGCCTCCTGCCCCTGTCTCCCCCTGCCGCCCCTGCCCCTGTGTC[A/T]TCCCAGATCACTGTCCTCTGCGGGACCTCCTGCCCCCTGCCTCCGCCCTGTGGGACCAACACCTGTGCG CTCTGGGGACCTGACCCGCCAGCCCGCAGCCTTTGTGAACCAACCTGTGCG

ID	Pos			Sequence
EST45311 0	151	C	T	GCCCTCCTCTTCCAATTCTGTCCCCTATAGTTTCCTCTATTAAGTGAACTACACATGCATTCTTTAGT GGATAGATGCACACAAACACACAAGCCATTATGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAAT[C/T]ACCTCTTTCATTTCATTTGTTGAAT GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80	A	G	TGCCCCATCACGCGGCCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTTCC[A/G]CCCTCCAAAATGACAGCCATGGCCGCCGGGTGCTTCTCTGGGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGACTTGAGGAGGGAGGGCTTGAGGTTGGT GAGGTTAGGTGCGTGTTTCCTGTGCAAGTCAGGACATCAGTTCTGATTAAA
EST38216 3	26	A	T	ATGCAGGGATGAAGGTGGACAGGGAGG[A/T]GAGGGCCAACCTGTCATCCCAGGGCCTGCAGATGTCG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 149		G	T	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTATTAGCATTTGTTTAGCATTACCTAA TTTTTTCCTGCTCCATGCAGACTGTTAGCTTTCACCTTAAATGCTTATTTAAAATGACAGTGGAAG TTTTTTTTTTCCTC[G/T]AAGTGCCAGTATTCCCAGAGTTTTGGTTTTTGTTTTGAACTAGCAATGCCTGTGAA AAAGAAACTGAATACCTAAGATTTCTGTCTTGGGGTTTTTGGTCATGCA
ESTD-KRT10b	183	C	T	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTTACCTTTTGGCAATATT AAAGGAAGAAAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACACTATGTAG[C/T]TGCTTTTTAAATAGT CTCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD-KRT10a	133	A	G	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTA[A/G] G[G]AGAACTGTACATGACAAATATTACATGAGATCAACTATGTAGCTGCTTTTTAAATAGTC TCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD-KRT8b	231	C	T	ACCCTCACCCCTCCCTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCCTGACATGAGACCTCAGACGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACCA[C/T]GTCAACATTGACACA
ESTD-KRT8a	21	C	T	ACCTTCACCCCTCCCTTAGCC[C/T]GTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGCCTGACATGAGACCTCAGACGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCATA GGCTGCCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
EST75099 6	82	C	T	CACTTGTGTGTCTAGATCTCCTCAGTGCCGCCTCTACTGGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGATGTCAA[C/T]GGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCCACC CCTTCTCCTTGGCCGTCTTGAGGTGTGG

Name	Pos			Sequence
ESTD-LF79	142	A	G	GGGTGATTTGAGGCTCAGTTAATATTTCAAAAATTGTAACCGTAGCAAAACTGCATTGGTATTTAGA AAAATAAAAATTTCCAATATGTAGTGCTGTGTTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACC[A/G]GGGAGGGCTTCCCTTACCACCCAGA
EST358799	142	A	C	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGCGTGTACCCAATTAGGTGAACATGGCTTCGAG AGAGTTG[A/C]ACAGATTCCTGGAAGACAGCAGCGCGGGATGGGGGCAGGAGAAGAGCTGCCTGGATGA A
ESTD-LMP2	35	C	G	TACACACTTTCCTTACCCATTCACTGAAACGACT[C/G]CAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113	C	T	TGTCAGTGTCCCCTAGGGCACCTCACCACTCCCAGCTCTTCTTCAGCTCTGCGCCTGTCCTGCGCCTGCA AGGGGTTTGCTTAATTCTCAATGTCTCTTCATCTTTAG[C/T]AGCTGTGGGGTTTTGTTGTTG TTCTTCTGTTTTTGCTTAGTATCTGACTACATTTATTATAAAAAGAGATGTATCTAAACAAAATAG AGATTGTTATCAGAAGTTCACAACACATTTATTAAAAATTTTTCACCTG
ESTD-MCC	45	C	T	TTGTCAGGAGTGGTGCTGATGCTGCCTCCCCAGCTC[C/T]GAACTTCAGGACAACGTGC AG
ESTD-METH	118	C	T	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGTCTTCCAAGGGTTGGTCAAGTTGCTGATTACC[C/T]GGATTTTTCTGACG ATCTTTCAACTGCTAGAGCATCGGTTCCTGTTTGAG
ESTD-NF1	25	A	G	ATTATCCAGATGAATTACAAAACT[A/G]TACCAGATCCCACAGACTGATATGGCTGGT AACATGGACTTGTATATTGTACAAAAAAAGTTTTATTTTCTAAAAAAGAAGAAGAAA AAATTTAAAGGGGTGTACTTATATCCACACTGCACACTGCCT[A/G]GCCCAAAACGTCTTATTGTGGT AGGATCAGCCCTCATTTGCTTTTGTGAACTTTTGTAGGGGACGAGAAAGATCATTGAAATTCT GAGAAAACTTCTTTTAAACCTCACCTTGTGGGGTTTTTGGAGAAGGTTATCA
ESTD-NFKB1	107	A	G	TGTCCCTAGGCCCAGCCCTGCTGTCCTCCCGTCGTTATCTTC[A/G]GTACTGCAAAGAGAACACA GACAT
ESTD-NPPA	45	A	G	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTCTTTCTGCAGCATATAGAATTTGGT GGGTTTCTTTTTTATGTAGGGTGATATTGGATACTTTTGTTTGTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATGCTTGAATAGATTAGATATGCTTATTTAACCTTGGCAATAGCATTGT C[T/T]ATTCCCTGTGGTTTTTAATAAAAT
ESTD-NRAS	202	C	T	GCCACCACCACCCCACCCCAGCACACCTCCAACCTCAGCCAGACCAAGGTTGTTGACACAAGAGAGCCC TCAGGGGCACAGAGCAGAGTCTGGACACAGTCTGGG[A/G]GTACCGTGTATCATCGGAGGCGGCCGGGG CACATGGACAGGATGAGGGAAAGACCAAGAGTCCTCTGTTGGGCCCCAAGTCCTAGACAGACAAAACC TAGACAATCACGTGGCTGGCT
ESTD-PAI1	100	A	G	

Gene	Pos	A1	A2		Sequence
ESTD-PAR	120	A		---	CTCTTCAGGAACCACCAGTCTTCTTACCAAACACGACTTATTGCTGTCCGAGAGGTACAACCCGTAGA ACTTCTTCCTAACTGTAATTAGTTAAAGGAATCGAAACTGGCTCTGAAACCATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTCACTTTCTGTGTTCTAGAACGTTTTCTAG GACTGGCAGTTTAAGCTTTCACTTAGGCTTTCTGTATACCCATGCCC
ESTD-Per/RDS	74	A	G	---	ACCTACAGACGTCGCTGGATGGTGTGTCCAACCCCGAGGAATCTGAGAGCGAGAGCGAGAGGCTGGCTG CTGGAGA[A/G]GAGCGTGCCGGAGACCTGGAAGGCT
EST683085	29	C	T	---	GGAAAGAGATTTAAGAAGCTTGATTTGGA[C/T]AATTCTCGGTTCTTGGTGTGGAAGAGTTCATGTC TCTGCCTGAGTTACAACAGAATCCTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTTA
EST540456	39	A	G	---	GGAATATTAAAAATATTTTAAAATACCTCCATTTGCTT[A/G]TCCTTTAGTGAAGATGATACCTGC AAAAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTGTTTTCTTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTTGCCTTGGAATTGGATTTTAATGTTGACTTTATCAT
ESTD-PXMP1	88	A	G	---	ATGAAACACATGGTTCTTAATTTATGATATGTTTGTTATAGCTATCTTAAAGGGCTTCTTTTTTTA ATGCAGAAAAGAGGGGGAAAAA[A/G]GAGCGAGCTGTGGTGGACAAGGTGTTTTCTCAAGGCTCATAC AGATTCTGAAAATCATGGTCCCTAGAACACATTTGTAAAGAGGTAAGTCTTATGAAATTATAATCTT
					CCCGGAGGAATCTGAGAGCGAGAGCGAGAGCGTGCCGGAGACCTGCCGGAGAGGAGGG CCTTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGGCAACCAGGTGGAAGGCGCAGACGCAGG CCAGGCCCCCAGAGGCGTGGCTGAGGGCCCCTGGGCGCCCCTCCCGAACACTGAGAAATAGTGCACT CCAAGAAACGTGGATCTCCCCCTGCATCCAACTCCGAAAGTCTGAA
ESTD-RDS	127	A		---	TTGGGAAGTTAGAGCCTATATTATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTC[G/T]CTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
ESTD-s14544	94	G	T	---	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCCTGGGAGAGATGG[A/C]TGGTGGTCTCGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST529080	45	A	C	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGT[C/T]GGCTCAG GATGCCGGAAATGAC
EST19590	55	C	T	---	TGAAGCTTCTGCCCAGCTTGCATTGTTTCTAGGAGAACC[C/T]GCGTCATACCTTTATCTATAGCCTT CCCTAGGTCTT
EST76136	39	C	T	---	TGAAACACCCTGTGGTCCGGAGCCAGGTTGTGTTTCTCCTGGGAGCCTGAGGAGTTTGTTGTCTGTGTG CAGTGCCCCGCGCCACCTGCTGGTTGAGCCTGGACATACACCTTCACCTCCTTGGCCCGGAGAAGAC ATTTACCCACCTGCCACTGCCGCCATGTCCCTGCCGTCTTGTGTGCACA[C/T]CCTCGTCTGTGAAGAGACCCAACCCCTGC
ESTD-SPTB	176	C	T	---	CTCCCCCACCCAGCCAAGCCAGTTTCCTAGCAGCAAGGGCAGGAC

			Sequence
ESTD-TAT	224	C :--:	AAATGGTCAGGACCCTGATCCACACAGAAGAAGTGGTACCATTTCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAAATGACTTGTGGGACAGGATCA ATTTCCTCTCACCTAGAACGTTTGTTTACAACTTTTCTTCCCAGTATGGATTATGATGGGGGG GAGAAGCAAAATTTTAAATAGGACCCATGAGACACATCA
ESTD-THRB	125	A C :--:	TGCGGCCTTTCCTCCGGCAGGGTAGACTTCTTACTTGGCTGTTGATTCCAAGAGAGAAAGAGTCCCAAG CACACGAAAACAGAAGTTGCAGATCCCAGTCCCATGAGGCCCAGTCTCAAATCACACAGGATC[A/C]CTTCAT CCACACTGGATTGGCCCAAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCCCTGTAGATGGG TAGTGAAGTTTCATCTCCTGTCAGCTTCTGGATTTCTTGTTCCCACCGCAACAAGAAGAGTCTATGC CAAGGCAGAAAAGCTGGTGCTTCATGGGCAAAATCAATCAATGTCTCTCCAGATTTCA[G/T]ATCCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCATAAATATTGATGTCGTTAAA CATGGGTGTTGATCCATTTTCATTTGGCCATAGGTCCCTATGGGGATGACA
ESTD-TYR	122	G T :--:	AGTAGTGGATGAAGCTAACCAGCCTCCTCCTCACTGAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAACTGTATTTTCTTCACTTTATTACCTTCTTTCT AATACAAGCACATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD-TYRP1	222	A C :--:	AGTAGTGGATGAAGCTAACCAGCCTCTCCTCACTGATCAATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAACTGTATTTTCTTCACTTTATTACCTTCTTTCT AATACAAGCACATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD-TYRP1	222	A C :--:	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGAGACACAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGACTGTCA[C/T]CAGACTGAGAACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGGCTGAGCTGATCCATTACTCATAT
ESTD-VB12	148	C T :--:	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGAGACACAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGACTGTCA[C/T]CAGACTGAGAACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGGCTGAGCTGATCCATTACTCATAT
ESTD-VB12b	148	C T :--:	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGAGACACAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGGCTGAGCTGATCCATTACTCATAT
ESTD-VB12a	74	A G :--:	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC[A/G]TGGATGCTGGAATCACCCAGAGCCCAAGAGACACAAGGTCACAGAGACAGGAACACCA GTGACTCTGAGATGTCACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGC ATGGGCTGAGGGCTGAGCTGATCCATTACTCATAT

Name	Pos			Sequence
EST58607 0	105	A	G	CTCTGGGATGGGTTCACAGGTGGCAGGCACAAGCCAGTCCATCCTCCTGTAGTCATCATATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAAGGACAGCCAC[A/G]TGGCGCGGGATGGCCGGCGGGAGTTC TGGTTGCGGCGGCCACGGCTGTGGCCCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGT TTCTTGGCCAAGGAGGGGCGGGGTGCCATGCCTGAGATGTAGATGCGGCC
ESTD-VWF	36		G	AGGTAGGAAAAGCAAAGAGTTGATTAGTGAAGGAGAATGGACCTTCCACACTGTCCTTTGG TCCCCTAGAGTCTG
EST71770 6	189	C	G	AGCACCACCTCTCACGTCAAGCCTCAGCACCAGATGCTGTTCTATAAGGATGACGTGCTGTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGTTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAAGAGAAAAACCACTGCAGAGTACCAG[C/G]TGTTGGTGGA AGGAGTGCCCAGTCCCAGGTGACACTGCCACTGGACAAGAAAGAGGCCATCCAAGG
ESTD- TNFAb	152	A	G	TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGGGACGGGGTTCAGCCTCCAGGGTCCTACACACAAATCAGTCAGTG GCCCAGAAGACCCCCCTC[A/G]GAATCGGACGCAGGGGAGGATGGGGAGTGTGAGGGGTATCCTTGATG CTTGTGTGTCCCAACTTTCCAAATCCCCGCCCCCGGATGG
ESTD- TNFAa	88	A		TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGGGACGGGGTTCAGCCTCCAGGGTCCTACACACAAATCAGTCAGTG GCCCAGAAGACCCCCCTCAGAATCGGGACGCAGCAGGAGCAGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCCAACTTTCCAAATCCCCGCCCCCGGATGG
EST52418 6	113	A	G	CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCAGTCACCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGGCGGGCTGCCGAGTACGGCGGCCATACACTTA[A/G]AAGTGAAAACTGTGAGTG TGG
EST13586 3	89	A	G	CCCACTCTATTTGCCCAGCCCCAGGGACAGAGCTGATCCTTGAACTCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC[A/G]GGGCTGGCTTATCAGCCTCCCAGACCCTGGCTGCAGA CATAAATAGGCCCCTGCAAGAGCTGCCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCCTGCTGCCTGCC CCGGTCACTC
EST51976 7	123	A	T	AGGCAGAAACTGGGCCCCCATGCGGGGGACGTGGAAGGCCCACTTGAGCTTCCTGGAGAAGGACCTGA GGGACAAGGTCAACTCATTGCAGGAGAAAGAGAGCCAGGACAAG[A/T]CTCTCTC CCTCCCCTGAGCTGGAGCAACAGCAGGAACAGCAGGGAGCAGCAGGTGCAGAGATGCTG GCCCCTTTGGAGAGCTGAGCTCACTC
EST11458 6	140	A	G	CCACTTGGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTTCTCGAGTTTT CTCTGCCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTCCACAGTGGT CCC[A/G]TTAAAAACATTCTATGAGCCAGGAAGAGAATTACGTATTCCTGCAAGCCGGGCTATGTG TCCCGAGGAGGGGATGAGAAAGTTTATCTGCCCCTCTCACAGGACTGTGGCC

ID	Pos				Sequence
ESTD-AT3aa	60	C	T	...	AGACCTCAGTTCCTCTCTTCTGTGTAAAATGGGAAGTTTGTTCTTGGATCTCCATGGGCCCAGC[C/T]AGCA CTGGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGGACCAGGTGGAGGAGGAATTTGAAAGGGCA TTGGAATTCAGAGAGCAAAGAGACAGATATTAAGAGCGTGGGGAAATGTGG
EST398528	106	C	G	...	CGGTCTTCCTTCCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACCACCTTCCCCACTCTCTTA[C/G]GGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAAAGGCCTGTTTCCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGCCTGCTAT AATACAGCCCT
EST624480	112	A	G	...	ACCTGGTGTTGCTGGTGCTGTGGGTGAACCTGGTCCTCTTGGCAATTGCCGCGGCCCTCCTGGGGCCCGTGG TCCTCCTGGCGCTGTGTGGGTAGTCCTGGAGTCAACGGTCCTTA[A/G]GTGAAGCTGGTCGTCGTGATGGCA ACCCTGGGAACGATGGTGCCCCCAGGTGGTCAACCCGGCGATGGTCGCAACAAGGGAGACACAGGCGCGGTTACCC TGGCAATAT
EST360272	120	A	C	...	AGTGACTTCCAAGGAAATGGCTACCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCTCAGA ACATCACCTACCACCTCGACACGCAAGAACAGCATTGCATACATGAGGATGAGGAGGACTGG[A/C]AACCTGAAAA AGGCTGTCATTCTACAGGGCTCTAATGATGTTGAACTTGTTGCTGAGGGCAACGCAGCAGGTTCACTTAC ACTGTTCTTGTAGATGGCTGCTCTAAAAAGACAAATGAATGGGGAAAGACA
ESTD-COL2A1cc	112	A	G	...	AGAATGTATATAGTCCTCAAACTGGCCATCTCCATTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGTCTCTTCCTGTCACTTTC[A/G]GGGTGTTCAAGGTGGAAAA GGTGAACAGGGTCCCGCGTGGTCCCGGCTTCCAGGTAAGCTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1dd	97	C	T	...	TGAGAGAACACCTAGTCCTCCTCTCTCTCCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGCTGGGACCTGGAACA[C/T]TGGACTTCTTTCTACTGCAGCAGCAAGACTTA CCCAAGAGAGATTAATGGCAAAGATATACAATTTTATTTGACCAAACACTACTCATGGAACA GCATT
ESTD-CPT2	150	A	G	...	GCCGCAATGCCCGGGAGTTTCTCCAATGTGTGGAGGAGGCCTTAGAGAAGACATGTTTGATGCCTTAGAA GGCAAATCCATCCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCCACTTCCTCCTCATGAAAAC TGGGAGGCCGGGCATA[A/G]GTGCTCATGCCGTAATCCCAGCATTTTGAGAGGCTGAGGCGGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT
EST122740	135	A	G	...	CCCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAGTGTAT TACATAAAGAAGTCAAGTGGTTTTACTCCTCCATGACCAAATATTCTTTCCCTCCTTAGGATGAGGTG[A/G]TAGTAAATGAACCGATGGGGTCAGAACTGTTCCTGTCACCATGGGAGGATACTATAACTGTGAAGA TAAATTCAAGCCACAGAGCTTGCCAGATC
EST768070	91	G		...	ATGCTAAGGGGATCGGACATGAAAGGACCCTGTGAGCCGATTGTCCTATCTCCAGGCGCCCTGTCATC CAGCTCACTCATCCATCAATGGGCGCCAGTCAGGCCCAGGCACTGGGCTCCGGAGGACTCACCACTGCGCCCCT GCTGCCATGTGGGACTGTGGCTGTGCAAGTTGAGGACTTCTTG

Identifier	Position	Allele		Sequence
ESTD-SSA1	111	C	T	TTCACTTGTGGATTGTTCTTTTGCTGTGCAGCACCTTTCAACATGATGTGATCCCATTGTCCAAG TTTGCTTTGGCTGCCTGTGCTTGTGTGGGATATTTGAAAAGAGAT[C/T]TTTGCCAGTCCAATGTCCTAGA GAGTTTCCCAATGTTTTCTTGTAATAGTTTCATAGTTTGAGGCCTTAAGTTCTTTAATCCATT TTGATTTGATTTCTGTA
ESTD-RYR1	109	A	G	CTTCGTGACGGGAGGTCACGTCCTCCGCCTCTTCATGGACATATGGATGAGTGTCTGACCATTCCC CTGCTGACAGTGATGACCAGCCAGCGAGACTTGTCTCTACTATGAG[A/G]GGGGAGCTGTGTGCACTCATGCC CGCTCCCTCTGGAGGCTGGAGCCACTGAGGAATCAGCTGGGAGTGGGAGCCACCTGCGCTGGGGCCAGCC ACTCCGAGTCCGGCATGTCACTCACTACCGGGGCAGTACCTAGCGGCTCACCGAGG
ESTD-WT1	70	A	G	AAGACCTACGTGAATGTTCACATGTCTTAAAGCCTCCCTTCCTCCTTACTCTCTGCCTGCAGGATGTG CG[A/G]CGTGTGCCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCCAGTGAGAAACGCCCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2	100	C		GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCAACTGTGCATGCACGCCTTAACCTCT GCACCAAATGGCCTCCAAGGCCGTGGGGGATCTAGGGGGATGGGTGAGGAATGGCCC AGCCCAGTCCCGGCCCGGTGCCTGGGTCCCAACAGAGGAGGGCCGTGGAGGAGGAGCAGGAGGATGGGC TGGATGAG
EST44438 7	100	C		GCAGCCAGGAGCGCCGCTGCACCATGCCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA[C/T]G TCCTGCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGGAGGTGGG
	62	C	T	CCTTCTCATGCCCAGATGGAAATTCCAGTCCCTTCCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCCAGGAGCTAATCCAA[A/G]TTCTCTACCCGCAGCTTGCTCGCCATACAG ACGGACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
ESTD-PBDA	103	A	G	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGCCTGTGGAGAGCAGAATATGGTCCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAG[A/G]TCAAGTCCA AGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAAACTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
EST12839 3	122	A	G	ATGGCTTGCCTTGGCATTTCAGCGGGCACAAGGCTCAGCTGAACCTGGCT[A/G]CCAGGACCTGGCCCTG CACTCTCCTGTCTCTTTTCTTCTCTCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGT GGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTGTGTGTGAGTATGCATCTCCAGGCAAAGCCAC
ESTD-CTLA-4	48	A	G	GATCAAGCAGTGCACACGGGTCACGATGACCAGCTCTCCACAGTGCACCATGAGATGGGCCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC[C/T]GTCTCCCGTGCGTCGGGGGGCCAACCCCGGCTTCCA TGAGGCCATTGGGGACGTGCTGGCGCTCTCGGTCTCCAACATCCTGAACATCTCGACAAAATCGGCCTGC
ESTD-ACE	96	C	T	CTTCTGCCTAATTTGAATGATATTGTTGCTGTGTGTGGGACCTGAGCACTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTAC[A/G]ATCCTGGGAGAGTGTATTTGGGTTTAGCGTGGTGGTATGTTGTCTA CTATAGTCCAAGTGAA
EST54419 8	88	A	G	

Marker	Pos			Sequence
ESTD-PS-1	99	A	G	GGGGAGTAAAACTTGGATTGGGAGAGATTTCATTTTCTACAGTGTTCTGTGGTTGGTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCT[A/G]TTTCGTAGCCATATTAATTGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCAATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTA
ESTD-B3AR	104	C	T	GGCTGCCAGGGGTTCCGTGGGGAGCGGGCCCTAGCGGGCCCCTGCTGGCGGCGTGCCGGTCGCTGGCCATCGTGGCCATCGCCGCC[C/T]GGGACTCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTCGGCCGCCAGCCGACCTGGTGATGGGACCTGGTCGGTGCCGCGGCGCCACCGTTTGCGTGCCTTGGCGCGC
WI-567b	48	A	G	TCTCACACTGACCCCTTACCTTCATCCTCACCTCTGCTGCTTGGTTC[A/G]AGCCCTCATCTCTTTACAGGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGTCTTCTTCTCCAATCCATTCTTCAAAAGGCTGCCACTGTGATCTTCCCAAAGGTCATCTGATTCTGATTCTATCCATCTTGCTTACCATCTTGCTTCAAGCC
WI-801c	58	G	T	ATGGAACACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCCTTTCT[G/T]AGATGGTATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTGCAGGGGGTGGGGGCTGTGCATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCCTCAGCCCACCAGAGAGTTAACATTTCTGCCACCCTC
WI-801b	58	G	T	ATGGAACACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCCTTTCT[G/T]AGATGGTATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTGCAGGGGGTGGGGGCTGTGCATCTGTGTATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCCTCAGCCCACCAGAGAGTTAACATTTCTGCCACCCTC
WI-1099b	76	A	G	GAAATTCACCTATACAAGAACTATTTTCTCTAATTATTATTACATTAGTCTCATTATTCTGAAATATTATTTTTACA[A/G]TACCCTTTGATTATTTGATTCATTTGTAACGAGAGATTACAATATCAGTAACGCTGTTCATTGATAGTGCTATCACAAATGTCTAAAATACTTTGGGTCAACATCAAAATTAGAAAGAAACTTACACAAAGTTTATTTGCTTTATGGTTTA
WI-2529	71	C	T	AGGAAATGGCTGATACTCCTGGTGGCTTCATTATTGAGTAGTAGTAAAAGGAGATGTAATTGCTTGATGAGCCTCTCAA[C/T]TCTTAACTGCTGCCTTCAGTCGTGCCTTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGTAAGTTGTAAATGCTGAATAAGCTTGAAATAAAGTGAAAGGAGGTAAAGAAGGAGACAACTGTGCTTTTTAAGAAAATAGAAGAGTCACTTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205	C	G	TAAGGGCCTGTCTTCCCCCAGAGGCCCCCAGGGGACAGAGAAAGCATCTTGATACCCAGGCCCACAAATGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCTATGGAGGTAACCTGAGGATGAAGGAGTGAGTCAGTCATATTGGGTGGCAATTAAATGACCCAGCCTCCTCTCTCAAGAAGACTTTTACATTTTAGACAGG[C/G]AGCAGAAGCAGCAAGGAAGGAAGT

WI-2625	98	G	A	...	GGGCAGTCCTGGCTGTAGTGGTAGACAGCACTGAAGGAGGAGGAGAGAGAGAAGAAACAGGCAGAA GCACTGTGGTAGTTAACAAGGCTTATTTAGGA[G/A]CAAATTGATGATACTCCCTGAGGACTCGCAG AAATTACCAGCAGTGGACAGGGGTTATCTGTGGTGAATTCAGTTCAGTTATTCCACTTGCAGGAGGAAAGCCA GCCAGCAAAG
WI-2924	54	G	A	TGACCTTCCTA GTCTTCTCTTA TAGG / GCCCTAAGTGT AATCACAGGG	TCTGTTGTCATATTTCCCTCTTTGACTCTGACCTTCCTAGTCTTCTTCTTATAGG[G/A]ACCCTGTGATT ACACTTAGGGCCTACCTGGATTATTTAGAAACAATC
WI-2939	72	G	T	GGCTTGTCTCA GTGCCTTT / CTTGTTGAGGG AAGGTCTTG	CCATTGTTGAGGTGGGGTCACTGTCATTCCCTCGCACTCAACAAAGTGGCTTGTCTCAGTGC CTTT[G/T]CAAGACCTTCCCTCAACAAGAATGTCTTTCCATGCTCCGTGTTCTTTGAAAATTCGACT TTATCCTGAAAAACTCAGCTGCAGTGTTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99	G	A	GGTTATGCCGC AGACGAG / TCAAGTATTGC CTTGTGTGG	CTTGCTACCATGCATTTCACAGCATACAACCCTCAGTGAAATGCCGTAAACCCCATTATAAAACAT CTTGCCATCGCAAGGGGGTTATGCCGCAGACGAG[G/A]CCACACAAGGCAATACTTGAAGTGACTTGGA GAATAAAGATTTTGGATGGATGAAAGCAGAGGAGATGCTAAAAGTGA
WI-3473	101	A	G	AAGCATTTTA GCCCTAGGGA / CCTGATGTCAC CAACATTTCT	GGAAAAAGAAACCTGAAGGATGAGTGAGTAAGTTAATTGGGAGAATAGTTGGTGATAGGCCCTGTTGGA GATTGCAGAGAAGGAAGCATTTTAGCCCTAGGGA[A/G]TAGAAAATGTTGGTGACATCAGGGCT
WI-1796b	29	A	G	...	ACACACTTTCTGTATGCTCTTCATCAAA[A/G]TGCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTGTCTTGGCTCCCC
WI-1796	29	A	G	...	ACACACTTTCTGTATGCTCTTCATCAAA[A/G]TGCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTGTCTTGGCTCCCC
WI-4360	93	C	T	GTAGTCACATT AGGTATTTTCC AAATAA / GAGAGATATTT TTCAGAGGCAT TTT	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCGAGAGTAGGAAAGAAAGATGGGGTGAGT AGTCACATTATTAGGTATTTTCCAAATAA[C/T]AAAAATGCCTCTGAAAAATATCTCTCCCATGTCCCTGTC TAAATATAACATTTTCCC
WI-1959b	87	C	T	...	GCTGAGCTTTGTGGCAGAGCCAGGAGGACAATTCAGCTGCCGGATTTAATAGATTCTGCAGCACTGCAA CAGGAACCAAAAATCAGTC[C/T]GGGTAACTGAGAGTGGTTTCACACCCAAA
WI-1973b	28	A	G	...	GTTGTGCCTGTAGCAGCACAGCACAGGCA[A/G]AGAGGAAAAAGCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1980b	140	C	T	...	CTTGAGTATGCGTGGATTTGGTATACACAGAAATGGGAGAGCTGGAACTAATCCCCCATATACCA AGGGACAAAATTGTATCTGTTTCTACAATTACACAGTAGGAGACATTATGTTCCATGACAATGGTAAT TTTTAA[C/T]GACAGTTTTAATTGAGTGAAATTACCATAAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGCCTATAAATAGC

WI-2015b	190	A G	TGTCAGATAGTCCGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCTATATATTTATACACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCCACAAGAGACTATGTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACACATGGTGCTTTTTCCAACT[A/G]CATATACTTCTAATACCATAGAG
WI-754b	49	C T	GAAGGCACAGGGGAGAAGATGGCTGTCATCTACCAGCCAGGGGAGAGAAGC[C/T]ACATTTATTGGTAATCCTATAAAGTGCATTCTTAAAATTTGTATTTACTTTAGA
WI-754	22	T C	GAAGGCACAGGGGAGAAGATGGC[T/C]GTCATCTACCAGCCAGGGGAGAGAAGCCACATTTATTGGTAATCCTATAAAGTGCATTCTTAAAATTTGTATTTACTTTAGA
WIR-1b	56	A G	AGGCAATCAGACCTACAGAAGGAAACCCAATAAAAACTCTGATGATCGTACATCC[A/G]TGCCGCTGGAGGGTGATGCCTCCTGAGGGACTTCATGTTTGGAGCCCTCCTG
WIR-1	56	A G	AGGCAATCAGACCTACAGAAGGAAACCCAATAAAAACTCTGATGATCGTACATCC[A/G]TGCCGCTGGAGGGTGATGCCTCCTGAGGGACTTCATGTTTGGAGCCCTCCTG
WIR-3b	72	A G	TAATTTAAAATGGGGCCAATAACACAGTACTTATCTCTAAAGGCTAAATAAGAAGAAGT[A/G]TCTAAAAGTTATTAGCTCAGAGCCTCACACATTCTCAGTGACTGATAAACAATAAGCAAAGCTGGGTGCTGAGATAAGA
WIR-3a	69	A T	TAATTTAAAATGGGGCCAATAACACAGTACTTATCTCTAAAGGCTAAATAAGAAGA[A/T]GTATCTAAAAGTTATTAGCTCAGAGCCTCACACATTCTCAGTGACTGATAAACAATAAGCAAAGCTGGGTGCTGAGATAAGA
WIR-4	47	T	GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGCTCACACATGTGCAAGGCAGCAGCAAATTTGCCCAGCTGCC
WIR-5g	209	C	CGGGACAGAGAGACAGAGAGAGAGAGGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACACCAGCTGTGGTCCCACTGTTAGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG
WIR-5f	196	C	CGGGACAGAGAGACAGAGAGAGAGGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACACCAGCTGTGGTCCCACTGTTAGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG
WIR-5e	194	C	CGGGACAGAGAGACAGAGAGAGAGGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTGTGAGNCATCCACACTGGAGGATGAGAACCCAGCCGCTGTGGTCCCACTGTTAGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCGGTGGCTCTATGGAAACACAGGTTTTACGTCCAG

Marker	Pos	A1	A2		Flanking	Sequence
WIR-5d	191	A	---		TTTACGTCCAG	CGGGACAGAGAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG
WIR-5c	177	C	---		TTTACGTCCAG	CGGGACAGAGAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGAGCCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG
WIR-5b	159	A	---		TTTACGTCCAG	CGGGACAGAGAGAGAGACAGAGAGAGAGAGTTCTGCAGCATTCACAAGAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG
WIR-5a	37	A	G	---	AGGTTTACGTCCAG	CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTC[A/G]CAAGAGGTTATTAGGACTCAGTTCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCTGTGGTCCCACTGTT AGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACAC
WIR-6	63	A	C	---	CGCAGTCTTGGGGTTGGGGCAG	TAACCCTGAAACTTTGTCTTCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C]
WIR-7	12	C	T	---		TTCGTGACTATT[C/T]AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-8	46	C	T	---		GGCGTCCTATGACTATCCTGGTCATTCATTGACTAATGATTCCTG[C/T]GCCCTG
WIR-2	56	C	G	---	GACAAC	AAACAGAAAAATAGAGGTTATAAGGATGGAACTAAAGTTGTCAGAAGAGGTATGA[C/G]CTGAAG AAAGAATTACTCTCTTTGACCAATAAATACAATTGGGAAACACTGGAAAACCATGGCTTGATTACT
WI-7069	93	G	A	---		TGTCCTTGCTTATGCCTGCCCTCTTTGCTTGGCCAGGATGATGCTGTCATTAGTATTCACAGAGAGTA GCTTCAGAGGGTAACTTAACAGAGT[G/A]TCAGATCTATCTTGTCAATCCCAACGTTTTACATAAAA TAAGAGATCCTTAGTGCACCCAGTGACTGACATTAGCAGCATCTTAACACAGCCGTGTGTTCAAAT GTACAGTGGTCCTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTC
WI-18694	41	A	T	---		GGTCATTTCCTTTTTATCTGTCAGGCAGCCAGCTCTGACT[A/]CTCTCTGTTCTGTCATCTCTCCC CCACATACCAAACTTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37	A	G	CCTATATTTCA AGTTTGGAAA G TGC	TTGTATTGCTG CTTGCAAAT	CACACTGTTCACACCTATATTTCAAGTTTGGAAATG[A/G]TATTTGCAAGCAGCAATACAAAGTA TTCATGAAGAATGCATAATCTCTGAAAATTATGAAAACATCCCT

ID	Pos	A1	A2			
WI-18517	87	C	T	CAGGAATCAG CAGCCTGA	TGTTTGGACAA GTGCAACA	TTAAAAAATCAACTAGGGCTCACCCTCCAACACCCCCTCCATTTGTCAACCTCTCACAGCCTGCATGCC ACAGGAATCAGCAGCCCTGA[C/T]TGTTGCACTTGTCCAAACAACAACTGACTGC
WI-18668	76	C	T	GGCGAAAAAC TAGGCAAAAA	GCTAAATTAAA CTGCACTTTTT GC	CGATTGACAACCTTTTATTTTCAACTTAGGTAACAGTCCAAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAAA[C/T]AGCAAAAAGTGCAGTTTAATTTAGCAAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTTCCCTCCTACT
WI-18680	75	T	C	GCTGTCACTCT AGCATCTGGA A	CCTCCTGAATA TACAACGGAGC	TAAAACATAGCAGTACTGTACACGCAAGCATGCATCCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAA[T/C]GCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A	C	GGGGTTCTCCGA GGGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTTCTGTGCGAGCACCACACCAAGGGCTTGGGCTTGAAGGAGGC CTTGAGGAAACACGGGTTCTCCGAGGGGTACIA/C]CCAGCAGGGCCTTCAGCTTAAAGTCG
WI-18673	29	A	G	...	...	TGTGGGCCAAACCTTGTTTAATTGCAAAC[A/G]ACTTAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAACATATGAATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T	C	GTCGTGGGGGTG GCGG	GCAAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTTGGAGGTTAATTCCTATTAGGATATGAAAGGATTCAGCAACGATTGAGATT GTGTTCCTCACGGAGGGGCTCGGGCCAAGGTCGTGGGGGTGGCGGGGGTGCAGAGT[T/C]GTGTCCTCTTC AGTGGTATTTGCGGACC
WI-18533b	91	T	C	...	...	GGGGAGGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTTAAACTCCCGAGATTTTCTCTTTATTT TATATTTCATTTTCATCCTAA[T/C]TTACTGAAGCCATTTCTTGGTTAACTTTAGA
WI-18533a	59	T	G	...	...	GGGGAGGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTTAAACTCCCGAGATTTTCTTT[T/G]CTTTA TTTTATATTTCATTTTCATCCTAATTTACTGAAGCCATTTCTTGGTTAACTTTAGA
D11734	83	A	C	TCATCTGATAC CTTGTTCAGAT TTC	AACCAGGATA AGGCTACAACT ATTT	GAGCATATGCTGCATGAGGACCTTTCTCTATCTTCACATTATGGCTGGGAATCTACTCTTTCATCTGATA CCTTGTTCAGATTTC[A/C]AAATAGTTGTAGCCTATCCTGGTTTACAGATGTGAAACTTT
D49493	159	A	T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGGC	CAGGACTTGTGTGCAGCTGCAGCTGCAGACAGAGCAACATCACTGGGGCCCAGAGAG AGCTGTCCGCCAGTGCCATCATTAGGGGGTCTTTCATTGCTAGTGACTGCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATT[A/T]GCCCTGGCCTGAAAGTGGCCCATCATTCATACCCCACTGTT CT
EST100307	98	T	C	CATTTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTCATAGAGGAGACCTAGGAGGAGGTTGACACAGCACACTGCTCAGCAGATGACTTAAAATTTT CCCTTAGCCATTTTGTTCTCTCAAGTCCCT[T/C]TCATCCATACCACCACTGCTGATTTG
EST100522	24	G	A	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG[G/A]GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTGAGTCATAACCTGGTCATGTGGCAAGAGCATGGCAAGAGCAAGAGGAA A

Clone	Pos	A1	A2			Sequence
EST10605 2	118	C	G	---		CTTGCGTAAATCACAGTTCTGTGTATTCATACAAAAACTTTGTTTTCTCTGACAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACTTAAATTTGTGGAGATGCCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61	T	G	TAATCT	CTCTCAAGTAG ATAAGAGGCA TTGTTT / GCTAAATTTC AGAAAGAATT	CATGTGTCAATCCCATGATTGAAAAGACATGTGCTCTCAAGTAGATAAGAGGCATAATCT[T/G]AA ACAAATTCTTCTGAAAATTAGCTTATGAACTCATTACACTGCAAACCAGAAGGAGCAC
EST11260 8	101	G	T	---		TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAAATATCATTAAGAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109	C	T	---		TTTGATGGAGAAATCCGAGGCCTGCCAGCATCCCCACCAGTAGATTTCTTTGGACGAAGAAAATCCT TCTGTGGATTCAGCTTACCGCCTTTCCTCATCTGCTGGTGT[C/T]TTCCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI-16632a	71	A	G	TGGAGCCCT	CCAACCTACTT / TCCAGCTTTCT CTAAAAACTCC T	GAATTCTGGGTATTAAATAGCGGGTGCCACAGGAGCACATAGGAAGAAGCATCCAACCTACTTTGGAG CCCT[A/G]AGGAGTTTTAGAGAAAGCTGGACCCGAAGAGCTAGTAGGAGGTAGCCAGACCAA AGGGAGGAGGAGTGGGAA
EST11772 6	74	A	G	---		CCAGGAATAAAAGAAAAAGAAGAGTCAGAGGAAACAGTCTTGATGTTATGAGGCTGAGACACTACTC TTCCTTCA[A/G]GACTATTTCATTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGGAGCTCA
EST11795 3	82	G	A	---		CTTGTCCATTTATTTTGTGCATGTTGTTCTTAAAAGGCTTGTGAAAGATAACTTGGAATGTGGGAAAC ACATAGATCCCAGA[G/A]ATATTAAAGGGGCTGGAAAAGTAGCCTTAAGAC
WI-16644	42	G	A	TATACC	CAATAAGCAG CTCATTTTGAT TAC / ACTTCATGAAT TTTACTTCATG	AGAGCAATGGTGCGATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAATTC ATGAAGTAAAATTCATTATACCAAAAAGCCTCCCACAGAACTTTCATGCACCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST12005 9	56	A	G	TTGTATAATA ACACTCAGTA CAAAGTCTGT	GGCTGGTCACT TCCTGGAT	GCCTAGTAATTCCAAAAGGAACACATGTTGTATAATAACACTCAGTACAAAGTCTGT[A/G]ATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTCCATAGTTTTGAAATC
EST12055 9	32	T	C			GTGGAAAATTTTTATCTGTTACGTCTTTCC[T/C]ATTATATTATCTTGTCCTTGATTTCAGCACCCC CACCCGATTTGCAGGCAGTGCTTTCTAAACTGTGCCCTGTGAGCTGTTAAAAGTCTCT
EST12492 1b	95	A	G	---		CCCCTAGCAAATGACTTGGAGTTGTGTGTCCAATTACCAAGTTACATACTGTTGCCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[A/G]GGAAACGCACAGCAAAATTGACGATGCAGCTTTTA CCTTTTTA
EST12492 4	25	A	G	---		ATCTTGAGGTTTCTGGGCCTGTCAG[A/G]AAGTGACATCTTTACTTACCCACAGGTCAGGAACCCTAT AAAGAAACTGTGTAGAAAAGATATCAGGTCAGAGACTTTTTAAAGGGGCTTCTTATCAGCTCATAAA

EST ID	Pos	Allele	Seq frag 1	Seq frag 2	Sequence
EST125022	52	C G	---		ATAACTAGGGAGAAAACCAAACTGGAGGCAAGTCCACAGGTCACACTTGTCA[C/G]CAGCAAGTAT AAACAAAGTGGGTTCGATGAAGAGAAAATGCTCACGGGGGAAATGACCATTTTAAGGGCCATGTG GTCGTCGAGGCAGTAGAGG
EST126198	105	T C	---		CCAGAGAAAAAATTAGAATGTATCGGTAAAGAAATAGGAATGCATATTCAACTCACTGTCACAAA CAGGTGTTTATTATCCCAAATGACAGTGT[T/C]GATGCATGTGGCAGACGAG
EST126200	67	A G	---		TTTTCTCTCTCCTTCATTTATTCATTTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGGC[A /G]TTGAGAATACATATTGAAGAAAGAGTCACTGCCTGCCCTCTGGAAAAATCAGAGTATTTGA
EST128179a	22	C A	---		TTGGGGTTCTCCAGGGATTCCCAG[C/A]CTCGTAGCTGATGTGCATGGGTTCTCATCCATGCTCCACGG GTTCTTGGGGAGTGACCGGGGATGGGAATCCATGTTGCTTTGCGTACTCCATCAGGTCATTGCG
EST129418	23	T A	---		TCTCAGCTTCCACCTGACCTGCA[T/A]CAACAGCCCAGTTATTTCACCAGAATTTTGTTTGCGTTTCA ATGTAGTGTTTAGCTTTAATACACTGCCACTTGTTTTG
EST129492a	52	A G	GGCTTTAATCA TAACCTAATA ATACTGTT	TGTGTCCCTGT GGGTCTC	AGGATTTCATGAGGCTTTAATCATAACCTAATAATACTGTTAAAAAACACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACCATTCTTCCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST130674	104	C T	---		ATTTTTGTTTCTTAAATGAAGCATAATAAAACAGTTAAAAATTCATCAGAAAAAATCATCTATAGTTGA GTGTAAAACTCCCCTAAATCAGTCTTCTAGGGCCACA[C/T]TGGAGCAGAAGCAGCTTCCCCACCCAAG CACCTCTGAACT
EST131176	66	A G	---		TGCTGTCTGCATCAGTCCTTTAAAAATTAATCGCTTTATACAATTGACACCAAATAAAATGCAC[A /G]TATTTAAAGTTTACAATTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST131216	44	C T	---		TCTGCTTTTAAAGATTCTTCATAGCTGCTTAGGTTGTTCTTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCCTCCACAAATATTTCCTGTGTGTGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST132266	74	T G	---		AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATTAATGAAATAGTCT GGCCCATTT[T/G]GACTAACCAGTTCTACAAATTCACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST132306	72	G A	GCTCAGATGTG AGAGACGC	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCGGCTTTACTGAACTTACAACCAACTTGCGCGCTCAATATGCAGCTCAGATGTGGAGAG ACGG[G/A]TCTGTACAGGAGCCGGTACTGTCTTCAATCCTTGCATGCAGGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST132369a	70	T C	AACCAGATTT CTCTCAGGCCT	ACAAGAGGGT TGACAAAGA G	AAAGATATAAAAACAACTCCCATCAGTAGCAATACAAGGTTATACATTTAACCAGATTTTCTCAGG CCT[T/C]TTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAACCCTCTCTTGTATATAACCA

EST	Pos					Sequence
EST13278 2a	51	A	G	CTTTCACCGAA CAATATTTTAG G	CATATTCTTGG GTGGTGAGAA	TTCGCAGAACGTTTACAAGCTCCAAACCTTTCACCGAACAACAATATTTTAGG[A/G]ATTTGAAATTAT TTCTGTAGTTCTCACCACCAAGAAATATGACAGCTTG
EST13282 0	99	A	T	CCACACATTTC AGTCCAAGA	GATGGAAAATT TGAGGAAGGTT GG	GCTCACTAGATGAGCATTGACCAAATATTTAGATATAATACCTGTTGGGAAAGTGCTGAATTACTAGCC TGCCTGAGAATCCCACACATTTCAGTCCAAGA[A/T]AACCTTCCTCAAATTTTCCATCTCCCATCAGA GG
EST13290 9	39	A	G	CAATTTTTAGA AGTTTGGGGTT CTT	AAATCACTTCA TGGAAATTTCA G	AGCTCATCTGCAAGCAATTTTTAGAAGTTTGGGTTTCTT[A/G]CTGAAAATTCCATGAAGTGATTTTT TTTCTGTGTTAACTTCAGTTACTTAAAGACCTAAAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTGTGGGCTTTTTG
EST13518 2	45	C	G	---	---	GAAACATCCTCCAGTAGTATTGAGGTTAAAAATGATTCAGCATTA[C/G]ACTTTAAAAATTACCTCA ATGTTCCTCGGAGTCGTCCATAGTTTAAAATGACTTCTGCACCTTCCTTATAACCTTGATTG
EST13522 8a	66	A	G	---	---	CAGGTTGGTGATTCTCAACTAGGAGCTATTTTGCCCCCCCCATCCCCACCGGCAGTGTCTGGAGAC[A/ G]GTTTGATTGTCACAACTGCGAGAGGTGGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69	T	C	---	---	CTTTAAGGAAGTGAGCCAGATGAATCAATGACCAACCTGGTTGAGAGCCATTGGTCTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGGAGAAGAAGGAGGTTCGGGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101	C	G	---	---	AAGATTACGGACCATAAGAAACTGCCCCCGACCCATACAACAATTTATAGCAGGTAAAACCAA CTGAAAGGAACAACAAAGTAATGACTTTCTTGAACAAA[C/G]TGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25	A	G	---	---	CCTCAACCATCTGTAACCGAGCCC[A/G]CAGTGACCGGACTTGCTGCTTCCCCATCCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23	A	G	---	GGAACAAGTC	CAATGGTGTCCATGTGAACATAT[A/G]ACCTATTCATAAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAAAGTCATCTGCTAAAATGACCGAACAGGAGGGGTAGGGAGG
EST14221 5	42	T	C	GCATGCTAGA CAGAGGCATT	AAAATATTTT AAAAGA	AATATCAATGCATTCTTGTTGGCATGCTAGACAGAGGCATTA[T/C]TTTGAAGATCTTTAAAAAT ATTTGACTTGTTCCCCTTCACACTCATTTTAAATGT
EST14812 2	50	A	G	CAAGTCAGCTT CTACATTCTGA ATA	TAAAGATTTAC TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCTTTCAAGTCAGCTTCTACATTCTGAAT[A/G]AGTACATAATGGG ATTTAAGTAAATCTTAGAAGTCCCGGAGTTGCCTTTTCTAACATTTCATATCAGGTGAAAACAAT TTTTCATATGGGTGATT
EST14815 3	128	A	T	CATCACCCACC ATACTGGTT	CGGGAAAACA GTACCGGAA	TTTGCTTCGGCAATACATAGTGCGCAATGCGCAGCCGGTCGCCGCCGTCTCCCCACTGAACCAGTAAT TCACCAGACAGAATGGCGCACCACTTAAATAAACTTGCCCGTCATCACCCCACCATACTGGTT[A/T]TTCC GGTACTGTTTTCCCGTA

ID	Pos			Seq	Sequence
EST15420 6	109	C	A	--	TTTTAACCCCAAGACTTGTGTAGATGTCAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTAATCTCTCCCTTTGTCATCATAAATCATTATAGCCAAGGGACT[C/A]GGAATTTTGGCTGCTTCAAGTCATTCCAAAACCTCTCAGG
EST15700 6	48	G	C	GGAATAGCTGA AACAGAGATA TTATTCTC · GAAAAGACAA AGACAACAGA GGA	GTCACCAGCACTTTTATTAAGACGTGAAAAGACAACAGAGGA[G/C]AGCAGAGAATAATATCTCTGTTTCAGCTATTCCAGGATGTTATGCCAAGAGTCCTTGATCTGATGTAGTA
WI-16739	57	G	A	GATAGTTGATG TTCATTATTCC CTATAA · GGTTTTGCCAT CACAAGC	AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGGTTTGCCATCACAAGC[G/A]TTATAGGGAATAATGAACATCAACTACTACACAGCTAAACCTAATGAAGACCAAATTGCCTCCAAGGT
WI-16782	96	C	T	CTTCTATCTTT CTGTTCCTCCA TC · GGTGGGGAGTCT CACTGTAAGG	CTTCTTCCTTCCTAGACGTGGAATACACACGGATCACAGTATCTGGAGATGTAGCAGCTGGCTCTTGACCATAATGGTGGGGAGTCTCACTGTAAGGA[C/T]GATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGTGCTGATGAAATTGTGGGG
WI-16783	64	A	G	CTGCTGGTTC AATCCTTATTA G · TCCTGAGATGT CTTTTACCTGA G	AAAAATGTAAAACTTAGAGGTTGCCTCTTTGTGTCACTTTCCTGAGATGTCTTTTACCTGAG[A/G]CTAATAAGGATTGAACCAAGCAGTATTTTTAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58	T	C	--	CAGGACTTAAGGTCATTTGCCTGGAAGACTTAACTAAAGGTCAGGGCAACATAGGA[T/C]TGTGACAGCACCACTCGGACCAGGAAGTGCTGAAAATCGTCACACTAGCGTGCCCAGCCCCTTTTTCCTGGCTGCTCTGCCCTCCCAGAGC
EST16088 8	89	G	C	--	GGTTTTGAAGACGCAGCTTATCTCCACCTGCCACTGGGATTCTCATTTTGAGAGCTGTGTTTGTCAGCCTTTTCCAGAAAAGGCCGCTCG[G/C]GGGTTTCTGAACCCTCTATGGGCATTTTAGAAT
EST16089 9	96	C	T	--	CGTCTGAAGTTTTCTTTTATCACAAGTCACATCAAATCCCTCGGGCCCCTGCTCAAATGCCACCTCTTCCTGAAAGCCATCCTAAGTAGTCTCTC[C/T]AAAGAGCCATCCCTGCCCCTTCTTTGCT
EST16100 1	24	C	G	--	ATCCCAGCTGTGAAGGAGGACAGGAG[C/G]GTAAACACAGTCCATTTATAAGGGGTGTGCACATTCCCAGGGCTCCAAATAATGCAACATTGTTTCACTCGTCGATAGTTTCATAGTAAAAAAGTCACTCCAGACAGGGTTGGCTC
EST16104 9a	83	A	G	--	TTCTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAAGTGATTTGCAGCTGGTTCCTCCAGGGA[A/G]TTGGCCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119	T	C	--	ATGGTATAACAAAATCAGTTCCAGGTTTTTT[C/G]TGAACAAATGATCCTTTGGTCTTTCCCGTGGCATGCTCCTAAAACAACTAAAACAACCCTCTACGTCTAATCAGTCACGTCACCTAAGATATCGAGTGGCAAGTCTTTCACA
EST16118 0a	32	C	G	--	ATGCTCCTAAAACAACTAAAACAACCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGTCTTTCACA

Clone	Pos			Flank		Sequence
EST16151 2	53	C	T		---	AGCCAATTCAAACGAACTCTATCAAAAACACACAAAAGGCCTAGAGAGGAGAGATTA[C/T]AATGAACGT AATAATTCAAGGCAATTTTGATCTAAAGCATTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54	G	A		---	CATTGGTTGGGTAGGGAAAGATAGTAGTGTGTGCAAATAAAATGGTAAAACAGCAG[G/A]AAATGGAA TTATAGCTTCTTTCATATAGGGAATTGAAATTTATTTACTGAGGGTGATAGGCAGAAGTAGTA
EST16183 2b	59	A	G		---	GCAGGTAAACTGTGGTTCACAACGTATTGTTCTTTCATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACTGTCTTCCTGGCCCTTCCTTCTGTCCATATTTTATGTCACTGTCCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28	G	A		---	AATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACACAGATAAGAGCTTTAAGTATTTCGCATTT CCCCAGAGGAGAAAAGTCAGCATCATAAACCACATGGGTCACATGCTCACGCACATGGGTGTC
EST16229 2c	52	T	C		---	TGTGAACTCGAATTCGCTTGTCCAAGTCCTGAGTCACAGTTTCATTTGGGAG[T/C]CCCTGTGCAGCC CTTGCCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
EST16229 2b	45	T	C		---	TGTGAACTCGAATTCGCTTGTCCAAGTCCTGAGTCACAGTTTCATT[T/C]TGGGAGTCCCTGTGCAGCC CTTGCCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
WI-16816	124	A	G	GGAGCCATTGT GTTCAGGACAG		CAGACTTTCCTCACACCTCATTGGCTGGAACTGGGTCACATGCACATCCTTGAACTATCATTGGCAA AGGGAAATGGGTCATCAAAATTGCTTAAGGCCAAGCAGGACCAATTGTTGGGGTTA[A/G]ACTGTCC TGAACAAAATCTAGGCTC
EST16269 5b	49	G	A		---	GCCACTCCTCGTGTGGCTTGCTCCTGTCCCAGCTGCTGCTCCCAGTGCCCACA[G/A]TGTCTCAGCCTCATGG CAGAAGCATTTAGCCAACTCCTGTGGTCGTCCACTCTCTCGCCGGGCTGGGGCTCCACCACC TCTTCCTCTCCAATC
WI-16824b	83	G	A		---	GTCACCCCAGCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCCTGGTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47	T	C	TGATGGTGCTG TTCTTCATAAG CAGCTTCTGAC AA		GTCACCCCAGCCAATGCTTCAGGAATAAATGATGGTGCTGCAGCTGT[T/C]GTTCTTTATGAAGAAGTC AGAAGCTGATAAACGTGGGCCTTACACCTTTAGCACGGATAGTTTCCTGGTCCCAAGTGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96	T	C		---	TTGCTTTTATTAATCCAGAACGGACATGCTACAGATACTGTACAGCATGAACATTTATTCATTACAAA AATGGCTTCCAAACCATTAAAAATGAACT[T/C]GGAATAAAGAGCATTAAAACGGAACAGTAACATCA
WI-16857	47	G	A	CAAATAAGCA GCTAATGGCA A	TGTGAATTGGG AAGACCACT	TATAATCCATCCTCCAACACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCACAAGACCTGTGTTCAAATTGTTTCCTGATAATGTGGAGAAATCTGCTCTTTATGTA

ID	No.			Sequence		
WI-16879	79	C	T	GATACAGGCC ATATTCCCA	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAACAAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCCATATTCCCA[C/T]ATAGGACTCTAGTTCTAGAAAGCCTTGGGGAGAACAGGCACCCAG
WI-16882	99	A	G	GAAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGGTGGGAGAAGACAATTCTCCCCCCTTTCACCCAAAGGTTACTCTGAC AAGGCTATGAATGAAAATGCCACGTCTCTGAC[A/G]GCGATTTACCTGACATGTGTCATCTCCCT
WI-16888	70	G	A	GCTAACTTTGG GCAGGTTC	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTCATCATCACTACCCGGGGAGAGCAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC[G/A]TAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75	C	T	ACTTGGCCTGT GTTGTTCA	GTCTATACTCT TCTAGGCAGTG GG	TTTGTTGTTGTTATTGCCTCCCAACATCAGAACATAAGTTCCATGAAAACAGGAACTTGGCCTGTG TTGTTCA[C/T]CCCACTGCCTAGAAGAGTATAGACA
WI-16910	74	G	A	AAGAGTAAAG ATGGCGCTAG AA	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTCATCTCAGAGAGTAAAGATGGCG CTAGAA[G/A]GTATCGTTATAGAAACGATACTTCATTTGGGCCTGAACCAGTGAAGGT
WI-16918	93	C	T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAAATAAACTACCACCATTCTCTGTCCTACCACAGAGCACTAAAATCTAGGAATTTGAC TTTACTGCAGCCATTAACACCAGCAC[C/T]GATGCCACCTTCTGTATCAGGAACTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127	A	C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGGG[A/C]CCA TGGCTGAGGCTTTCAACTGACATCAGAACAAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16947a	58	C	G	CATGGAAATA GGGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAG[C/G]ACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGAACAAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16966	43	T	C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTGTTTACTTTAAAAATGCACACTACATAACAACCTAATA[T/C]CTTAACTTGGTCCAACTATTT AGTATAACTAATATGAGTTTTTATACTGATAACTTGCAATGCCATTAAA
WI-16995	55	T	C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATTT CCAGCCGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAAATAGTATT[T/C]ACGGCTGG AAATCAACATGCCTCTTCTTCTGTGAAGTTGTCAGCATGGAGGCTGAGTCAATCT
WI-16992b	60	T	G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAGTACACTGTC[G/A]CCCTCATCTGAGA[T/G]GTG TAGGACTGTAAGGGAATGTGTTTGGGGGTTTAGGAA
WI-16992a	46	G	A	AAGCACCCAG AAGTACACTG ATC	CACATTCCCTT ACAGTCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAAGTACACTGTC[G/A]CCCTCATCTGAGATGTG TAGGACTGTAAGGGAATGTGTTTGGGGGTTTAGGAA

ID	Pos					Sequence
WI-17010	23	T	C	TTCAACAGGA AAAGCCATG	AATAATACGGT GTTTTGAATGT CA	ATGTTTCAACAGGAGAAAAGCCATG[T/C]ATGACATTCAAAACACCGTATTATTAGAAGCTCATTTAAT TGTTTAATGCAGACAAAAATCAAGGCTAACTAAAAGCAGATCCAATGACCCAGTGATCAACCTAGA GGTTCCCACG
EST17127 9b	74	C	T	CACTCGGCAC AGACAGAGT	GGGAGGCCAGG GGTG	ATTCCGTCTCCAAACAGCATCCCAGCCGCGGGCATCTCCCCACGATTTATAATACACTCGGCACAGA CAGAGT[C/T]TGGGGAGGCCACCCCTGCCCTCCCCAGGCTTCCTAAGTAACAACT
WI-17040	94	T	C	AATTCTCTTAT CATCTCAAGCC A	GGACTATGGCT TATTCAGTGAT G	CACGCGGTTCATTAAATTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC GAGAATTCTCTTATCATCTCAAGCCAG[T/C]CATCACTGAATAAGCCATAGTCCCAGTCTCGTTTTCC AAATCTTTCTCATATTGT
WI-17044	47	G	T	GCCAAGGGAT TAACGTATAG G	GGGGATCCCCT TGTTTAAGA	TTGTTTTGTTTTGTTTTCTCCTCCTGCCAAGGGATTAACGTATAGG[G/T]TCTTAAACAAGGGGATC CCCACTTATAGCTGACAGCAGCAGCTGCAACCCACTGACTCTCTGCAGAATGGCAGGGAATCGAAT CAAAAGAAAAGCAAGTG
WI-17021	62	T	A	TGGACTTGTCA GCCTATAACT ACTC	TGTAGAGTTAG TGGCAGCTGC	GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAGTGGACTTGTCAGCCTATAACTACTC[T/A]G CAGCTGCCACTAACTCTACAGGCACAGTAACTAACTACACTTTATACAGGAGCACATGCCAAAGTGCCTGG GAGGTGCCAATAAAATCAA
WI-17065	90	T	C	CCAGAAAGGA AAAGCATAAA CTT	CCCAAGAGAC AATGAAATCCT	TGTAAAAAATGTAGACATGGGGGAAAAAACATTCGTAATCAACATGTCGTGTTTTCTACTTCCGTA CCAGAAAGGAAAAAGCATAAACTT[T/C]AGGATTTCATTGTCTCTTGGGT
WI-17066	32	A	T	TGTACAGCCA ACATCACTGTT T	GAGATGTTGAA AATGTTCTGGA A	TTCATAAGGTTGTACAGCCAACATCACTGTT[A/C]ATTCCAGAACATTTCAACATCTCAAAAAGA AACTCTGCACCCATTAGCAGTCATTCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86	T	G	---		TGCTGACTGTCATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAGCAT AACCTCCTACACAGGCCTT[T/G]CTACATAGGAGTATATTTGGCCAAGACTCACCACTAGAAGTGATT
WI-171104b	108	T	C	---		CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTGTGCGAGCTTCATTCCATTCATTCCA AATCAGAAGCAGTCAGTGGTTCCAGACGGCTT[T/C]CTCTCTTTGTTAAGAAATTA
WI-17114a	37	T	C	TTTCCATCAAG GACTTTGTTTT	TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAAACAGATGTTTCCATCAAGGACTTTGTTTT[T/C]GTCTCTTCCACTCTGCTATTTATAATAC AAGCTACCTCCCAAGGCCAGATGTGCTCTAAGTGCTAAAAGAAGAGACTGCAGCCACAATCAGAGTTACAT GGGA
WI-17150	76	T	G	GATGAAATTC AGATAGTCTTC GCTCTT	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGCTCTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC TTCCTCTTT[T/G]CATATCTTCCAGGATTCTGAGAAGGCCTCCTTTGTCTGCTCTAATTT
WI-17163	43	A	G	CATTTCTTGT AAAATAACAA GTAACGTT	CAGAATCTTGC TTTTGCCTT	GAAATCGAATACGTCCATTTCTTGTAAAATAACAACAGTT[A/G]AAGGCAAAGCAAGATTCTG TAAACCAACATTGGAAAAGGGACACAGGGAGGGGAAAAGGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAAA

ID	Pos	Allele 1	Allele 2	Sequence
WI-17178	127	T	C	AGCAAATGTCCCCTCCAATTTCATTAGCTATGATGGAGTTATCAGTTCATTCAGAGCGAATTACTGG GGCGAGGGGGTTTAATATCCTGATGTGGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGC[T/C]AGAA GCAGTTGAAAATTGAGGG
WI-17180b	81	C	G	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAATCCTGCACTTCCCAAGTCTCGTGCGCACAG GCTTCAACAATTAC[C/G]AACATCTTGCCCATTTGTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17180a	47	T	C	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAATCCTGCACTT[T/C]CCCAAGTCTCGTGCA CAGGCCTCAACAATTACCAACATCTTGCCCATTTGTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17156	54	G		TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCAT[G/C]TTCCACAGA ATCAAATATATATTCTTGGTTGGAAATTTAAATGTTCTTAACTGTCTTAACTATCTGCCTACCATCCACCTCAAT TAATATTCTTG
WI-17149b	79	T	C	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTGAAGGAGGAACATCTCATGCACGTGCGTGGAA ACCCAATTGTCAT[T/C]GTGTATGAACTACAAAAGGATGGGGAAAAGAACACATTCCTCACA
WI-17149a	48	C	G	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTGAAGGAGGAACAT[C/G]TCATGCACGTGCGTG GAAACCCAATTGTCATGTGTATGTATGAACTACAAAAGGATGGGGAAAAGAACACATTCCTCACA
WI-17197	67	G	A	ATTTTGCTATGTTGCCTGGGCTGGACTCCAGCAATCCTCCTGCCTCAGCAGAAGTAGTGGGGCTAC[G /A]GGTATGCACCACCTCACCCTGCTATCAGTTTCGTTTAATAGAATATTTGACTTTTAGATGCGCA
WI-17198	38	A	C	TGTATTTCAGTACTTTTCTCCCCCCTTGTCCCTAGTTT[A/C]TAATTTCTCAGTGGACAAATGGACAA ACCATCTCTGTTTGAATTGAATACAGATACAGCAAGATATCTTACAAGAAACAATGCACATCC TTC
EST187538	27	C	T	TCGCTATGCTACCCAGGCTGGTCTCAT[C/T]TCAGGCTCATCATGCGATCCTCCTGCCTCCTGCAGTGGCTGG GATAAGACACAACTGCCACCAGGCCTGCCCTAGGAGTAGTCTTAATGCCTGATGTGGG
WI-17108b	74	C	T	TTATTTTAAAACATAACCAGCATGCACACTTGGTTTTTACATTCTCTGGTTGCCATTCAGTCTCAAAGT AAACAC[C/T]GGGAGCATATGATAAATCGTAGTTTAAGGAAGCCATAGCACTTACAGAGT
EST190672b	41	A	G	ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCA[A/G]GTGGCATTAAGTACATTCAACT TTTTGAGCAACCCGCCATCCATCACCATTCATCCATCTCCGTT
EST190672a	40	A	C	ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTC[A/C]AGTGGCATTAAGTACATTCAACT TTTGAGCAACCCGCCATCCATCACCATTCATCCATCTCCGTT
EST191258	28	A	G	CTGTTTCTCAGAGATGACGACTAGTGTGTTTTTCCCTCTGAAAAA TATTCACAATTACAGTAGTGTTTTATTGGC

ID	#	A1	A2	Col 1	Col 2	Sequence
EST208248	115	T	G	AGTCGGGGAGT	AAGATTTATC TTGGACCCGA ATCTTAGG	GTGTGGGAAGCCGGAGTTTTATTATTCAAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTGT[G/T]CGGGTCCAAGATAAA
WI-17347	50	A	G	GCTTCTCAGCCT CTTGTGCTA	TCAAGCATCCA	TTGGTTAAATGATGCCCAGATGGGGTCACATCCTCCAGAACTTCTCAGCCT[A/G]GTAGCACAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGGGATGTGAGTGGGACCA
EST21904b	128	G	A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTC AGAAAGCAT	TGATTGTGGGGTCTGGGAGCAGGTGGGCAGTTCAGTGAGGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAGAAATGTACTAGGCTTTCATATGGCCATTTTAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST221113	82	T	C	GAAGATCTGT CTGGCATTCTT CT	TGGAAAAACA GCCCCAC	CAAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAGTCACCATGTTTGCTAAGAGAAGAT CTGTCTGGCATTCTTT[T/C]GTGGGGCTGTTTTCCAAGGCACA
EST221972	78	T	C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGCGGGT	GTTTAATGATCACTCACCAAAATCCACAGGAGAATCTTAAATGTTTACAAGCACCAATTATTCTGCT ATTCCTGCCATT[T/C]ACCGCCATCCTTCATGGTAGAGTATCACAAGTAAAAGTTTCTGGTTGTTTCATC TACTTAAAACCA
EST223119c	92	T	C	...	...	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAATCCACCACTGTAAACAG TAGCATTCAATGGTTTTTACTCTA[T/C]GTCAAGCTGGGCAACTATCATCTACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST223119b	54	A	G	...	...	TTTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAATCC[A/G]CCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST223119a	41	T	C	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATA[T/C]ACATAAAAATCCACCACTGTAAA CAGTAGCATTCAATGGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCATCTACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST223199	19	A	C	...	...	TCGAGGAGCTCTGAGGAGC[A/C]CACCAAGGGACGTGTCCCAGGGCCACCGGTGCAGGCAAGTGTG GTCCAACTCCTCCTCCCTTACAAACTCCAGCCTCACCCACACAACACTGGCTGACAGGCCTTCT TAAGCCTTTTTAACTGT
EST224333c	103	A	G	AAGACATGTT CACCAAGTGA AA	CAGCTTCAGCT TAACTGACAGA	GATGTTAATGACTTCCTTTGAGATATGATGAAAAATATTCCAGTACACATGGAAAAGACATGTT CACCAAGTGACTGGGAGCTTACC[A/G]TCGTGTCAGTTAAGCTGAAGCTGAAATT
EST226579	71	A	G	AAATGGATCC GCATGAATTTT T	AGTTTCAGTTT	TATCCATTTCAAGAAAAAAAAAAAAGACTTAAAAAATACAATTCTATCCCAGAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAGAAAAAAAAAAAAATTCATGCAAACTGAAACTATGCTTT

ID						
EST22993 5b	71	T	C	ATCCTTTTGTT TCTACCCCC	TTGCCTGTTAA TTTGACTGTAA TG	GCCTTTTATTGTGTCTCCTTTAACATCAAAATGTTTATAACACACTTGATCCTTTGTTCTACCCCCA ATT[T/C]CATTACAGTCAAATTAACAGGCAATATAATAGGTCTAACAGAATGCTTGCATTT
EST23021 0	108	T	A	...	...	TTATTTCTCAGCTTACCATTTGTGTACTTATATCTCTGTACAAGGTGTTTTCTCCATGGAGAAATG TTAAATCTTTGTGTGAGGTTAATTTATTAATCTTTGCCTT[T/A]ATGGTTTGACAGTTGTGTCTTTCT T
WI-17387	55	C	G	CCTTTGCAGAT TGAAGAAAAA	GCTTTTGCCTA AGATTAATAGT AACTACT	ACAGAATTTAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA[C/G]AATATTAG TAGTTACTATTAATCTTAGGCAAAGCCATTTCTTTG
EST23669 1	101	A	C	AATGTAAGCT CCAGAGGCAG	CCTTCCCCTCC TGTAAGC	TTTTTTGGCTGTCTGCAGAATAGATGAAAAGAGAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGCACACTAGGCAATGTAAGCTCCAGAGGCAG[A/C]GCTTACAGGAGGGAAGGGACGCTGAGGC CAAGAGTGCTGGCTCACTG
EST23733 9	31	T	G	GGCTGTTAGTT TTGTTTTGTTT GTT	TGCACTTTAAA TCCCATCAAT	AAAGGCTGTTAGTTTGTTTTGTTTTTCCT[T/G]TATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCCTAGAGAAAGATATGAGGCCCGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
WI-17470	83	A	G	GTCCCGTCCCG CCAG	CCAGTGACGAG GCCGA	CTGACACGTCCCTGTGTCGCGGGGGTGTCCATGTGGCGGTGTGTGAGTGAGACTTTTTACTGCGTCCC GTCCCGCCAGCCCTA[A/G]TCGGCCCTCGTCACTGGCCTTGTATTTCTGTCTTGGTTGGAAA TACCATCAGCCTTCC
WI-17519	55	T	C	GTTGTCCTAGC TAATGAATGC A	AATTATTATTT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAAATGCATTGTTGTCCTAGCTAATGAATGCAT[T/C]AGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAGAAGCTTAGAACAGTACATGGTCATAG
EST25356 3b	95	C	G	...	...	TCTTTGATACAGGTAACCAGTTTGTAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGATAT CAGCACATCTCTGTGGAGAAAGCAGTGT[C/G]TATAAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26	A	C	...	...	TCTTTGATACAGGTAACCAGTTTGTA[A/C]ACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGCTATAAATGTCAACATCAGGATTTCTTTT
WI-17581c	99	C	T	...	...	GGGTGACGCGCTCCAGAATGGGAGGACAAGCCAATTGGGAGGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTTGATAATGATAGAACCCAA[C/T]TTAGGCGCAATTACATTGACGGCTCATGC
WI-17581b	86	T	C	ATTCAACATT ACTACCAGTT ATTTGATAA	CGTCAATGTAA ATTGCGCCT	GGGGTGACGCGCTCCAGAATGGGAGGACAAGCCAATTGGGAGGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTTGATAA[T/C]GATAGAACCCAACTAGGCGCAATTACATTGACGGCGTCATGC
WI-17596	86	A	G C	ACTTCCTTGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAGGCCTACT TCCTTGTGTGTAAACACTCCC[A/G]ATATTGTCGATTTCTAGCTATAAGAATGGGGCCACTAAGTGGGTC

ID	Pos	A1	A2	Seq A	Seq B	Sequence
WI-17623	46	T	C	...		TGTGGTTTTAATTTAATTTCCCATAATAATTAATGGTGGGCACATT[T/C]GCATGTGTGCTTACTGGGTC ATTCATATATCTTTGTGAAGCATCTGCTCCAATCTTTGCCTGACTTTGGAGTTTTTGGT
EST26419 1b	46	T	C	...		ATTTCATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGA[T/C]GGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTGAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGGACAGAGAATG
EST26419 1a	35	C	A	ATACAAAGGCAACTATGTGCAG	CAAGAAGTTTGGACTGCCC	ATTTCATACAGAGATACAAAGGCAACTATGTGTCAG[C/A]AACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTGAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGGACAGAGAATG
EST26780 5	69	G	C	...		TCAGCTTAATTTAAGGGACATGTAAATAAAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC AG[G/C]AGGTTAGACCAGTAACAACAACCAAGAAAGCAAAGTGCTCGTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39	A	G	...		TACTTCAGTTAAGGCAAATTCCACACAGAGACTGTCTC[A/G]GAGACGGGCACAGAACCAGACACC GTAGAAACACCACCACCATGCATGACGGGGAAGCAGAG
EST27152 1	101	C	T	...		CAAAGGATTTTATTTGTTCCCTAAAAAGTAAAAATCTAGAAAATAGCAACCCACTGCAAGAGAGTT CTATACTAAAACATTTTGTCAATCATTCTCTCT[C/T]TTCACATGGTGTACTCTTCATGTACACAT CATCGGAAAAACAGACTGA
EST27504 0a	33	G	A	GCACTTTGCAACAATTTAATAATTT	GCTGGTGTGATGCTACTGTAATG	TTTTTGCACTTTGCAACAATTTAATAATTTATC[G/A]CATTACAGTAGCATCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTCAGTATTTCTGTTACACACATTCTGTTAACAAGAACCCATACATT GGTAAATTCATTCT
EST27662 4	51	C	T	CACATTCTGTTCTCCAGTCTTG	TTATGGAAATGGCTTATGTAACC	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTCTGTTCTCCAGTCTTG[C/T]AGGTTTACATAAG CCATTTCCATAAAATTCTATAGCCTTCTTAGAGTAACACACTCTTGTTTAGGAATGTTC
EST27788 3	100	A	G	...		ATTTTATTAGGCGGTACAATTCCAAGGTGTAAGGGTGAAAGGAAGGCAGGCAAATACAT TATTGAGCTGAAAACAACTTACATTCAAGGAC[A/G]GCTTCCAGACAAGCCATGTAGAACCAGCAT GCCCTTGGGACTGTGTGGAT
EST27828 4	58	G	A	GGAAGTCATCAGAACCCCAC	GTGCAGAGAGGTACTCCAAGTAC	TCTTCTAAAACTTTCCTTCTGTTGGATCCCAGTGACGTGGAAGTCATCAGAACCCCAC[G/A]TACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58	G	A	AATAAATTTCAATCTGTCACACAATC	TCAAGAGGCCTTATCCATTT	TAAAATTTGAGATACATTCCCCAATGTAAACAATAAATTTCAATCTGTCACACAATC[G/A]AAATG GATAAGGCCTTCTTGACAAATTTCTGCCACCTCCGTTAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37	T	C	...		TCCCGGCTTCCAAAAGCTTTATTGGCAAATATGCTCTA[T/C]AAAGAATGATCAATCCTGTTGCCTCT AAGTCAATGGAAATGAAGAGCTGTGTCCAGGGACACACCGCCGTGCTGAAGGAGACTGCTGTGTGTG TCCACCTCTTATTCATAG

ID						Sequence
EST28483 7	31	T	A	GGAGTAAAAG GTGTTTCTTCT TTAAA	TTTCTCGCATT TATTTTTATAC CA	CATTTGGAGTAAAAGGTGTTTCTTCTTTAAA[T/A]ATGGTATAAAATAAATGCGAGAAACATTAAC GGAGAATGTACAGACAACAGACGAAGACATGAGTTGTTTCTGACTGTGACACATTGGTGAAA
WI-17724	50	T	C	TGGGGOCTOCC TGTC	TGGGTTGGCAG TGTCC	AGAATTGGTCGTAGTAATCGTTCAGGATTTCGGTGATGGGCCCTCCCTGTC[T/C]GGACACTGCCAACC CACAGCTGGAGGGGCACTTAAGGCACGTCATTTTGTGATTAGA
WI-17730b	68	T	C	...	...	TGAGCCTGGGGGAGAAAGACCACAGAAGTGAAGTGCTATTAGTTACATCATACCAAGTGTACATACTG T[T/C]CACATGATTTATGGCTGTGTTGATGTGATGTGAGTGTGTCA
WI-17730a	39	A	C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGGAGAAAGACCACAGAAGTGAAGTGCTATT[A/C]GTTACATCATACCAAGTGTACATA CTGTTCACATGATTTATGGCTGTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
EST29041 5b	53	G	A	GGAACAAACA CATTAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTCATGAGGAACAAACACATTAAGCATCATTGTCACT[G/A]GCTAACTCCT CAAATCAACAATACCCTTTATTTTAGCCATGAAAAC
EST29128 4	58	A	G	...		CTTTTAGAAGGACACCAGTCTTGTTGGACTTAGGGCCTACCCTATTCCAGCAGGTGCC[A/G]TTATTT TCACTTGGTTACGTCGTGTAAGGACCGTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTGCTGGGGACACT
EST29912 3	103	C	T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCTTCTG T	ATTTATTAGGTATCTGCTGTTGTGGGGGTGGGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAGAAAGAAAGAAACATTCTGCCAGCTT[C/T]ACAGAAGAAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121	G	C	...		TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAGTTAACTCACCATGAAA TTTAACCTTCTGTACTGGCTTCACTGAGGCAGTAAACTACATAGGGATAAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCCTG
EST30223 2	99	A	G	...		AAATAAATACATCATGGGGAATGGGGATATCCCCTCAAGCATTATTCTTGAGTTACAAGCAA TCCAATTACACTCTCAAGTTATTTAATATCC[A/G]GGGATTTAATTTCTTCCTAGTTCAATCTTGGGA GG
WI-16260b	86	G	A	...		CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAGAAAAGACCCAGA GTTCACACATATAGGTAGC[G/A]ATAACCAGGTCTCACTTCCCGTGAGAACTTCGTGGGAC
WI-16260a	59	G	T	TGAGGTGGATT CAAGAGAAA GTGAAACTCTG A	CTACCTATATT GTGAAACTCTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAGAAA[G/T]ACCC AGAGTTTCACAATATAGGTAGCGATAACCAGGTCTCACTTCCCGTGAGAACTTCGTGGGAC
WI-17835	30	G	A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTTCTTG[G/A]GCCTGTTTCCTATACCCCAAATATCATAAGAATT GTTGTTGCTTCTATAATGTTCAGCTTCAAATTCTTTGCTTAATCAATGAATTACCTGAATT TTCTCCTCTTGTTCAAAA

EST31951 4	87	C T	GGGTTGTCCAG CCAACA	CCCACCAAAT CACCTCC	ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGAGACTGAAACATTTCACTCTTTAGCAATGACA TCGGGTTGTCCAGCCAACA[C/T]GGAGGTGATTTGGTGGGGAATTCTTATCACAATTATTCT
EST31968 8b	95	T G	---		CGAATTTGTCTCTCTTATTTGTGATTCTTAGTAATCCTAAAAGATTTGGGGGCGGGGTTACTATAAGT GCATTTTATAATGGGGATTTTCTGCT[T/G]AACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTCCC
EST31968 8a	75	T C T	GCGGGGTTACTA TAAGTGCATTT GTGGGCAGTT	TGTAAGAATCA T .	CGAATTTGTCTCTCTTATTTGTGATTCTTAGTAATCCTAAAAGATTTGGGGGCGGGGTTACTATAAGT GCATTTT[T/C]ATAATGGGGATTTTCTGCTTAACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTCCC
EST32063 2	103	C T	---		TCCATGGATGAACAGACGCTACCATGCCACATCCCCACTTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCCTTCCAGACCTAGCTGGCTTTGTAGT[C/T]GTTCAGGCCCATTGAAAATAGCAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A G	---		AAGGCTTTCCAAGCATTCAAAGGCACTTGGGTGTTGTGCTCTAAGTTCTGGTCACTGCAGCCCC[A/G] TTCTGTATTAGGGAGCACCCCAAGCCCAGTAACAATATGGTTCTTGCAG
WI-17800	29	C G	GGGAGCACAA GAGAAACTCA TT	TTTCCTACAAT TAATCCCAGTC	TGGACATGGGAGCACAAGAGAAACTCACT[C/G]AAGACTGGGATTAATTGTAGGAAATATTTCACAG TTTCCACAAGTCAGAGAGCTAATCCCTGTATCTGGAACATACACTGCTGCCATTTCTGC CCATGAAGGGAAATACCC
WI-17857	34	T G	CCTAAAGTCTG GGATGACTTTC C	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCATTCCTAAAGTCTGGGATGACTTTCC[T/G]ATTCTACATCAAGTAGAACCTAAGCCAAT TCAGAATCAGAATCCTTTTGTCCATCAAATTCCAGCTAACTCCAAGCTGAATTAAATGTTCATTCT
WI-17860	121	T A	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTTAACCATGGCCTGTGTCATGATTATATTGCTATAAGGAAGGGAACAAAATCTTA TAGTGTCCAAAGATAATAATTCTTGGTTAAATCTTGCCAGCAAAGCAAATA[T/A]CGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43	A T	TTTTATAGCCT ACTTCTCAAA ATTGTT	CCGTTGTCACT AATCACACAA A	CAGCAACCTTTTTTGTTTATAGCCTACTTCTCAAAATTGTT[A/T]TTTGTGTGATTAGTGACAACG GGGGAATCTACAAATGCTCACATCACAGTAAACTACCA
EST33301 4c	80	G A	---		GAAAAAAAGTCAAATGTGTTCCCTTATGGGTGATGCCACCATGTGCCTCACACAAGCATGATC AATCGCCACGAGA[G/A]ACTGGATGCCAAAGAGTATGG
EST33301 4b	63	G A	---		GAAAAAAAGTCAAATGTGTTCCCTTTATGGGTGATGCCACCATGTGCCTCACACAAGCAT[G/A]TGG ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44	G A	AGGCGTGGTTTT CAATACTAAA ACA	CTGTATTTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGCAGCGCGTGGTTTTCAATACTAAACA[G/A]TGTAAACAATGCAAATATT TAACAATAAATACAGTGATTAAATAAGCCATGCATATCCAGTTGATGTAATACTTTGCAA

Name	Num					Sequence
WI-17904	50	A	G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACAC[A/G]TACGGGAATTAC TATTAACATAAGCGATAACATCAAAATGCAGTTAAAACAACAACAAATGA
EST341495	69	A	G	TGCCAAATAC TCAAGTGTGA AT	AACTACTAGCCG CG	GTTTTTCTTTGAGTGACACAAGCTTGTTCATTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA T[A/G]GATTTTATTAGTTGTTCTCGCTAGTAGTTTTGGTATTCATGAAAAAAGCAGCTAGTTCAGC TTACAAATCACACAAGT
EST343438	95	C	A	---	---	TGGGAAAACATAAGTAACTCAAGAATATATTCCAGTCTTTATGTTACTAAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTC[C/A]TACAAAGATTAAAGAAACTTACCATCAAACACTTC CAGTGCATCAA
WI-17982	98	C	T	GGACCATATG ATATATAACT CCTAAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAATTTAATGGAAGGAACCACAGGTATGTTGAAAGAACATCAGCTGGAGACAGG GAGGGGACCCATATGATATATAACTCCTAAAAGC[C/T]GGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118	A	C	---	---	CTCAGTAACTCCGGTGTATAATCTGCCATTTATTGATTTATTTATGATAAAACAACCTCTCATTGTGA AAAACAGCTAAGGGTGACATCTCCAGACCCAACCACTGTCCCTGTAATGT[A/C]CTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84	A	G	GTAGAGGCGA AGGGAACAG CAGC	AGGCACATGGG CAGC	CCCATCCAGAAACCCCAGTGTGATGGTGGAAGCAGCATGAAAAACAACATCTCCCAGGCCTCGCAGT AGAGGCGAAGGGAACAG[A/G]GCTGCCCCATGTGCTGTCTCTAAAGACGGCCACCCTCAGGTTGATGT CACCTGTGGGGACGGGGT
WI-17136	33	C	G	---	---	ATTCTTATAAAAACACCATGTCCCTAAAAATGTC[C/G]ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAAGACAGAGAAATGTGTCCCT
WI-18041	24	A	C	---	---	GCCACTGAAAAAGGTGCTCTTCC[A/C]GTTTCTAACTCCCTGACTCCCTCATTGGAACTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTAGACTTTGCTGTATTTAAAAGGCAGTGTTGATGCTCCAGGAT TCAAATACTTAATCA
EST351648a	57	A	G	CACAGCCCTGC CCCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCTCAAGCACAGCCCTGCCCCC[A/G]TCTTGA GATTCAGAATCCAGAGGGTGCTCAGTCCTTGGTTAGGTGCTTCTGTGACATTCCTCTTG
WI-18052b	67	A	G	---	---	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTTCTTCATGTACGAAATC[A/G]TTGGTTACACATCTTAG A[G/A]CAGCAGAGCTGCCTGAGGGAGGGGTTGTGTTTAATGTCGTATGCATGCTCAGCACAGTGCTGGC ATGGCCCCATCCATGCTT
WI-18052a	50	T	C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTTCTTTCATGTACGAAATC[T/C]TGGTTACACATCTT AGAACAGCAGAGCTGCCTGAGGGAGGGGTTGTGTTTAATGTCGTATGCATGCTCAGCACAGTGCTGGC ATGGCCCCATCCATGCTT
WI-18054	46	G	A	GGGAGTGGGG GAGTAAAA	CGTCACCCTGC TTCCA	CTGTTGTGCTGAGAAGAGCTGAGAAGAGGGTCAGGAGTGTCAAGGGAGTGGGGGAGTAAA[G/A]TGGAAGCAGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTTTGCTCAGGTTGGTAGCAACAGAGGTAATG

ID	#	Alleles	Seq 1	Seq 2	Full Sequence
WI-18064	54	G A	GTAGCTGCTA AGCTGTATTTC AGA	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAACCCTGTGGGTAGCTGCTAAGCTGTATTTCAGA[G/A]GAATGTCAC AATCATACCACTGGGGAGAAAGAGTAAGCACAGTGCTTATTAGGTGCCAAACTGGGGTACCTGGGAG GCAGAAA
EST355347 2	97	T C	GCATAAAAATT TTCCAGTTGGT AA	CCCTCGGCACC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATTCTTGATCATGGGGTGGAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAAATTTTCCAGTTGGTAAG[T/C]AGCAGGTGCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28	A C	AACCCACTAC TTACTCAGAGT CGTGTAT	AAAACTAATA AGAAACTGGA GGTTTTT	AAACCCACTACTACTCAGAGTGTGTAT[A/C]ATATTAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTTGATATTTTCTGTACTCAGAAGCATTTAGGTTGCAAAGGATATAA
WI-18080c	80	C T	---		TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTGTAATTAAAATCTACTATGCCGTG TTTGACTTTTAT[C/T]TCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTCTCCTTTGGTGTAT
WI-18080b	65	G A	---		TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTGTAATTAAAATCTACTATGCC[G/ A][T]GTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTCTCCTTTGGTGTAT
WI-18080a	41	T C	GCAAATATCA ATATCAAACT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTC[T/C]TTGTAATTAAAATCTACTATGC CGTGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTCTCCTTTGGTGTAT
WI-18086	63	G A	---		GTGGGCATCCTATAAAGCAGCCATGTTGAAACAAATGATATGCACAGAAAGCATACTTCT[G/A] TGGCTTGTTACACGGGTTCTTCTTCAAGGAGAGATGACTCAGCCCTCCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTTGAA
WI-18115b	71	C T	---	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAAGCCTTTAGTGTACCTTTGGTATTCCC TTC[C/T]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAGGGGTGGAG TCAGT
WI-18115a	70	C T	TTAGTGTACCT TTGGTATTCCC TTT		AACTACATAGTAGTGGTGCCTGGCTTAGAATCAATGGGTAAAAGCCTTTAGTGTACCTTTGGTATTCCC TT[C/T]CTTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAGGGGTGGAG TCAGT
WI-18136	78	A G	---		TTTTGAGAAGCACTCTGTAAGGCAGGATGCATTCAAAAAATGGCTTTGAGGATTAATCTTCTCTTTA GGTAATTTGC[A/G]TAAGAACAATAAAAGCATTTTAAAGTCCACTGCCGCCTTAGAAACT
WI-18169	115	A G	CCATCTTTCCG GAGTTCTGCTT GTGCTCCA		GGCAAAAATATTTTACATCACACCTGGAATCTGCCCAAGTCTTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTTCCGAAGCTC[A/G]TGGAGCACAAGCAGA ACTCGGTGGGGTAGAGTGGA
WI-18190b	26	G A	---		TGAAAGAAGTCGACACAGCGGACACT[G/A]TCATAAGTGGAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGACGAGGAGCAGGACAAAATCAAGAATCAAGAATGAGCTGGAGACATTAATCCTGGCGA

ID	Pos	Allele	5' fragment	Sequence
WI-18190	62	G A	---	TGAAAGAAGTCGACACAGCGGACACTGTCATAAGTGGAACAAAGGATGAAGCTAATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGGACAGGGACAAAATCAAGAAATCAGAAGTGAGCTGGAGACATTAATCCTGGCGA
WI-18181	100	A C	AAATATATAC AACACTCCCTT CAGATC	GACAGTGAAAAACATTGAAAACAACAAATACAACAAACAAATGTAAATCCAA TGTGTGAAAAATATATCAACACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAACGTA TGTGTTCTTGAAC
WI-18215	78	G A	AGCAGAGTTC CTGCCCCTC	ATTCATACAAGCATTCCTGAGTACAAACTAGGGGACACAGGTATTTCACAAAACAAACATAGAGCAGA GTTCCTGCCCCTG[G/A]GTGTGCGGGGGAGAGGAGGGGAGGGGATTCAGCATTTGGTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60	T A	TGGTGTTGATT GTGATACACTTT AA	CATTTCCGAAAATCTGATAGTTAAAATATCCCGTCTGGTGTTGATTGTGATACACTTAAGT[T/A]GAA CCCCTGAAAACCTTTATTTGAAATTGAAGTTTTGCTCAGAAACTGGGCAGAACTTTCACATTCTG AC
WI-17892	76	T C	GGAAAACTTG AGTTTGAGATC ACA	TTTAAAAATGCTTAGATTTCCTCAGTATTTATCAATAGTGTGTAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C]CTGTCTCCACTAGTCTATTCACTTCTGTGGGCATTCGGCAGAAGTGGC
WI-18242	30	G A	CCCCAAATGTT TACTGTAACGA AATCGTAACA CTTTC	AATATCCCAAATGTTAATGTTAACATATACTACT[G/A]GAAAGCTGTTACAGTAGAAGTGTTAGCAAAAAT TGGATGCCACAACTTATCTCACCATTCCTTTCAAGCAAGTGAGGGTCAGGGTCTTCTTGCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119	C T	---	GCATCAGAGACATCACCACTCCTGAAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAAATAGGAAAATATGGACTATCTTCAAACTGCACAAATGATCGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124	T C	---	GCATCAGAGACATCACCACTCCTGAAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAAATAGGAAAATATGGACTATCTTCAAACTGCACAAATGATCGCATGAATCCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97	C T	AAATAGGAAA TATGGACTATC TTTCAAA	GCATCAGAGACATCACCACTCCTGAAAAAAACCTTCTACAAGAATTGAAAAGTGTTGCAGGACCTAATA CTGAAATAGGAAAATATGGACTATCTTCAAA[C/T]TGCACAAATGTGAATCCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73	A G	GCTGTCAGCTA TTGTTATTTCA AA / GGAGAAAAGG GAGCAGAGAGA AA	CTGAGCCTCTTGGATATGTGGTTAGTGTCTATCATTAATTTGGAAAGCTGTCAGCTATTGTTATTTC AAAT[A/G]TATCTTCTGCTCCCTTTCTCCCTTTTCTGGGATTCTCATTCTGCATGTGTTATA
WI-18330b	66	A G	---	AAACATCTACAGCTGTCTCTTAGGCCATCCTGTAAGAAATCAGGATAAGAGCTGAGGAACAAGAGGG[A/G]TATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAAACATAATTTTTTGTTGAT TCACA

Marker	Pos					Sequence
WI-18330a	49	G	A	TCCTGTAAGA AATCAGGGAT AAGA	AGTCCTGACTC ACTGCCTACA TCACA	AAACATCTACAGCTGTCTTAGGCCATCCTGTGTAAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGAGGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACCATAATTTTTTGTTGAT
EST375645	85	T	C	AAATTCAAGC CATCTACACAA AGA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAAATTCAAGCCATCTACACAAAGAT[T/C]TCTCATTGAGGCCTCCATAGGCTGCAAACACATCAAAGGCATTACTGTACTGGAGAGGACTGAG
WI-18327	104	G	A	AAACAGCTTT CGTTAGGCTAG TT	CGCATACAATG GCTCAGC	CAAAGGGATTTTATTACCTACAACAACAGTAAGGAGGACAGCTGGGGGCAGTTTCCCAAAGCAGTACCTCCCAAACAATGGTGAAAACAGCTTTCGTTAGGCTAGTT[G/A]CTGAGCCATTGTATGCGGAGGCAGAGT
EST376246b	102	G	A	---		GTGGCAAGAGCAGCTAAAACACACTCATTTGCATGAACTCCAAATACGAACAGTGCACGCTGATGGCCTGCAGTCCTGCCGGTGCTCTGCCGTGCTCTGGACG[G/A]TTCATTCTACATGGCTGCTGCTTTGCGTCCTCTGACCTCCCATTCC
EST376246a	58	C	T	---		GTGGCAAGAGCAGCTAAAACACACTCATTTGCATGAACTCCAAATACGAACAGTGCA[C/T]GCTGATGGCCTGCAGTCCTGCCGGTGCTCTGCCGGTTCATTCTACATGGCTGCTGCTTTGCGTCCTCTGACCTCCCATTCC
WI-18357	89	C	G	CCCAGCCCCTTA AGACTGAAGAT GA	AAGGACTCAA	AATGTTTTAAAAAGTCTACCGTGCTGAGGTGGCCATGAAGCCAAGCCCATGGAGAGACATTTCAGATAATCCCAGCCCCTTA[C/G]TCATCTTCAGTCTTGAGTCGTTCCAGCGCCCAGGTCCAAGCTTGTGGACCAGCAGGACAAGCC
WI-18012g	117	A	G	---		TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTCCAGACTTGGAAGATCCCCGGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCCTCGTGA[A/G]GTGTTTCCTGATACACGCTGACGTTTCGAGGG
WI-18012f	113	G	A	---		TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTTCCAGACTTGGAAGATCCCCGGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCCTCG[G/A]TGAAGTGTTTCCTGATACACGCTGACGTTTCGAGGG
WI-18012e	112	C	T	GCCACTTTGC CCCTT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTTCAACTTTCCAGACTTGGAAGATCCCCGGCTGTCCACTCTTAGAATTGAAGCCACTTTGCCCCCTT[C/T]GTGAAGTGTTTCCTGATACACGCTGACGTTTCGAGGG
WI-18012b	46	T	C	---		TTTTATCTGGGTCAGCTCCTTCTTAATGGCCTGAAGGTCATCTCCTT[T/C]TCAACTTTCCAGACTTGGAAGATCCCCGCTGTCCACTCTTCCACTCTTGAGAATTGAAGCCACTTTGCCCCCTCGTGAAGTGTTTCCTGATACACGCTGACGTTTCGAGGG
EST383904	75	A:G		GCAAAAAGGA CTCTGCATTG	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCCAGAGTAATTCCCATGGTTATGTTACATGGCAAAAAGGACTCTGCATTG[A/G]ATTAAGTTTATTAATCAGCTGACTTAGCATTGGGAGATTATTCTGGAT

EST	pos	a1	a2				
EST385127	91	T	G	TGACGATGCC AATACTTCG	GGGAAGC	CACTGCACTCT	TAATAAAAACTGACCCAATTGGTAAAACTGTGTCTGGACTGAGAGAGAAACAATGAAAAAATCTGTAAAT ACCTGATGACGATGCCAAATACTTCGT[C/T][C/T]TCCCCCAAGTCCTAACAGAGTATATTCCTCTGGAAAA
EST385190	24	C	T	CCTGCACCTCC TAAAAGATCT T	TCTGTTAGGAC TTGGGGGA		CCTGCACCTCCTAAAAGATCTTTT[C/T]TCCCCCAAGTCCTGCTCTCGTTCAGCTTGATTTTTTGTCCTTGAGAACCTTG TCCTCCCTGCTGATT
EST385751	66	T	C	GAACATCCCA TGTTTCTGTTT AA	AGGGAAGGTA GTATAACACAT AAGAGA		AGTGGTCAAATGTAAAACTAATGGGACACCAAGCCTCAGGAGGAACATCCCATGTTTCTGTTT[C/T]TCTTATGTGTTATACTACCTTCCCTTCTCTTATACACATAGATTTTCCTTAATTGCAGC CCA
EST386169	101	C	G	CCTGCTCCGCC CTTC	GAGGAATGGAT GGTGGC		CCATCTAGGCAGGCTACCTGAGCTCTCTGTGCTCCCAGAGTGGGTGCCTCACGCCCCGGGCCCCGTGG AGTCTCCGCGGGCCCGGGCCCCTTC[C/G]GCCACCATCCCATCCTCCAGGGG
EST386528	59	T	C	TCTGAACTGGG CATTTCAA	TTGCAAAAATG AAAGGAAAAA		TATAGTAGGTACTTCCTTGCTGCAGCAGGAATTATTCAGTCTGAACTGGGCATTTCAA[T/C]GCGTG GTATTTTTCCTTCATTTTGCAAGTAAAAAAATCAT
EST386545	42	T	C	AATGGTCATTT TAATATATCA GTTTACA	CAGTGATGGTC CTTAATCTTCT ATC		CTCAAGCTGAGAATGGTCATTTAATATATCAGTTTACATA[T/C]AGATAGAAGATTAAGGACCAT CACTGAGGTCACATAGCTCAGAGGCAGAGTTAAGATTGGACCCAGGCAGGTTGGTTCCAGCATATA
EST387079	75	A	G	...	...		GGATCCTCACTCACCTGGGACAGCCTGAGAAGGGACATCCCACCAAGACCTACTGATCTGATCTGGAGTCCCA CGTTCCCC[A/G]AGGCCAGCGGGATGTGTGCCCCTCCAACTCATCTTTCAGGAACACGAGG ATTCTTGCTTCTGGAAA
EST387592	86	A	G	TGTCTCCCTGA GGGTGATATGG	TCACCATCGTG GACTTAAGG		TGACCTTGTATTCTTCACTAGAGGGGAGAAGAATCACCTACCTTTTGGATGCCTCCCACTCTACTTGT CTCCCTGAGGTGATATGG[A/G]CCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAATTCTTGCC TAGCAGCACC
EST387751	40	T	A	AATCAATAGG AGAGGATTGG C	GGCTTTGCTCT GAATTCAAA		GACTCTCAACCAAAGAGAAAATCAATAGGAGAGGATTGGC[T/A]TTTGAATTCAGAGAGCAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCTTCCATGAGTTAGGATCTCCTAAGTGGTAC AAACAAACCAACATGGTGG
EST388154	91	C	A	TGTTTTATGAGA ACCCATTACA CA	GCTGACTGGCA CATGCTTT		CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACTTATGTGTTGTTCATTCAACAAG TGTTTATGAGAACCCATTACACA[C/A]AAAGCATGTGCCAGTCAGCAGATTCAGTAATAA
EST388584	98	C	T	CACGAGTAAA AAGAAAACTCA TGAC	GGAGCGAGTCC AAGGAGAA		TCTTTACTGTGCTTACAACTTTCCTCCCAAGTTTGCGGTGGTTTCCTTGGACTCGCTCTCCCCAATCTCGAT TTCAACACGAGTAAAAAGAAAACTCATGAC[C/T]TTCTCCTTGACTCGTTGGTCTGTGAGAATTTGTGTCG ACCGGACTGCACTGTTG
EST388652	72	T	C	GCTGTAGAATT CTGTGTCGATGC	GGAAGGACGG AGGACACAG		CCTTAATGGATTTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTCG ATGC[T/C][C/T][C/T]TGTGTCGATGCAGGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGTCTTAGTTGTTAA

Name	No.					Sequence
EST38878 9	47	T	C	AAACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCCT CA	CCAATGAGAACCAAGTAATTAAACATCATTACTAGCCTAGATCCTAA[T/C]TGAGGAGGACATGAGATTTATTGAAGGGAAATCCTCAATTAATATGAACATTCTTTATTTGTTTATTTGTTTCACTTTCTCAAATATCGGATTGTTGC
EST38882 6b	113	G	C	---	---	TTATTCAATGTCATCTCACACATTCTTTATTTTA[T/C]TTGTTTCACTTTCTCAAATATCGGATTGTTCATGAGAATAATGGCTGGCACGGCAGTCTTCTCAGGCTCCCTGGATAGCTAAATTTTA
EST38882 6a	35	T	C	TGTCATCTCAC ACATTCTTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	TTATTCAATGTCATCTCACACATTCTTTATTTTA[T/C]TTGTTTCACTTTCTCAAATATCGGATTGTTCATGAGAATAATGGCTGGCACGGCAGTCTTCTCAGGCTCCCTGGATAGCTAAATTTA
EST38909 5	47	A	G	GCACAGCATG GCTAAAACG	GGTATTTGTTG ATTCCCATCTT T	GCACTAAACTAACTTTCATTGTGGATTGCACAGCATGGCTAAAACG[A/G]TAAAGATGGGAATCAACAAATACCATTGAAGATATGGAGCAAAGAAGAACTCTCACATACTGCTGAGGGAATATAAATT
EST38911 9	85	G	A	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	AACTGAATGGCAGTGAAAACACTACACATCAAAACTTAGGGAAATGTGGTTAGTGTGGTACGTTGAG GGAAACTTATAACCTCAC[A/G]CGCTTGTTTCACAAACAACAGCAGAACAACAGAGATTCCAACTCCAGCAATGACAGGCTAGGG
EST38955 5	30	G	C	TGAATTCCCTT CACTGCAATCT GGTGGG	CACCCCC	TAAACATTCCCATTGAATTCCCTTGGTGGG[G/C]GGGGGGGGGGTGAGATTGCAGTGCTCAAGATAAATATCACAAATATATCAAAAACTTCAAATTGTCTATGCATTCACACACTGACACTGAGCCACAAACATTCCTTTCACAGGGGACTGTAC
EST39002 0	42	G	A	GGACCCCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGCAGATCCCGGACCCCTTCGGTGACC[G/A]CAGGCTCCCTGCCAGGGCTGGCCCCTGACGTGTGGAGGAGCTGAAATACGCTGAACATCCGACAACCTC
EST39004 8	79	T	G	GGTGGTAAGG CCTAAGGAAT CGGC	ATCTCGGCTGG CGG	CACGTGGCCCCTAAGTTCCGGGTCTTCCTCCAGTCTGGATGGCCGCCAGCCGAGATGGTCCTGTAAGCCTGTGGGTCGGTGGTAAGGCCTAAGGAAT[T/G]GAGGGGCAGGGGGCGGGGGCGGATGCCGGCCAGCCGAGATGGTCCTGTAAGCCTGTGGGTCAAAGACCTAACTTCTGGA
WI-16398 0	90	T	C	TCCCTATTATT CCATGATATTT CTCA	GAATGGTTGT GAAAAATATA TTGATAT	AAAGATAATGTCATCACAACGCAACATATAGAAACATAAAGAAATAAAGTATCCACCCTAAAATCCCTATTATTCCATGATATTTCA[T/C]AGCAACTAGTATATATTTTTCACAAACCATTCAGTTACAC
WI-16403 9	69	T	C	CCTTTGTCCTC AATTTTTAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGTCTTTCATGTATTTTTCTCATTCCTATCAGGTTTCTGGTCCTTGTCCTCAATTTTTAACACT[T/C]TTTTTTATATAGGGAATTAGCCCTTAAACTGTGGTACATGCTGCCAAATTTCCTCCCAGTT
WI-16406	24	C	T	GCTTTAATGGC TACAGAAAGA AGG	ATGTGTTTAAA AA	GCTTTAATGGCTACAGAAAGAAGG[C/T]GGTTTTATTTTCTTTTTTAAACACATCTGGTTCTGCGGCAGCAAGTTATATTATTGCATTTAGAGCAATAGGTGCCCTGAA

Marker	Pos	A1	A2	Seq a	Seq b	Sequence
EST392360b	57	C	G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTTATTCATGATTGTTTCATCTGAGAATAAACTTCCTGTCTAATTTTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATATGAGACTGGAAATATTACCTGGCAAATGAATGAGGTGTCTCTC TTT
EST392944	63	G	T	CCTGAAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAGTTACCCGGCCTTTACCCCACGCC AGCTCGCTTGCTGTCTGCAT
EST393662	72	T	C	...	...	AGAAACACATTCTGTCTGATCAGAGGAAGAGATGTATGTAGAAAATCAGAATCTGACTGAATTCCTAAA ATCTAT[T/C]ACACTGAGAGGAAAAATGAAAAGAAAAATGTTTGCATAAAGCTTTCCCTGACTCTCA GAGGGGTTCAGA
EST393719	86	A	G	CATTTGGATTA GCGGTGAGAGG	TGATTTGAGAC ATTTCACATTT TT	AAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTTATGTGTGTAAATTCCCAGTTGAGCATTTTTCAT TTGGATTAGCGGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAATCAAATGCTTCCTTCTAAAGATTA GACATTTGCCCAACCCTGC
WI-17177	23	A	G	...	...	ACAAGTGACATATCCAACCAACCA[A/G]TCCATCCCACCTGTGCCCTATTCTTTCCTTGTGTTTCTTT AGAGCCTTTCAGCTATTTCCTGTGAAGCAAACTGCACGAAGGCCTCCCCCGTACTCCTCCCCCCTGGAA G
EST394288	31	C	T	GCTCCCCACA ATTTTGATT	GGTCCCTTATG AAGCCACC	AGGTTCCTGGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCTGCATT TTCTGGGTGGGGGCCTAGGTAATTCTGTTGCCTTTGGTCCCACAGAGCACAATTAAAGAAGATCAGGTCT GGCTGTTGC
EST394302	45	A	C	GGCAGAGGAA TAACTGATGTT C	CAGGGGTCGGG GTATTG	AATTTAGCAGAAAACAATGAAGTTGGCAGAGGAATAACTGATGTTC[A/C]CAATACCCGACCCCTGA CCCAGTACCTTTCCCTCAGGCCCAGGCTCCGGTGGAGGATGTCCTGGG
EST394467b	117	C	T	CTACTGACAT AGGGACTTCA GAGTAA	TCCTGGAAAAC TGACATAAACC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAGAAAATAACAGGAACCTATTTATAT ACGTAAATCACTTCATACCTGCCTACTGACATAGGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST394652	80	A	G	AATGCAGGAG GGTGGC	CAATCTCGGCC CCTCT	ATGGTGTCATTAGAGGGCCACAGGGGGCCACAGGGGGATGGGGGGAGTAAAAATAACATAAACGAACAGAAA TGCAGGAGGGTGGC[A/G]AGAGGGGCCGAGATTGGGGTGTTCAGGGCAGAGAGGTGGAAGACCAG
EST395010	81	A	G	AAAGATTCCT GTAGACATCT AACATTAG	CACTTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTCAGACATTCTTGACAGCCTAAAGATTCCTGTAG ACATCTAACATTAGT[A/G]TAGCCTTCAGAATTGCAAGTTCAAGTGCAAACCAATTC
WI-18387b	84	A	C	...	...	CACAAAATGGGACTGCTGAAGAGTGGGACAGTTGGACCTTACTTTGGTGACCCATACATTTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGTAACATTGACTATGTAAGTGTAATGTGCGATG GCTATGTGTAGAGACATAAAGA

Name	Pos					Sequence
WI-18387a	57	A	G	CCTTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAAA	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGTGACCCCATAC[A/G]TTTGTG GTCACATGCTTTAGCCATACACACATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAATGTGCGATG GCTATGTAGACATAAAGA
EST406019	78	A	G	GCGTGGAACCT GAAACAC	TTCTTGGAAGA AAGGCGTC	TCCCAGGATGGTTATTCCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGGTGACTCGGCGTGGA ACCTGAAACAC[A/G]GACGCCCTTCTTCCAAGAAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32	A	G	AGTGTATCAC ATCTTCAGGAT AGGT	GCACACCCTTC ACACTGTTA	TCCATTCAGTGTATCACATCTTCAGGATAGGT[A/G]ATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTTGTTGA
EST43091	28	C	T	CATTCTGGTCT TTATTTTTGGA CA	AAAAACTGATTT GTTAAAACATG CTAC	ATGTCATTCTGGTCTTTATTTTTGGACA[C/T]GTAGCATGTTTAACAAATCAGTTTTCATAGGCAA CCTTTTGAAACATCACAAAGAAATACAATATATTTTCACAAATTTCTCATCACTGTAAATTCA
WI-18420c	108	T	C	TTCCATTAAAC AGGAAGTTTC C	AAATTCTCAGC ATTGCTATAAG C	AGAGAGACAACAACAAGAAGAAATGGGAAAATTAAAGCAAATCTTGGA TTCAGATTCCATTAAACAGGAAGTTTCCTCAAAAAAATCAAA[T/C]GCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38	C	T	GAATAAGGGA AAATGGGGAAG AA	CCAAGATTGC TTTAATTTCAC TC	AGAGAGACAACAACAAGAAGAATAAGGGAAAATGGGAAGAA[C/T]AGAGTGAAATTAAAGCAAATCTT GGATTCAGATTCCATTAAACAGGAAGTTCCTCAAAAAAATCAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101	T	C	...	...	AGCTGATCAGCTGTCGTTACTGTGTTTTATGTGTGGCCCAGGGAAGCCAAAAGATCAGACACCCTGTC CTAGACAGATTCAATGCACAACAACAGGAGG[T/C]GGGGGTCACGGGGTCACGGGAGAGCCAAAGAC TAGGGC
WI-18425	81	A	C	CACCCTGTCCT AGACAGATTC A	CCTCCTGTTGT TGTGTGCA	AGCTGATCAGCTGTCGTTACTGTGTTTTATGTGTGGCCCAGGGAAGCCAAAAGATCAGACACCCTGTC CTAGACAGATTCA[A/C]TGCACAACAACAGGAGGTGGGGGTCACGGGGTCACGGGAGAGCCAAAGAC TAGGGC
WI-18449	129	C	T	CTTTTGGCTCT AAGTGGGACT A	CTCCCCTGACT GTATCCAGA	AAATTGAGGTCCGGGTGGAACTATAAAAGGAAAGAGAAGTAATCAAGGGAGGCCAAAGTG GGAAGCTGTATTGCTGATCTAACGTGCTGTTCCAGTTCCTCTCTTTTGGCTCTAAGTGGGACTA[C/T]TC TGGATACAGTCAGGGAG
WI-18457	120	T	C	...	...	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTGCCCCCAAGACATTATTTTATTCTT AAATGTCCAATATCTGCCTGATGTCTGTGTTTGTGCACATTGGGCACCACAG[T/C]AAATAGGCTAAA AGGCAGTGCCCACCTGCT
WI-18462	39	A	G	CCACAATGGC AGAGGTGA	TTTAGGCTTTG AGATGGTTTCT	GGTGCTATAGCTGCTTGTGTACCACCACAATGGCAGAGGTGA[A/G]TAGAAACCATCTCAAAGCCTAAAA TATTTACCATACAATCCCCTCACAGCAAAGTTTGCTAATCTCGGGTTTAGGGACTCCATTGAG
WI-18476	60	C	T	GGTGGGGGTGC GAGG	GCACGGATGGGA GTGACC	TGAGGACGTGTGACAAGCTCCAGCAGGGGTGGGGGCCGGCGGGGTGGGGGTGCGAGG[C/T]GGT CACTCCCATCGTGCCCCTGCGCCTCCCCACCACCACCTGCCCACCTGCGGGGTGCCAGTTCCACGTTGAGGT

Name	No.			Seq 1	Seq 2	Sequence
WI-18491	109	G	A	AACAAATGGT AGGTGGTATT AATACTATT	CGTGTGCATT TCTTGTAATCC CGT	CTAATGAGATGAATACATGGAAGGCGTTTAGCACAGTGCCTAAAACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAATACTATTATTATTAAATCCCAGAATGAC[G/A]GGATTACAAGAAAATGCACA
EST50757b	79	C	T	GAGCTCGAGG CTGCTTCT	ACCCTTCACCC GCCC	AGCCCCTCCACTCCACTCTGCTTCCACAAAGTCGGCTCCGAGAGCTCCGAGGCTCGAGGGCTGCTTCTTTTTATAT GTGCAGGGCC[C/T]GGGCGGGGTGAAGGGTCAGAGA
WI-17675	103	T	C	GGACATTTGG ATGGTGACTT CAGG	GGGGAACCACC	GATCTTGGAAAGCACTAGAAACTAAACATCTTCACCAGGTGCTGAAGAAAAGTGTCTTCGTTTAAT TGCCAAGCAGGGATGTGGACATTTGGACTTT[T/C]CCTGGGTGGTTCCCCATAGATTCACCAT TGCCTCTAATGTGTCTA
WI-16543	67	G	T	AGATAAACTA CATTTGGGTTT TGG	GATTCATCATT ACAGGGGACTT	GATCCATTACCTAGGGTAAAATTCTCCTGAATGTCAAACAAAGAGATAAACTACATTTGGGTTTTGG [G/T]AAGTCCCGTGTAATGATGAATCAAGAATCCTCAAGTGTCTTGCCACCCATTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C	G	GCCAAAAAGG TTGGGGGAA	TTACTTTGTA CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAAACCATCTCCCCCTGACCCCCAGTCCAGTCCATGGAAAAATTGTC TCCACAAAACCGGTCCCTGGTGCCAAAAAGGTTGGGGGAA[C/G]TGCTGGTCGGTACAAAAGTAATT G
WI-17690b	79	A	G	---	---	ACAACATGTGAAAGAAGAGATATGTTGTCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTGTTGATTT GGCTTCCCTAT[A/G]GATTCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTG
WI-17690a	63	G	A	AGGCATTTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCCTGAATC	ACAACATGTGAAAGAAGAGATATGTTCCCTATAGATTCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTG TTTGGCTTCCCTATAGATTCATCATCCCAGATTATTCTGAAGTGGAAACCACCCTCCGACCCCAA
EST51717b	128	C	T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAATCTCAGTGTCTAACTCATCATCCCAGATTATT[C/T]TGAAGTGGAAACCACCCTCCGACCC CAATGGCAACATCACCCACTACCTGTTTCTGGGAGAGGCGGGAAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCTCAAA
EST51717a	39	C	T	---	---	TTTCCAGGTTGACAGGTTTTATTCCACCCCTTCACCCCTTGGGGCGCC[C/T]GGCGTGGCAGAGCCCACTGGGTTTACATTCTCTGT
EST53012	97	C	T	TGGTCACTTTG GGCTCTGCCCA GGCC	GGGCAGGTGTGGACAC	GATCCAATCTCAGTGTCTAACTCATCATCATCCCAGATTATTCGGGAGAGGCGGGAAGCCAGGAGGAGGAGGACAG
EST53349	96	A	G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTCACATT TT	AAACTGCAAATAACAAAACAAAACAGAAGTCCAAGAAGGCTAAAGTCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACAATGTAC[A/G]AAAATGTGACAAGATATCCAGATGTTTAA
EST53389	74	A	G	GGAGACCTGC AGAACTTAAA CAATAAATGCT GCA	GCCCTTTCTAA CAATAAATGCT C	TTTCGAAATGTCCTCCATGAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAATAGGTTTTAACATGAAC TAAACAC[A/G]... ACATTAAAGGGAGATGGCC

EST	Pos			Fragment 1	Fragment 2	Sequence
EST53477	61	T	C		...	TTTGAGAGGTTGTGCAAAACTACTGTATTTACAAAAATGGCACAAAAGTGAATTCAACAGTT[T/C]AA TGCACATGCATACTTCACATCTTCACATCTTCAACAACAAAAGGTATTCTAACTCTACAGAACTGAATATT AGCTTCAACGGCAGCTGTT
EST64622	91	T	C	CGAGATTTTCT TCTTTATTTTA TATTTTCA	CCAAAGAAAA TGGCCTTCAGTA A	GGGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTTAAACTCCCGAGATTTTCTTCTTTATTT TATATTTCATTTTCATCCTAA[T/C]TACTGAAGCCATTTTCTTTGGTAACTTTAGA
EST67268 a	77	C	T	TGTGTATAGCA CATACTTCAGG C	ATGGGGTGGTG CGGC	CTCATCTTTATTATAAATGCATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATAGCACATA CTTCAGGC[C/T]TGCGGGCACCACCCATAGAGATGGTGAGGAAGTAACTTCTGCTTCTCATTGAAACT GTAGATCCATCGGGGA
EST78503 a	26	C	T	ACGACGCCCGG GCGAGT	GCATTTCCGCG GCAC	GAAATGCAGAAACGACGCGGCGAGTT[C/T]GTGGACCTGTACGTGCCGCGGAAATGCTCCGTTAGCA ATCGCATCATCGGTGCCAAGGACCACGCATCCATCCAGATGAA
EST80253	92	G	C	...		ATGCACTTTATTGGCTCCCAGGGAGTGGGATGCAGGATCAGAGTGGACGAGGATGACACGCGCAGGGGGCTGGTGTG GGGGAGCAAAGCGGCGGCCGTCGCCC[G/C]GGACCCTGGTTCCCTGAGGACCAAGCGTGAATGGGGCCC CACTGGAAAGATGCTTG
EST91254	73	T	G	...		TATTCTGTAGGGAGGAATAACCATGCTTCCATGGACTATCCATGGATAACTGGTTTTTTGTTGTTG TTGTT[T/G]TTTTAATTATTAAGAATAATAATATGTGCTCATCATCAATGCCCTTTCTCAGTAGAGCCCAG ACCTGG
EST91332	100	T	A	...		TCCAAACTGAAAGGAGGGTGGGGAAAACAAACGCATCATATGTAAAGCACTGAGTCCAGCCTGCGCTC TTAGTAAGCATTTAATCACCTTCAAAAATTAA[T/A]TGTGACTTACGGAAACAGGTCACTGAATAT TATT
EST91495 b	58	T	C	...		CTGACTCAAAAGACACTCCTGAAAGCAGGTCCATCCTGAGCAGCAGCTTGTATTACTT[T/C]ACAAG TCAGACCTGTTATTAAAGACGACTGGCATTTAAATCAGGCTGTGTCACCCCATCCTGGGTCTTT GTTCTTGGCTCCTATGGTG
EST91921	114	A	G	...		CTGGCTGAGGATCTCAAAGACATTCCACCACATTGAATCTTAGGCTGGAGGACATTTCGTATTCTT CAGTCAGGAATAGCACACTTCCTTTCATGAATAGCAGCTTTAGGG[A/G]TTATATCATGAGGTACA AATAAAGAGGCCCTCACC
EST92026 a	56	T	C	...		ATAGCCAAGATTTGGAAGCAACCCGTGACCATCAACAGATGACTGGATAAATAAAA[T/C]GTGGTA CATGTACACTATGGAGTACTATTCAGCCATGAAAAAGTCTAAGATCTTGTCATTAGCAACAACATGG ATGGAACTTGGGAACACTGT
EST92040 b	38	C	T	...		TTTCCATGAGGAATAAATTTGTTTATATAAAACCTG[C/T]AGATGAATATTTTTTAACAGCATG ATTCACAAATGCCAAAAACAATGCAAATGCCCTTCAACACATGAATGATTAACAGACCGTGATAC ATGA
EST98276 c	69	T	C	...		GAGTCTTGCTATGTTCCCAGGATGGTCTTGAGCTCCTGGTTTCAAACAATCCTCCTTCCTAAGCCTCC [T/C]AAGTGCCAGGATTATAGGTGTGAGTCACA

Clone	Pos	Alleles	5′ flank	3′ flank	Sequence
EST98276 b	61	A C		...	GAGTCTTGCTATGTTTCCAGGATGGTCTTGAGCTCCTGGTTCAAACAATCCTCCTTCCT[A/C]AGCCTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA .
EST98276 a	22	A C	GTCTTGCTATGTTTCCCAGG	AACCAGGAGCTCAAGACCA	GAGTCTTGCTATGTTTCCCAGG[A/C]TGGTCTTGAGCTCCTGGTTTCAAACAATCCTCCTTCCTAAGCCTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98800	53	A T		...	GCCTCCAGCTGCACTGACTCCTAAGCCATCATTCGAAGATTTGGCTAATTG[A/T]TAGTCTTACAAAGGCAGTCGAGTTCACCAGGCAGAAGGGGTTTGTGTTGGGAAAGCCGCTGCTATCTTTGTTTCAAACTGTAAAGCAAGTTCCTC
J02931	138	G A	CAGCATTAGTCACTTTGAAATGTAA	TTGGAATTGGTTGTAGTACCATT	AGAGGATAGAATACATGGAAACGCAAATGAGTATTCGGAGCATGAAGACCCTGGAGTTCAAAAAACTCTTGATATGACCTGTTATTACCATTAGCATTCTGGTTTGACATCAGCATTAGTCACTTTGAAATGTAAC[G/A]AATGGTACTACAACCAATTCCAAGTTTTAATTTTTAACACCATGGCACCTTTGCACATAACATGCTTTAG
L41680	88	G A	GAGAAATCGACTACCAGCTGA	TTTAGAGCACTTTGCAGGTATTT	GGATCCAAAACACGGCTGGGTTTCAGCATCCACCAATGAACTGAAAGGTGAATAAAGGACGTTCATGAGAAATCGACTACCAGCTGAT[G/A]AAATACCTGCAAAGTGCTCTAAAATAAATATTTTGACTTTAAGGGTCCTAGTAAGTGCCCACTTCCACTAAGAATACAGTTGAATGTATAATCAGTAGTGTTTACAAGATCCAACAGTGCACTCA
M15796a	84	C G	CAAATTTGTACCTCTAAGTACATATGTAGA	TTGGACTTTATTCTTTAAACAAATTG	CTTTTCTGTCACCAAATTTGTACCTCTAAGTACACATATGTAGATATTGTTTCTGTAAATAACCTATTTTTTTCTCTATTCTCTC[C/G]CAATTTGTTTAAAGAATAAAGTCCAAAGTCTGGTCTGGTCTAGTTAACCTAGAAGTATTTTTGTCTCTTAGAAATACTTGTGATTTTATACAAAAGGGTCTTGACTCTAAATGCAGTTT
M20472	103	C T C	GTTGAGTTCTTTTGGACCAAAC	ACAATGAACAACTCTAAAGACAAAAA	AGAGCCACCCTGTGGAAACACTACACTCGCAATATCTGCAATATCTTAATCCTACTCAGTGAAGCTCTTCACAGTCATTGGATTAATATGTTGAGTTCTTTGGACCAAAC[C/T]TTTTTGTCTTTAGAGTTGTTCATTGTTTGTGATTGCATGTTCCTTCCTCCGGCATTCAGAGAGGAGAAAGCCTCTGCTGCCATGG
M32315b	129	T C	GCCTCTGCTGCCATGG	GCCTTCCGAGAGGGACAC	CCCTCTGACCTGCAGCCAAGAGCAGCAGCGAGTTGGGGAACAGCCTCTGCTGCCATGG[T/C]GTCCCCTCTGACCTGCAGCGAGTTCGGGAAGGCTGGCTGGCGGCCAGTCCCTGACTCTCTGTG
M33875a	131	C T	GGTTACAGCTGGAGGTGTGT	ACCTTTGTTAAAATTTAGGTGGTTAT	TTCCCAGGAGCAGCAGCAAAGGGGCCCTGCTGAGCTCTGGTTAGGTTACAGCTGGAGGTGTGTATATACACACACACGTGTATATACACACATATATGTGTATGTATATATATATGGCTTT[C/T]CAATAACCACCTAAATTTAACAAAGGTTCCTTCTAAGTGGTAGAACTTGGGGTGTATTTTACCTTCCTTCT
TIGR-A003M18 a	29	A G CT	TTTTTGTAGAGATGAGGTTTTC	GGCAGACGGATCACTTGA	TGTCTTTTTGTAGAGATGAGGTTTTCCT[A/G]TTGTTGGCCAGGATGGTCTCGAACTCCTGACTTCAAGTGATCCGTCTGCCTGGCCTCCCAAAAGTGCTGGGATTATAG

ID	Pos			Flank	Sequence
TIGR-A003P30	117	C	G	---	ACAAGTTCAAAAGGAGAACTTCCTTTGTTTAATGCAGCTGTGTCAGAGAGCCTGTGATTTCCTAGGAAACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAAGGTACCCTTGGAGATACT
TIGR-A004S34	156	C	T	A CCAAACCTCCT CATTCCTATAA TGTAAACAGCT AACTGTTTTG TTAAA	GCTTGTCTTTATGTTTAGGTTCGGGGGAAAGGAAGGGGCTGACAACCGCAGACATCTGGACACCAGCAAGGGTCCAGGGGGAGGTTTGCAGAACTTCTTTGTCCTTGGCTAACAGTGTCGTCATGTGACAATAGCCAAACCTCCTCATTCCTATAAA[C/T]CTTAACAAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTTTACATG
TIGR-A004T44b	97	A	C	---	AACAACAGTGTAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCAAAATGATTGAGTATGATAAAGAATTTGCATGGCGATT[A/C]AAATAGAAAACCTATAAATGTAGAAAAAGCAGGTCTGGACTTAGCAAAGAAACAATATGACCTTAGCAAAGAAACAATATAG
TIGR-A004T44a	69	G	A	GGAAGATAAA CCAAATGAT TGA	AACAACAGTGTAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCAAAATGATTGA[G/A]ATATGATAAAGAATTTTGCATGGCGATTAAAATAGAAAACCTATAAATGTAGAAAAAGCAGGTCTGGACTTAGCAAAGAAACAATATGACTTAGCAAAGAAACAATATAG
TIGR-A004V08	60	T	C	CAGGAAAACA TCCTTCCCACA GGCCATTCTCTT AAAGGC	CCTACAAATCCTATAATATTGCAAGGGTTGGGAAGGATGCAGGAAAACAGGCATTCTCTTA[T/C]GCCTTTTGTGGGAAGGAATCAATTGGGTGCATGCACTTAGGGGACAATTTGGGCAGTAGCTGTCAAATTTCAGTAGCTGTCAAATTTCAAA
TIGR-A004V26	125	A	G	---	TCTAGCTATAAGACCAGATTTAATATTCTAGATATAGAATTATCCAGAATAATTCTATTGAATTGACTGATTACAAAATGTTAACAGCTGGATAAACGGTAAAATATGCATTATCTTCACATGA[A/G]AAGGTTTCAGTTTATAAAATGCTTAAATACTGTATCTATTTGCTTAAATACTGTATCTATTGG
TIGR-A004V28a	29	A	G	TGTTGTGGGGTG CGGAGGTTGCA CGATCTC GTGAGC	CCAGGCTATAATGTTGTGGGGTGCGATCTC[A/G]GCTCACTGCAACCTCCGCCTCCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTCAGCCGCCACCGCCACCTAACTAATTTTTGTATTTTTAGTAGAGACATTGTATTTTTAGTAGAGACAGG
TIGR-A004X20	25	T	C	AAGTTTTCCTT TTTTATAGTTG CTCTTCTGTAG ACTGTAACATG GA GAGAC	TAAGTTTCCTTCTCTGTCTGTAGGA[T/C]GTCTCCATGTTACAGTCAACTATAAAACATGGCTCATGTTCACTCTGGCCTTCGCGTCGCCTTCTTCATTCTTCCAAGGCGTTGATATTTGGAAGTGGTACCTTTGTTGTGTGCTTTTCAGACCAACCGCCTTCTTCCTTCCAAAGGCGTTAAATCATCATGTCCAATCATCATCATGTCCTT
TIGR-A004X30	26	T	C	TTTGAAATCTT TTCTTTATGGA AGAGTAGAAC AGTGTTTAAAA CCAC CTATTTT	TTTGAAATCTTAGAGTAGAACCCAC[T/C]ACTCTAGTAATACTTGTAATAAAATTAAAAATAGTTTTAAACACTTCCATAAAGAATTAGGGGTGCCCAGCTCCTTGATTTCCCCCTAGGGGATAAAGATATCCATGTTAGGGGATAAAGATATCCATGTAC
TIGR-A004Z04	102	T	G	CTTATAATTAG AAATTTCATGA TTCATTTGGGT ATGCAAAACT AAGCAA	CACGGTATATGCCTTATATATAGGTATATATACAGATCGTACACAATATATTTACACAGTTTGACATGGGGTCCACAGTACCTTCATTTGGGTATGCAAAACT[T/G]TTGCTTTCATGAAATTTCTAATTATAAGGACTGTTGCTTTCATATTCAATGGACATTATACAAAATATACACAAAATATACAGTCTCTTTAGTGATTTAAGACTCTCTTTAGTGATTTAAGACTG

TIGR-A004Z19	85	C	T	GAGAACAACT GCAGCATTTTT	AAGATGGTCAT CGGGGAAGA	TAAGTGGGAGACAAGTTTATTGGAGAGGAGCTTGACACCCCTCTTCTGCCCTAGCTTGAGAGAGAACAACTGC AGCATTTTTCTTTTTTC[C/T]CTTCCCGATGACCATCTTTGGGCGTGGCGGCCAGCCCTGGGGGTGTC TCCCATCGCGTCGTCTTTAGTGAGACTGAGGATCTGGTATAAGGAAACAGATC
TIGR-A004Z42c	89	C	T	TTGGGGGGAGGT AGGAGACT	CAGGGCTGCCG GTCC	GTCTTAGCAGAGGAGAGATAACTTTGAGGGACAGCAGCCCCCAAGGCGCCAGGTAGCCTTCAGGGGCGGGCA GGGTTGGGGGAGGTAGGAGACTC[C/T]GGACCGGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTT CATCATCTGTGTCTTC
TIGR-A005D17c	81	T	C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCCAAGGC[T/C]GTCTAGATTCTTCTGTGCAGGATTCCTTCCTTCTGGGCAC GGGGTGGGACCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAACAC
TIGR-A005D17b	79	G	C	GGGGAAACCC AGCAAG	GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAG[G/C]CTGTCTCTAGATTCTTCTGGCCTCTCTGTGCAGGATTCCTTCCTTCTGGGCAC GGGGTGGGACCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAACAC
TIGR-A005D44	97	G	T	TTAACATTATT GAACTTAAAA CTGTTACAC	TTGTCTATTAT TTAAAGCCAAC AAAA	CATCAGTAACAATATACACAATTGGTCATCAACTGAACTTTGCCTCCAATATATTTCTATACAATACTT AACATTATTGAACTTAAAACTGTTACACT[G/T]TTTGTTGGCTTAAATAATAGACAATGATTTTTG TCTATTACTTAGTGATAGACAAAGTGATTACTTTGTTAGACAAAGTGATTACTTTGTTAC
TIGR-A005E31b	27	G	A	---	---	GGAGTTCAAATTTATAACCAGGCCTCT[G/A]CTCACAGCTGTACTGGCTAGGCAAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTGCCTGCTTGCCCCTACAAAGCCACCTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR-A005E39	182	G	C	---	---	CTCAGTGTGTAAAAACTTTGTTTAGGGAAAAAAAAAAATCCAATGGATATATGGGAAGAGAAGAGTG CCAGGCTGGATGGTGCTGAGACAGAATGACCCCCTGGGCTCCTTTATTTGTTCTTTCAACAGGACC CCACAGATATTTGCGGTATGTCATGAGGACTGGGGATGTCTTCTTCTATTG[G/C]CGGATGTCTTCTATTTT
TIGR-A005E42a	42	A	G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTCTTAGTAAGGTTACTACTGCACAGAG[A/G]CTCAATTCCCCTGATTTAGGA AGGCGATGCTAATGGGTATTGCATAGGTGTAAGTATAAAAATGTTGTATTTAAGAGAATCCCACAAG CTTGGTATAAAGGCAGAAAATAAATGGTATAAAGGCAGAAAATAAATAG
TIGR-A005E46	76	A	G	CACCTGACTCG GTGCTTTAC	CCCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTGTATTAGCCTACCGTTTGCTAAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCTTTAC[A/G]TACATTACCTCACAGCCAGGGTTGGCAAATGGTCATTTTGACAAATGGTCATTTTG ACAC
U20979	24	C	T	GCAGGGGTGA CGTATGTAGA A	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA[C/T]GCTTAGGGTGTCCTCCCACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGCACTTTGTCCTGCTTCACGGACCTCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGATATTTGTAAAAATTCCCCAAGAGCCGCATATGAATCTGCCC

ID	Pos	Alleles	Flanking	Sequence
X57830	106	G C	AGTGGAACCA ACGATCATAT CT	CATTGACAGAA TAAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAAAAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAACCAACGATCATATCT[G/C]TATGCCTCATTTTATTCTGTCAAT GAAAAGTGTGGTTCAATGCTACAAAATGTTCTGACAGCATTCAGCTGTGAG CTTTC
X74070b	72	T G	TGGATC	CTTTTTAAGAA ATTTTTGTTTA TATTAGAGATC TAGATTT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATTATGACTGCTTTTAAGAAATTTTGTTTATG GATC[T/G]GATAAAATCTAGATCTCTAATATTTTAAGCCCAAGCACTGCACCCCTTGGACACTGCAGCTCTTT CAGTTTTTGCTTATACACAATTCATTCTTTGCAGCTAATTAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44	C T	---	ACTGCCGAAGTGTAGCGGCGCCCCAAACCTTGCTCTCATCACCAG[C/T]TAGAGCTTCTTCCCGAAGGG CCTTTAGGATAGGAGAAAGGGTTCATGCACACAGTGTGAGAATGGAAGAGCCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGTAAGG TCCA
D28513b	133	A G	---	ATGACCAAAGCACCACCACATTTAGAACTTTGGCTGCTGCCTTTGGAAGTCCAGAGTCTCAGCTCC CGCCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTGATTGACTGCAGTGAATGC[A/ G]TGTGCGTGCAAGCATGAACCCTTGTTTAAATCAAGAGGCTTACATAATTTTAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G	---	CCACTCCATCCTGATGCCCCAAGTTATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAA[A/G]TTCTCCAACTGATCCTGCACCCCCAAATATGAA CAACTGCAGCAGGTGCCACCACCACAAAAGACACCACTACCCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G	---	CCACTCCATCCTGATGCCCCA[A/G]GTTATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTCTCCAACTGATCCTGCACCCCCAAATATGAA CAACTGCAGCAGGTGCCACCACCACAAAAGACACCACTACCCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A	---	CTCCCTGCCTCCTCCTTCCTGCCTGTGATGCTCCGGTCTCAAACAGCCGAAACCTGTCTTGCAATGGGGG GAGGGGGCGTTTC[G/A]CTTTCCTTTCTTTCTCCCCCTCAGGCACCTCCTTATTCTCCACAAACCATTCTGAATAAA GCCAAAAATCTTTCTTCTTTCTCCCGTCCTCACTCCTCCTGTCCTGTGTGCTGGCTTTT CTGGA
D37931	64	T C	---	ATTATCGGCGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTGT[T/C] CCCAGGCTCTGTCTCCTCAGCTCATTTCTGCTCACTCTTTTCTGCTACTCTTTTCTCTATTAAATACATT GCACCCAAAGAGATATGGAGGAGACATAAACCTGTAATGAATGAGGCTGGGCTTTTTCTTGTAATAAGCTTCC TTT

D63807	101	C	T	CAGGCAGGACTTCAGTGTCAGTATCCCTGCCTTCAGTCTTCTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGAGGGAGTGTATTTTCCTGTTCCA[C/T]GAAGAGGACTTTTGTTCACAATTGGATCAC AATGCAGAGGAGTCGTCGTTCCTCCCCGGTGGGCTTCTCGGGTGCTGGGAGGGTGACCTGTCCCAGATGAC
D90145	21	T	C	TGGGAACATGCGTGTGACCTC[T/C]ACAGCTACCTCTTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGTGGGGACTCTCTTCTTAACTTAAATTTATTTATTATACTATTTAGTTTTTATAATTTATTTTGAT TTCACAGTGTGTTGTTGTGATTGTTGCTCTGGAGAGTTCCCCCTGTCCCCCTCCCACCTTCCCCTCACAGTGTG TCTGGTG
EST14035 1a	59	T	C	ATTATCACTCTCAAAAATTTGGTGTGTGTGTTAAGTACTTTCTTATTTATGAGCCCC[T/C]GAGGA CCAGACATGTTATTATCCAAGCCCCTTATATACCCATCTAAT
EST16668 5	71	C	T	GCATTTAAAATTCACATTGAATCATTATTTACTATTTATGATGTTTACATAACAATTCAGTATCATT ATG[C/T]GTGTAGATTTCAGATGTAGGTCGTCAATACTGAGCACTTATCT
EST16904 7	57	C	T	ACAGACTATCGCCAACTTATAAATGCTTAAACTTTATGATCAATAGTAATAAATTACA[C/T]GAGATA TTCACACTTTATTATAAAATAGGGTTTGTGTAAGATGATTTTCCCAACTGTAGGGTAAACAT
EST21863 9	49	A	G	TTTTTAAGTACCAGAGGCACTGCTGGAACAGAGTGAAAACTGATACACC[A/G]GTTACTACTTACTC TTCACTCTTCAAACTGATTCCCCTAAAGGTTCTACTTAGCAAA
EST21885 6	80	G	A	GGCTGTAAGTAAGAATCAAAGGTTAAGAACACATTTATGCCACTTATTCCACAAACATTTACTGAGCATA CTAGGTGCTGGGA[G/A]TGTGACAGTGAGCAAAAAACACAA
EST22623 8a	26	A	G	ATTTAGTGCAAATGACAAAGCCCAA[A/G]AGAACAGAGGATCAAAATAAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTAACAAGTATGGGAGT
EST22644 2	98	A	G	AAAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTGTTAAAACAGCACTAAAAATAA AAATTTTAAAATGATTATCCATTATTACAG[A/G]AAATGTGAAAAGATGGCTTTTAAACCC
EST23587 1	31	T	A	CCTCATTTATTTAAAAAGACGGACATAAAAA[T/A]TATACAACAAAAAACCCAAGTCACATTCAG GAGGTAAAAAACTAAAAAGTCTGATATGAAAATATGGTGG
EST24246 7	106	T	C	AAAGATCTGGCATTATTCACATCATTCTAAATATTTGTAATTACTTTTTCCATGAGTATTTTTTCA TGTCCAAGCATTTAACTATCATCATTTAGCGTAAATACC[T/C]GAATAACCCATAGTTACAGAATTGG GTCTGTGTAACCTCAATT
EST24308 3	45	A	G	TAGTTTAATTTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT[A/G]CATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24435 6	73	G	A	CTTGAACTTCTGGTCTCGGTACGTCCGTCTCAACCTCCAAAATGATGCGATTACAGGCATAAG CAGCC[G/A]TGCCTGACCCACATTTCTTTATCCGATCGTCTGTTGATGGACATTCAGGTTGTTTC
EST25089 6	25	T	C	TATTGTTGCATTATCAAAATGGTTA[T/C]AGTTTTCAATTAAAACTGTAATTGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAAAGTTGTAAATGTAGTAGTTCCAATCGTCGTTAGTTAATGCTACATT

EST					Sequence
EST254769	33	G	A	---	AATGATCTTTATTTTCAGACCTGCTCCTAAAA[G/A]CTTTCTCCTCCTCCTCCTCCTAAAAAACCAAACACAAGAGGTCCTGCTTGCTGCTGCCTTTCCATGGACTGTGGCCGGCTGTGGACCGTCTGCTGA
EST261832	70	T	A	---	AGATAATGCATTAGAGCCTGCCCTCCATTGTATCTGATTAACTTTGTAAAGATTGATCTCTAAATAAGAT[T/A]ACATTCTGGGGTACTGGGAGTTAGAACAAC
EST272311a	28	T	C	---	AGAAAATAAGGTGCTACCAGAACTCATG[T/C]GATAGCGCTTCTTCTTTAGGCACATATTATAGCATTCAGATGAAAGTTCTGTAATCACACACACTGTGCCTCTAACAACAAACACGGTGACTCTGA
EST278165a	26	T	C	---	CAACTCAAGGTACAAGACAATTGCAT[T/C]TAACATTGTTTATAAATAAAAGGAACATCAGATCAATCATTAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST285880	78	A	T	---	GTTTAATTGGCGTATGGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGGAGGTCTCAGGAAACTTACAATCA[A/T]GGTAGAAGGCAAAAGAGAGAAGCAGGCATCTCTCCATGACCACCAGCAGGAGGAACAGACAGAGGAGGGGGAT
EST302265	25	A	C	---	TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGCTATACTAACTTCATTGTAGTAGGGAATATAAACTACTGAACAGACAGACTTGTCTAACTTAAACAAGACAGACTCATTTCCTTGAG
EST309359a	59	C	G	---	AGCTATGTGTAGAGCAAATTCCAGTGGTGGTAAATCAAGAACTCTAAAGTTCAGTAGAGA[C/G]AGGTGTTTGAATGTCAAGGAAATCACTGAGGTAGATTTGGGATTACAATAAAGACAGCTGCCCTGTGAGGTCATAAGAGCTTTTGTGAGG
EST325157	25	G	A	---	CCGAATATAAGGAGAAAAAATGGTGGC[G/A]TGCCTCTAAAAACCTGTTGAATAGAATAATGGCCAAATATTACAGTTTCTCACTTCCTATGAATACTGGCACTGTTTATTTCATGTTTATATGTGAGTTTCTATGCATAAAAATCCCAGTAAGA
EST332744	27	T	C	---	TGCTTTGTTTCCCTCCAAATCCTAAAA[T/C]GTGTGTCTTCAAAGAAATTCGTGGAAAGAAATTTGAATACGAGTTTCAGTAACTATGGAGATGATACCATTACGGAGTTTGTACCATATTCAAGTATTCTTGAATACAGGTTGGACTAGGTA
EST333527b	75	C	G	---	TACACATTATTCAAGAGACCACCTGACATGCATCTCCTCCGCAGAATACATTCGTCCTCTCTCTTAGAGAAGTTTAA[C/G]GCACATAGTATTATTTACTAAGAGAATATCTCTTGGTGTCATATCTAGGGG
EST334241	126	A	C	---	ATTTTCCCACAGCAGAAGTACAGAAGTATATTTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGGGAACCAGTACAGAAGATGTTCACAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAACAAAGGTGTTGAATCCTCTT
EST334887	90	A	G	---	CCTTTGGGGGAGTTTTAAGCCAGAATGTGACAAGTCACTTACAGGAAGACTGGAATGTAGCCATAGTTGAACTCTAACATCGTCTCTATAG[A/G]ACCATTCCCGTCTCCAGTAGGTTCTAGGCATACTAAGCTGCTC
EST335081b	45	C	T	---	AAAAACATGCTATTTGAACAAACTTTTTATAAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTTTAAATAACATCAACTCACAAATGACTTTTAGAAGCCAAATAA

EST				Sequence
EST335081a	36	A G	---	AAAAACATGCTATTTGAACAAACTTTTTTATAAAGA[A/G]TAAGTTGACTGAAAAGCAGTTTTAAAT AACATCAACTCACAAATGACTTTAGAAGCCAAATAA
EST338634	77	C T	---	ACAACATAGGACTGGTTATTCTTGGTTTTGAAAAATTATGTTGCCACTTCCTATTGTTTAAAAATGA TCATTTAAC[C/T]TCTTTGAACTACAGCCTGAATCCCCC
EST347393	97	T A	---	GAAGTATCCTTCCCAGTGGCAGGAACTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGTGGGGAACCTC[T/A]GGTGCCTTACAACTCCAACTACTGCAGAATTTCT TGTTGTGCCTCATAAACA
EST347926b	104	A G	---	ACCTGACTGCTTTAAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCCAGGATGTTCCCTGA[A/G]GTATTCAGGAATTCTTAGTCCTATTACA AAGATTTTGTTGCTGTG
EST348359b	93	T G	---	GGAAAATGTTCCCTTGCAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTTGTGCTTTCTGGT[T/G]GGCCTTAAAAGAAACAGACAAATTTGTGCTAAAGAT
EST348359a	82	G A	---	GGAAAATGTTCCCTTGCAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTT[G/A]TGCTTTCTGGTGTGGGCCTTAAAAGAAACAGACAAATTTGTGCTAAAGAT
EST352300	93	G T	---	CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACCAGTCATCTCAATAAATG CAAGACATGAGCATAAAAGAGGTTCTC[G/T]GCCTTTCCAGCGTTGTTATTACAGAGAAACCT
EST353379	33	C T	---	TCTTTTCAAATTTTTGATGTAGGCATTTAATG[C/T]TATAAATTTCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTTGGGCATGTTGTGTTTCCATTTTACTTAGTTCAGAAACTTTTCAATTTCATCT
EST357089	32	C T	---	CTGCCCCAAATTAACTTTAGGCAAATGAAA[C/T]AGACTTACTGTATGGGGACATTTTAAAAAG ACAGCTTAGTAATGTTCATATGCAGCCGTGTTGCTTCCCTCTCTGAGGTTGGCACCTTCCTGTTGTG ATGTGCAAAGTGTGGCT
EST357479	51	C G	---	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAAACCCACAAAGGCTCCA[C/G]ATGTTAAAACGT TCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCTTCCAGTAGGGTTGAGATT G
EST357519	89	C A	---	TGGTCCATTATATTAAAACTGAGGGAACAAACGGTGCTGACATGGCAGACATTTATTTCAATGGAGA AGTTCCTCCCATGAAACCAAGA[C/A]CTTGTCCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAGGCCTGTGA
EST363014	93	C T	---	CACCTGTTCATTGGTTCACTGGGCTGTGCTATCTGTGGGCTGATGCTCTACCAAGTGCTCAGCCTACAGC AGTCAGGAGGCAGCCATGGCCCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST365190a	33	G T	---	GCCATCAGCCCACCAAAGACAATGACTACCAACGC[G/T]GGCCCCTTGCACCCATACTGCCTCAGCAC CTAAGACTGGACAACTTTGTACCTAATGACCGCCCCACCTGGCATACTGGCTGGCCTCTCTCTGT CACAGGGGTTCTTAGTCGT

EST366206	50	G	A	GACTTTATTAGATAAGGGGTTTCGGCTACCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATGGGGAAATAAAATACAAAAGGGCCACACCCGATGCAAAAGACTTT
EST366900a	89	C	G	CCTGTGATGTGCAAGTGGTGCCTGAGCAGTCGTACTTACTGTGCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTCGGGGATTCCTA[C/G]AGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTTCA
EST367299	62	C	T	GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCTCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACTTAGCTACCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST368236	103	A	T	ACTGTCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCCAGACCAATTAG GTCAGTATCTCTCGGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCCTAAGCTCATCATGAG TTAA
EST369874	126	C	G	ATGATCGCTTATGTATTTGAGGGGCGACTGGGTAATGGGAGATACCCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGAGGCTAAATTACAACTGACATTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST370543	88	T	C	GGTCTCACTCTCTTGCCCAGGACGGTTGAAACTCCTGAGCTCAAGTGACCCTCCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACCTGGTCCTTGGTTTAAAGTAACCACTGAA C
EST372693b	105	T	G	AATAGTCTATGGCTACGGGCCCGTGGGATGTTAAAAATTGGGATTTTAAATTAAGATTGTGAACATG CAAACCCAGCACAAATTTCTCAGCTTATATTTGAAAGTC[T/G]CAGGAGAAAAAATGGGGTCC
EST372842	93	G	T	AAAAGACCTTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAGGAA GCTCTCTGGATAATGTCACTCTAGGAA[G/T]AGTAAACAGGTGTTAAAACCCTGAGATAGCAACCCT CTTGGCTTGCTTGAGGAATA
EST373152a	90	A	G	AGATGGGGTCTTGCTAGCTTGCTGGCGTCGGGCTGAACTAAAGATATCCTCCTGCCTCAGCCTCCCAGGTAGT TGGAACTATAGTAGGAGTATCT[A/G]CCCTGCCCCTGCTAGAACTTCAAGTTTTGATGGGCAAATCCA CCCCAGAGGACAGGACAA
EST373741	45	C	T	CCTGCCATGATCGATAATGTTAAAACATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAAAGCATACC ATTCCATTTTAGTTGAAATATTCCTTCACATAGCCAACACACATTTTTTCAAGGCACTCTAGCTACTACACA GGA
EST373768b	101	G	C	GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAGT[T/C]GAGGCGCTGGGGGGCTGAAGTCAGACT CTCTGGGGTTCAAATCACAGTGCTGCTGTCCTGCAGCGGTGCCTGCAGGCAAGTTGCTGACTTCTCTG TGTCCAGG
EST373768a	41	T	C	GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAG[T/C]TGAGGCGCTGGGGGGCTGAAGTCAG ACTCTCTGGGGTTCAAATCACAGTGCTGTGTCCTGCAGCGGTGCCTGCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63	T	G	...	ACACACAAAAAAATGGTGGCAGAAAATCTGGAAAGATTCTAATAACCTCAATTCGTGAAAAC[T/G]AACATGCCTCAAAAAGAGAGGGGGAAAAAACTTTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46	G	A	...	AAGACATAAATCTGCAATGAAATCAGTTATGAAATCAGCCTATCGCATTTAAAACACCCTAAAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTATTACC[A/G]GTCATGAAATTCATTAAAAACCACAGCGAT
EST37613 6	34	A	G	...	CTAGGCATGGGGCTTTTACAGTCATTATTACC[A/G]GTCATGAAATTCATTAAAAACCACAGCGAT ATAGCAATGAGCAAAACAGACCCTCCCCAAAATCACCCTGCGTTCATGGATCTTCATTCTAA
EST38025 4	56	T	G	...	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTACATGTTTATATCACTTA[T/G]TTATCTCA ACAATCTTGAAAGGGGTGGTATTATTTCCCGTCTTATAGGTGAAGACTCTGAGGTTCAGAA
EST38068 6	57	C	T	...	TCTACCAGGTCACCAAAGTATCTGTATATGCTTAAGTGGCATTTCATGTCACTTA[C/T]CGCCATGG AAGAACGCTCTCCTTTTAATTCCCTAACTCTCTTCTTCTGGGAAGACAGAACGTGCACAA
EST38420 6a	100	T	C	...	TAAAATCAAGGCCTCTCTTCATTACCAAAACAAAACAAAAAAGGGAACAAAATACGATGGGAGGAGAGG GAAGAGATGATGCCGAAGTGTCATCCTGACTGAC[T/C]GTCCCTGCAGTGCCCATGGGTCCCGTGCCT TATTCATTCTCCTCTCTCA
EST38950 5	25	T	C	...	TTTATTTGCAAAAGTAAGCAGCCGCGG[T/C]TGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAAATACTTGGGACTTACATTGACACAGGCTAAAAGTATGGGGATGAGAGAGGAACAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90	T	C	...	TTTTTTGTTACTCTGTAGCCAGTCATTAATCTGAAGGTTAATATATCATTTATTGGGATGAGATCA TAGTCTTTACACAAATGCTATGT[T/C]AAACAAGTTACTGAATATTTTCACCTCGTGGAGTTG
EST39331 1	70	G	C	...	TCCTTCTGCTCTCTAGCACTCAGACCACCAAAGAAAGCCTGGAAGACCAGCCATGGAAGGAAAGTA TGC[G/C]GTGTTTAGGGAGAGCTGGCACCTGGCCCTCTAATCTTCCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31	C	A	...	GTCACCATTGACCTTACATAGTGCCTCTAGT[C/A]ACCTATGAGGCACTAGAACTCTATTGTACTTCT CACTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37	T	C	...	TTCTAATAGCATGCCCGTGTGACAGGGAAACTAAGCT[C/T]CTTCAAAATAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTTCTCCAGAAGGCTCAAGGTGTTC AATAAATCTGTGGGGACTCA
EST40549 1	42	A	G	...	TGTTTCTCTAGAGAACCCTGTGTGATACACTACGCATGCACA[A/G]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTTACCACCATTTCTCACTTGAACCTAGCTCCCTGCAAAGCACCTTCTA CCCTGCACTTTTGGGGAG
EST40579 1	81	A	C	...	TGTGAATTACACATCAGTAAGGCAGTTACAGAATTTCATTCTTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAAA[A/C]GGACTTGGAGACAGCGATTTAAATACGGAACAAGGTCTTCCAGGAAG
EST40584 3	68	A	G	...	TTGTATGGTTGTAGGAATTTGGGAAGAAATTATCTGTGAAGGAAATTTGCCACTGTAATGCACACCC A[A/G]TCTGTACTCCCACAATATCCTATGTTTAAGCT

EST51340	51	G A	GATCAAACTGTATTGCCCAGGCCAGCTCCTGAAGAAACTGTGAACTATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTGCACACCACCATCCATTGTCTCTTTCAAAACTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134	T C	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCTCTCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCTTATCCAACTCTCGA[T/C]TTTTCCTTGGTCTCCAGTGGAAGGGAAAAGCCCAGTGAGT AGCTG
K01506	63	T C	CTGAACTCCAGCTGCCCTACAAACTCCATCTCCAGCTTTCTTCTTCTCACTTCATGTGAAAACTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCCTTCAAGCTCTGTCTCCTTATCCATTACCTCAAAGCAGTCATTCCT TAGTAAAGTTTCAACAAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTC ATTGAGCCTTTTATCCT
L18877	69	T C	TGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGGAGGGAGTCTGGGCCAGTGCACCTTCCAAGGCC C[T/C]ATCCATTAGTTTCCACTGCCTCGTGTGACATGAGCCCATTCTCCACTCTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTTCTGTTCTATTGGATGACTTTGAGATTTATCTTTGTTCCTGTTGGA ATTGTTCAAATGTT
L31848	36	T C	GCTATTTACATATCCCAAGCCTTTAGGGCTACAG[T/C]CTTCCTGTCCTGGACCCTGTAGGGTGCCA TTTGGAGTTCACAGCCTAGAAGAAGAAAAGGCTTGGGCCTGGTGGTGGCTGCATAGGCCTGTAATCGT AGCGCTTTGAGAGGGCTGAGGCAGGAAGATAGCTTGAGAGCAACAAGTTCAGAGACAAACCTGGGCAAT GT
L38517	137	G C	GGGGTCCAGAAGCCCTCTCAGCCAGGAGGGAGCCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCCTGCCACCATCTCCTCTGCCATGCCATGATCATTGAGAAGATACCACCATTGAGACTGCTGGGCAACCAGCGGTCCCCAC CC[G/C]CGTCGTGTAGTCATAGAGCTGCAAGCTGAGCTGAGCTGGGCGAGGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123	T G	ACTTGAGAAGCAGCAGAGCTCGCCACCTTCTGGAGGCCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGACAGGGCAACAGGGCCAACAAAATACAGTAGTTCTTTTGTATATT[T/G]CGCCTGA AGATCATCCCGCAAGCCAGCAGGCTGGAGGTGCCCGGTGGCGGTGCCCTGGTCTTTAGTCTGTGTGGG GAG
L41268d	173	G A	CAAAGTTGTCTCCTGCCCATGAGCACCAGTCAGGCCTTGAGGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGGTTGCCAGCTCCAATGTACCACGACAGCTGGAATCTGAAGGCGGTGAGTCTGCAT CTTAGGGCCATCCTGCTCTTCCTCACCACCACAAAATCTGAAC[G/A]TGCCTCTCCCTTGCTTACAAATGTCT AAGGT

ID	No.	Var.	Sequence
L48728b	111	T C	AAGTGAACAGAAAGCAAAGATGGATTGTGTTCCTATAAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGAGCTCAAGTTTTGGTTTACTTTCAGAA[T/C]GAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGGATTTTTAGCCCAATGCTCCAAAAACTCATCCTGTACCTTGGAGATCCA GTC
M18079	52	G A	GCGCACAGTCCAAAATACAAATTGGACAGAAGATCTATATTGTACCAGAACT[G/A]TTTATTTCACC CCATCAAGTATAAGGTTACTGATTGGTCCTTTATAAACATTGGTATATTTCCATTCCATGCCAA AGCAAAAGAAGTAAAAGCTAA
M19169	113	T C	TAGGGATCTGTGTGCCAGGCCATTCGCACCAGCACCACCCACTCCCACCCCGTGAGTGCTCCCACCCC TGGACTGGTGGCCCCCACCCTGCGGGGAGAGGCCTCCCATGTGCCTGT[C]GCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCCTTTGTTGCTCAGCAGGCGCTCCGCCCTCCTTCCTTCTCGCTTCTAATA GC
M21539	114	T G	TCACCTCGTTCCACAGCTCCACCTGCCATCTTCTCATCAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCCTTAGCCTGTGATCTGCCCATGATCCCCGACAGCAAAT[T/G]GTTTCCTTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAGGAAGTCCTCAGCTGTACCGGCCTTTCAGAGCT TCTCTTTGGGTGC
M26041c	173	A G	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTCTCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTTGAATTATTCCCTGACTTC CTGATTTTTTCTTTCTCAAGTGTTACCTACTACTAAG[A/G]GATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCCTCAGTAA
M26041b	157	A G	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTCTCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTTGAATTATTCCCTGACTTC CTGATTTTTTCTTTCTCA[A/G]TGTGTTACCTACTACTAAGAGATGCCTGGAGTAAGCCACCAGCTACC TAATTCCCTCAGTAA
M26041a	45	C G	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTCTCCTT[C/G]CAAATGTTTCTCCTCTCACC TCTTCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAAATGCCTTTGAATTATTTCCCTGAC TTCCTGATTTTTTCTTTCTCAAGTGTTACCTACTACTAAGAGATGCCTGGAGTAAGCCACCACCTACC TAATTCCCTCAGTAA
M63967	57	G C	TAAGGCAGCTGTCAGGGAGGCCCAGTCACAGTCAGCAATTCCACAACCACCTTGAC[G/C]AATGCT TGCCAAGCTGTTTAAAGCCAAGAACACCCTTCTTGTTCCAAATTAACTCTTAGAGAAAACCCCA CAAATAAAGCAATTCAATC
M81695	34	G A	ACTTACTTACCCTCACCTGTCACCTGCAGGCTCAGGCTGACGGGGA[G/A]GAACCACTGCACCACCGAGAGAGGCTGGG ATGGGCCTGCTTCCTGTCTTCCTGTCTTGGGAGGAAACGTCTTGCTTGGGAGGGGCCCTTTGTCTTGTGTCAAGGTTC CAACTGGAAACCCTTAGGACAGGGTCCCGTCGTGTTCCCCAAAAGGACTTGACTTGACTTGCAATTTCTACC T

ID	Pos			Sequence
U06641d	166	C	T	CTCCTCCTTTATTTCAGCATGGAGGGTTTAAATGGAGGATCTCCTTTCCTGTGTGACAAAACATCTTTC ACAACTTACCTTGTTAAGACAAATTTAAAAAAGATCTTTTCACAACTTACCTTGTTAAGACAAAATT TATTTTCCAGGCTATTTAATACGTACTTTAG[C/T]TGGAATTATTCTATGTCAATGATTTTTAAGCTA TGAAAATACAATGGGGGGA
U09607	39	T	C	GAGGCCTTATGAGGGTCCTCTACTTCAGGAACACCCCCA[T/C]GACATTGCATTGGGGGGGCTCCCG TGGCCCTGTGTAGAATAGCCTGTGGCCTTTGCAATTGTTAAGGTTCAAGACAGATGGGCATATGTGTCAG TGGGGCTCTCTGAGTCCTGCGCCCAAAGAGACAAGGAACCAAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	T	C	GAGCAGAAGGCAAGAGGCGGCAAGATGAGTTTTGAGCGTTGTATTCCAAAGGCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[T/C]ACATCTGCCCGCCCTTCCCAGCCCTCCCAGCCCTCCTCGTTCTTC ATTCATTCAACAAAATTTGGC
U10694	20	C	G	GTGACATGAGGGCCCATTCTT[C/G]GCTCTCTGTCTGTTTGAAGAGAGCAATCAGTGTTCTCAGTGGCCAGTGG GTGGAAGTGAGCACACTGTTATGTCATCTCTGGGGTTCCTTGTCTATTGGGTGATTGGGAGATTTATCCTT GCTCCCTTTGGAATTGTTCAAATGTTCTTTAATGGTCAGTTAATGAACTTCACCATCGCGAAGTTAA TGAATGACAGTA
U13877b	162	T	C	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTGCTATCTTTGTGACCTTGCACAAGTTGTTTAAC CTCTTTGTTGTTCAGAAATTTCTCCATGGAGTAACAATATCTAGGTTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGAGGAAACAGCCAAGAGAT[T/C]TTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187	T	C	TTTCTGTCCACTTTCACCTGGTTTTAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTGGAAGAATTAAATAAGCAATGCTGAACATCAGGAATTGTAGATATCCGTACAGAGAGT TCCAGTAAAATTTATGAGTCCACGACCCCTTTCTAAGCAGTCTCGGTCCATG[T/C]TCGGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122	T	C	TCCAATTATTGGTCCCCAAAAGCAGCTTCCAACGTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTAACAGAACGTCCTTGCGAGACTGAGCGATGACACCACAC[T/C]TTGTTTGG ACATTTAAAATTCACTCTGCTGAATAGGAGGAAGCTTTTCTTTTCCTGGGAAAACAACTGTCTCTTGG AATTA
U18543	58	T	C	GCACATGCAGAATAGACTCAGCCTATGTCCTGATTCCAGCTGGGTAGTTCTAGAACTT[T/C]AGAAAG CTCCATCTTTAATGTTTTTATTGTTTATGTCCCCTCCCGGCTTCCCACCTAAATTTAGAGCTTTAAA AGAATGCACTGCCCCAAATAGGACACACGATGGTGTTAGCTGAAGTTTGATTAGCAATTAGGCACTTCC AAGGCTTTAGTAGAGAGAGCC

Clone	Pos			Sequence
U25975b	164	C	A	TCACTGCTGTGTGGCCTCCATACTCTTTTTCCATTTTCTACACAAGAGAAGCCTTTAGTATATGAAAATTATTACTCTTTTGGGGGTTTAAAGAAAATGGTCTGCATAACCTGAATGAAAGAAGCAAATGACTATTCTCTGAAGACAACCAAGAGAGAATTGCAAAAAGA[C/A]AAGTATGACTTTTATATGAACCCCTTCTTTAGGGTCCAGAAGGAATTGTGGACTGA
U25975a	143	C	G	TCACTGCTGTGTGGCCTCCATACTCTTTTTCCATTTTCTACACAAGAGAAGCCTTTAGTATATGAAAATTATTACTCTTTTGGGGGTTTAAAGAAAATGGTCTGCATAACCTGAATGAAAGAAGCAAATGACTATTCTCTGAAGACAAC[C/G]GAAGAGAGAAAATTGCAAAAAGACAAGTATGACTTTTATATGAACCCCTTCTTTAGGGTCCAGAAGGAATTGTGGACTGA
U25997	61	A	G	CAGGGAGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTAGGGGTGTTGACACACCA[A/G]TTTGAGTGTACTGTGTGCCTGGTTGATTTTTAAAGTAGTTCCTATTTTTCTATCCCCCTTAAAGAAAATTGCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCAGCATTCCCACCACAAAATCC
U28413	29	C	T	ATTCCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATTTTCCTCATGTTTTAAAATGAGGTTAATATTTGCATAAAATCCTAAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCCTTGATCCCAGATGTTGTGGCCTGGGAAAGCCCCTCATTGCTACAGTACAAGTAACACAAGTCGTTGTACCTCAGTG
U30884c	89	A	G	TAGGGGTAGCATTAAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGGACCTGCCGTATAATCTGTTCTTCTATTCCCACGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTATTGACGGAAGTCATTAGAATGGCTTGAACTTGCCCCACAGTTGAACACAAGTGCTGTCA
U30884a	34	A	G	TAGGGGTAGCATTAAAGATTCAGGAGTCATTAGCA[A/G]GTGATGATTTTGGGGACCTGCCGTATAATCTATATGAGTCATAGAACACAAATCTATGTTCTTCTATTCCCACGTTAGCCAATTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTATTGACGGAAGTCATTAGAATGGCTTGAACTTGCCCCACAGTTGAACACAAGTGCTGTCA
U31216b	78	A	G	GGGACAGCATATGTGGCACGGCCTCTCGTCTGTGCACGTGAAGACCAATGAGACGGCGCCTGCAACCAAACAGCCGTCATCAA[A/G]CCCCTCACTAAAAGTTACCCAAGCTCTGGCAAGACCTTTCAGATACCAGCACCAAGACCCTTTACAACGTAGAGGAGGAGGATGCCCAGCCGATTCGCTTTAGCCCGCCTGGTAGCCCTTCCAT
U31216a	70	G	A	GGGACAGCAGCATATGTGGCACGGCCTCTCGTCTGTGCACGTGAAGACCAATGAGACGGCGCCTGCAACCAAACAGCC[G/A]TCATCAAACCCCTCACTAAAAGTTACCCAAGCTCTGGCAAGACCTTTCAGATACCAGCACCAAGACCCTTTACAACGTAGAGGAGGAGGATGCCCAGCCGATTCGCTTTAGCCCGCCTGGTAGCCCTTCCAT

U31416c	76	G	A	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCTGCCTCCTCTCTCTTGCTTACAAATGTCTAGGTCCCACTGCCTGCT GGAAAGAAACACACTCCTTGCTTAGCCCACAGTTCTCCATTCACTTGACCCCTGCCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68	C	T	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCCTCACGCCACCACAAATCTGGTGCTGCCTCCTCTCTTGCTTACAAATGTCTAGGTCCCACTGCCTGCTG GAAAGAAACACACTCCTTGCTTAGCCCACAGTTCTCCATTCACTTGACCCCTGCCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78	C	T	ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCAACTCACATTGTTCCTCC AGACCGCAGG[C/T]CCCCCAGCCTCAGGTTGCTGGAGCTGTCACATGACTCCTGCCTGCCAGG GCTCAAAGCAAGGTCTTGCTTCTATCTGGGGGACGCGTGCTCGAGAGAGGCCGAGAACCGCAGAAC ATGCCAGGTGTCC
U37690	54	A	G	GACCACGCTGAAACCCACCCACCCGCTGTCGTGCTGACCATGGCCCTGAGCGTCCT[A/G]CCCCGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCCTGGCCGCCAGTGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGTCTT
V00540	39	T	C	TGAAACCGTTTCAACATGGAAATGATCTGTATTGACTAA[T/C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCCTATAACCACCGCATGAGTTGAATCAAAATTTCAGATCTTT TCAGGAGTGTAAGGAAAACATCATGTTTACCTGTGCAGGCACTAGTCCTTTACAGATGACCATGTGAT A
X15943	106	A	T	TCAAGAAGGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTAA AACCACTCTCTGAGCCCTCTCTGAGACGTGGTTTAAAA[A/T]ATCCATAAGGAAGGTACCCACAC CAGTATCTGAGTTCCAGTAGCTAAGACCCTAGAATTGGATTCATCTCTGTTTTTCATGTCTCTCCTT GTAACCCTGAGATCATCAG
X52011b	148	C	T	AGGAAGATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTCACATTAACATTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGGAGACACATTCACAAAGAAAGTTGCGAAAATTGCG AAATCTGTTGTGTGCA[C/T]GCTCAAATGAAAAACGCCCTTTCGGGCTTTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118	A	C	AGGAAGATCCCACCGACCCTTCCTGGCCTAATCCTTTAGATTAGGTCACATTAACATTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGGAGACACATTCACAAAGAAA[A/C]GTTGCGAAAATT GCGAAATCTGTTGTGCACGCTCAAATGAAAAACGCCCTTTCGGGCTTTTTATTTTTTGGGAACTG CGAGTGGCTTAGGTCTAGCCT

ID	Pos				Sequence
X54741	24	A	G	---	CAGGCCACCTGTCTTCTCTCCCAC[A/G]TGCACAGCTTCCTGAGTCACCCTCTGTCCAGCCAGCTCCTGCACAAATGGAACTCCCCAGGGCTTCCCCAGGGACTGGGGCTTGCCAGGCTTGTCAAATAGCAAGGCCAGGGCACAGCTGGAGACGATCTTGCTGGCAGGGCCTGCCTGTCCCCAGCCCCACCTGGCCCCTTCTCCAGCAAGCAGTGC
X54869	99	A	G	---	AAGCATTTGCGTTTACAGTGCATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATTGCATAAATCTGAAAATGAATTATGTTATTTGCTCT[A/G]ATACAAAAATTCTAAATCAATTATTGAAATAGGATGCACACAATTACTAAAGTACAGACATCCTAGCATTTGTGTCGGGCTCATTTTGCTCAACATGGTA
X66924	147	G	A	---	GCCGTGTCCTGACACCTCCAGAACGCAGGTGCTGGCGCGCCGTTCTGCCTGGGACCCCGGGAACCTCTCCTGCCGGAAGCCGGACGGCAGGGATGGGCCCCAACTTCGCCCTGCCCACTTGACTTCACCAAATCCCTTCCTGGAGACT[G/A]AACCTGGTGCTCAGGAGGCGAAGGACTGTGAACTTGTGGCCTGAAGAGCCAGA
X78932	62	T	G	---	GAAATGTGAAGAAATGTGACAAAGCCTTTAAGCGGTTGTCACACTTGATTGTATATAAGATAA[T/G]TCATACTGGAGAAAACTCCCAGAAGTGTGACAAATGTGACAAAACATTTAATTAATTCTCATACCTTATTGCACAGGAAAGCATTTATACTTGAGAAAAAATTGTATAAAGAATGGAAAAGTCATTATAAATATCTGCTCATATCTTAACATCAGCGAGTT
X80026	25	T	C	---	CTCAACCCATAACCTCAACCACATC[T/C]TATCCTCCACCCCACATCCCACCACCACTCCATCCCCAACCCATCCTCATCCCCAACTACAGCCCCAAACCCAGCCCCAAACCCAGGGCCATCCCCAAACCCATCCCCAAGCCAAACTCAACACCATCC
X80197b	99	G	C	---	ACCCCAACTCAAGTCCCAGGCCCCAGGCATCTTTCCTGCCCTGCTTGGCCCATCCAGTCCAGGCGCCTGGAGCAAGTCAAGTGCTCAGCTACTTCTCCT[G/C]CACTTTGAAAGACCCCTCCCACTCCTGGCCTCACATTTCTCTGTGTGATCCCCAACCCACAGTGGGAAAGGCCACCCTAGAAAG
X80197a	28	A	G	---	ACCCCAACTCAAGTCCCAGGCCCCAGGC[A/G]TCTTTCCTGCCCATCCAGTCCAGGCGCCTGGAGCAAGTGCTCAGCTACTTCTCCTGCCACTTTGAAAGACCCCTCCCACTCCTGGCCTCACATTTCTCTGTGTGATCCCCACCCACAGTGGGAAAGGCCACCCTAGAAAG
X85106	150	G	A	---	GGCACCCGAGAGTGACCACAAGTCCAGCAGGAGCGGCGGCGGCCTCGCCGTGTCCGCTCGGCGTGTCGTTTCTTTTTCAGCCCCGGAGGAGGTCCTGACCTGGGGGCTTCTCCAAAGCCTGGTTCTCCAAGC[G/A]AAACCAAATGCGCCCTTCACCTCGCGTGCCCGTGCCGAGGCCGGGGGCTTCTTTCAGAGC
X87160	128	T	G	---	ACCACCAGCCATGGTCTAAGGACATGGATGGGGTGCCCCAGACGTGTGCACAGGGACCCTCTGCCCCACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTAAACCGCAAGATGGGGCC[T/G]GGGGCATGCGCAGGGAGGAGCCATCGGGTACTACGCCAGCAACACTCACAACTGTCCCAGGCTGAGATAAATCCCGGGA

ID	Pos			Sequence
X87344	34	C	T	CATCCCAAGGCACTGGTGGTGACTCTGCTTCCCTG[C/T]ACTGACCCAGAGCCTCTGCCTGTGCACTGC AAGCTGTGTCTACTCAGGCCCCAAGGGGACTCTCTGTTCCATTCTCCCCCACAGACCTGTCAAGAG AAGCATGACAAACAAAATCATTTACCGACTTTAGTGCTTTTTT
X87838	179	G	T	GGTGGGCTGGTATCTCAGAAAGTGCCTGACACACTAACCAAGCTGAGTTTCCTATGGGAACAATTGA AGTAAACTTTTGTTCTGGTCCTTTTGGTCGGAGGAGTAACAATACAAATGGATTTGGGAGTGACTC AAGAAGTGAAGAAATGCACAAGAATGGATCACAAGATGGAAATTTA[G/T]CAAACCCTAGCCTTGCTT GTTAAAATT
Z14138	81	A	G	GTTCTGCTGCCTCTACACAGGGCCCTGTACAGTGAATGGTGCCATTTCGAAGGAGCAGCAGTGTGA CCTCCTGTGACCC[A/G]TGAATGTGCCTCCAAGCGGCCCTGTGTGTTGACATGTGAAGCTATTTGAT ATGCACCAGGTCTCAAGGTTCTCATTCTCAGGTGACGGTGATTCTAAGGCAGGATTTGAGAGTTCACA GAAGGAT
Z18859	191	A	C	TAATCCTCACCATTCCTCAGGTATAAGTTCTATAAACAGGCTTGGAATCTGGGTAATTAAAAACAGA AAATTATAGTAGTCAATATACCATGACACATGAAGAATGAATCCATTCTTTGGAGATGGAGTATACATGACT GCAACTGTATTTCATACGTCTCTTTCAAAGTGGGATAGCTATTGCCAGCTTAAAAGAGC[A/C]CAGGTTC CAGTGACTGGTTTTCCAA
Z23091	159	G	A	AGAACCTGACCAGATGTGGCTCGGAGGGAATCCAGACCCGCTGCTGTTGCTCTCTCCCTCCCCTCCC CACTCTCTCTCTCTCTCTCTCTCTCCACTGCCACAGCCTTCCTTCCCTCCTCCTCCCCTCTCCG CTCTGTGCTGCTCTCTCATTCTCAC[G/A]GCCCGGCAACCCCTCTCCTCTCCTGTCTCCCGTCTCTGGAAA CTGAGCTTGACGTTTG
11595b	125	A	G	GTTGGCCATTGTTAGTAAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAAACCTGACCCTAGTTGTGCTCCAGGACCTA[A/G]GCGTGC TCACTCTACCTTGTCTTTGTTGTTGAAAGGAGTGGTTTCCCATGACTGTTAAGTGACAAGTGCCATGG ATATCTACACGTCACCAGACTAGATTGTCTCAATGTCCTTGGCTTGCGAC
11595	125	A	G	GTTGGCCATTGTTAGTAAAACTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAAACCTGACCCTAGTTGTGCTCCAGGACCTA[A/G]GCGTGC TCACTCTACCTTGTCTTTGTTGTTGAAAGGAGTGGTTTCCCATGACTGTTAAGTGACAAGTGCCATGG ATATCTACACGTCACCAGACTAGATTGTCTCAATGTCCTTGGCTTGCGAC
1241	131	G	T	TATATCACATTAGTAGTATGTCACTGCCAATGGTCCATGTGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTTGAA TGGTCTTGTCCTTTCAATAAAAGAGTGACACATGTGTTTAGATAAAGGGCACTT[G/T] |GCAGGAGTGTTAGGATGAAGAGAAGAGATTAAGGAAGATCAGGAGGAAGAAAGTAGCAATGGGA ATGAAAAATAGGAGGGCCCTGAGATCCCACTGGATAATCTAAAAAACCAAGAGAAAG

ID	Pos	Allele 1	Allele 2		Sequence
1282	130	C	T	...	GTGCGGATCACCACTACAGTCTAATTTCAGATGTTTTCATTACCCCTAAAAGAAATCTTGTACCCATTA GCAATTATTCCTCATTCCTGCCCCTCACCCCCAGGCCCTACTCTTTATCGCTATAGATTTGCC[C/T]ACT TGACATATCATACACATGGAGCCATACATATGTGCCCTCATGATTGGCTTCTTCACTGAGAATA ATGTTTTCAAGGT
6810	68	C	T	...	AGTATCACACATACTACTTAATATATTAGATATACACAACAATAATAAAATCACTCCCTACCTTGAAAACTTT A[C/T]AGAAGCATTTTAATTTTACAACACAAAGCTCAAACGAACCTACAATAAGTCTAGTAGTCTG TTTACGTGCCAAGGGATAAGGCTGAACAATAAATTAACCCTTTAAAAATGTCTATGAACAAGTACAA TTTTCTTTTGAGTTCTGCAGAGCAATGACCACTAAGACCACTAAGAAATATTTTAAAGGC
6817	118	A	C	...	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTTGTAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGGTAAC[A/C]TGTGGATACCCTG TGTGCTTCTACTGGCCTCCAAAGGCATTCAGGGGATCATCAAAGATGTTGGACACCTTGTGTTCAAATC TTGGTTCAGGTGCGGCCGCCTGTGCAGATCGGCTTTTGGTTTGGTTGTTCTTAG
6819b	212	C		...	CCATTTATTTTCTCTAAATTTAAAATAGAAGACTTAATGGAAAACATTAGTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTACCACGCAGGAGAGCCTAGTAAAAGCCCCGTCAGTAGT ACACATTCTCTATGGTCCTTCAACAGTTTGCATATACAAAATTTCTGCTATTTGCTTTAGCAAA CAGCAATAAAACTTTGTGTTTCCTATATGACACCTAATATCCA
6819a	166	G	T	...	CCATTTATTTTTCTCTAAATTTTAAAAATAGAAGACTTAATGGAAAACATTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTACCACGCAGGAGAGCCTAGTAGAAAGCCCGTCAGTAGT ACACATTCTCTCTATGGTCCTTCAACAGTTT[G/T]CATATACAAAATTTCTGCTATTTTGCTTTAGC AAACAGCAATAACTTTTGTGTTCCTATATGACACCTAATATCCA
681xx	39	A	G	...	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCACCATTTGGGACA CAGATTATATATGTCAGACACCACGAATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGT TTAACAAAAGAAATGAAACGTCTAGG
6972b	149	G	T	...	AGGATTCCCTCTTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTCCTTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCTGGACTCTTTTGGTTGGTAAACTATTGATTATTGC CACAATTTCAGA[G/T]CCTGTTATTGGTCTATTCAGAGAGATTCAACTTCTTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122	A	G	...	AGGATTCCCTCTTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTCCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCTGGACTCTTTTGGTTGGTAA[A/G]CTATTGATTA TTGCCACAATTTCAGAGAGATTCTATTGGTCTATTCAGAGATTCAACTTCTTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

ID	Pos	Allele 1	Allele 2	Sequence
7598k	210	A	C	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTAATATTTGATCCCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTTCCCGTATTTCCTCAATGCAG[A/C]
7598j	208	A	T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTAATATTTGATCCCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTTCTTTATATTTCCTCAATGC[A/T]GA
7598i	192	G	T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTAATATTTGATCCCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTTATATTTCCC[G/T]ATTTTCCTCAATGCAGA
7598h	144	C	T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTAATATTTGATCC[C/T]ATTATGTGAGAGATTTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTTCCTCAATGCAGA
7598g	142	C	T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTAATATTTGAT[C/T]CCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTTCCTCAATGCAGA
7598f	120	A	G	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTG[A/G]GGATGCCTTTTAATATTTGATCCCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTTCCTCAATGCAGA
7598e	83	C	T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGCCGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTAATATTTGATCCCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTTCCTCAATGCAGA
7598d	77	C	T	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAGCCAAAGGAACTCAATGAAATAAGC[C/T]GCTAACCAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTAATATTTGATCCCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTTATATTTCCCGTATTTTCCTCAATGCAGA

ID	Pos	Allele			Sequence
7598c	56	A	G	...	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTACAAAAGACACCCAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAAATGAAAATTATTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTATATTTCCCGTATTTT CCTCAATGCAGA
7598b	47	C	G	...	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACA[C/G]CCAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTATATTTCCCGTATTTT CCTCAATGCAGA
7598a	30	A	G	...	AAAGGTAAATCAAAGTTCCCTCTATAAATT[A/G]TGATTTACAAAAGACACCCAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCAGATTTTACCTTGGAGAAATGAAAATTATTCTTGAGGATGCCTT TTAATATTTGATCCCATTATGTGAGAGATTTTCCTGATATGTTATCTTATTATATTTCCCGTATTTT CCTCAATGCAGA
7998c	116	A	T	...	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAATGAATGGGTAGTCCTATCTTCTCAAGGTCCCCAAATA[A/T]CCTTGAGGTTCCT
7998b	94	A	C	...	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTTAATGAATGGGTGAGTCCTA[A/C]TCTTCTCAAGGTCCCCAAATAACCTTGAGGTTCCT
7998a	75	A	T	...	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCTATTCAGACATCTTGCCAGCTCTCCTGTA ATACTTT[A/T]ATGAATGGGTGAGTCCTATCTTCTCAAGGTCCCCAAATAACCTTGAGGTTCCT
8071	119	A	G	...	AAATACAGAATTTATTTAGAAACTGTTTAAAGTAGAAAAAACCCTGTCAAGAAAGACCAGGTGG AAAATGGGTTCCCAATAAAATGGAATTTTAGGGCAACAAAAGTCTAAAAGGCC[A/G]CAAAAGAGA AATAGCACCACTGTCATTGAACAATGGCTAGTTACTTGCATTTTTGGCATTGTTAATCACTGAATC TGGGTTTCCTCTGAATTCCACACAGAGCATGCACTACACACAAACATTTTATCAT
8467b	93	C	T	...	AAGGCTTTCCTCTCTAAACATCAGTCCTACGGAGAAATCCTGGGAAAATCCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA[C/T]GGTCATCGAAAGCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAAGCTTGCAAAAGTATTAAGGAAAAAAATTACTG
8467a	70	A	G	...	AAGGCTTTCCTCTAAACATCAGTCCTAAACATCCTGGGAAAATCCTGGATATTTGGCTTATCACTT TG[A/G]CGCAAAATCCCACTTTGCTGTAACGGTCATCCGAAAGCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAGTATTAAGGAAAAAAATTACTG
8498	84	C	T	...	AGGGTTCAGGGTTTGGTTTAAATCAGGGTCGCACCTTTCAAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATACTTCATTAATACTTAACATTAGTCTTTAAAATAAAAGAAAAA AATCCAGTTTAAGAACAATTAACATTAGTCTTTAAAATAAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCAGGAATGTAATTTTCCTAACTCAG

Clone	Pos	Alleles			Sequence
WI-18562	29	G	A	---	CTAAGGAAAAATTTAATGATGGAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTTATTTCACATAGCTTAGTTTGGGGATAGAAATAGAACTAATGTTACAATGATTCTTACATT TAGCATTAATCAGAAAACGA
WI-18618	51	A	C	---	ATAGCAGACTTTAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTTCGATGCAAAGTATAATTGTAACCACCAGTGCTCGCACAGTTC AC
WI-18683	22	C	T	---	TAAGCTGTTCAGGACTGGACTC[C/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAATAAATTTCTCTCCCAAAGCCTGCCTGCAGT
WI-18520	75	G	A	---	GACTTTGGTGATTTAATTGCTTTTCCCTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTTCTTT ACTACA[G/A]CGGAGTGGTAAATACTACCTACTGCCAACAAACACGGCATCCACTCTGTCTTCAA TGCCTCTTCCGTGAGAC
WI-18563	94	A	G	---	AAATAAAGTTTTATTGGCACACAGCCCAAGCCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGGTTCACTAATGTGAC[A/G]GACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	T	A	---	GTCCTATTTCAATTTAGCTAGACCCATTCGTTTAATGGCTACATTTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTATTTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94	G	A	---	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTGAATCTTCATCCT TGGTAACAGGTACATAGGTAACCAAA[G/A]TATATAGCTTATTTGGTAGATCTTCATCCT
WI-18723e	71	T	C	---	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTGAGATTTTTGAAAG TGG[T/C]AACAGGTACATAGGTAACCAAAGTATATAGCTTATTTGGTAGATCTTCATCCT
WI-18723c	96	A	G	---	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTGAGATTTTTGAAAG TGGTAACAGGTACATAGGTAACCAAAGT[A/G]TATAGCTTATTTGGTAGATCTTCATCCT
WI-18619	44	G	A	---	TTTATTACAATATTAGGTGGCACAATAACTAACAAGCTTCTGA[G/A]ACAGGAGGTAACATTCTCA TAGACTTTGCAACTCAGCCAGAAGTAAAACTCGAAATA
WI-18715	76	G	A	---	TTATTCACAAAAAGTGATATTGCAGAGGGTCTGGGGGCTGTACATGGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGGTATTTTTAATAAAAAAATAA TGGAGCTACAACCACCCC
WI-18535	107	G	A	---	GTAAATAAAGTTTATTGGCACAGCCACGCTCGTTCATTCGATCGATGCCATTGACATCTGCTGTTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAC CTTCTGTGTGGTCCCCGTG
D17525	107	C	T	---	AGAGTGGTCAGAAACACAGGGCCGAATCCAGGCTCTCTATCACTTACTAGTTTTCAGTTCTCTGGGCAGGTGAC TTCATCTCTTCGAACTTCAGTTCTTCATAAGATGGAAA[C/T]GCTATACCTTACCTTACCTCGTAAAA GTCTGATGAGGAAAAGATTAACTAATAATAGATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAGGTCGATGTGTCTACCAGGCAGACGAAG

ID	Pos			Sequence
DWU-133c	313	A	G	TAATTGGCCACTGCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCAGATGACGACAGAATATTTGTTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGGTAAATGAATGTTTCAGTTTTGAATTTAATAGTAACTCC AATTCAGTAAATGGTATCACTCGTTTAAAGATATGATTAGACT
DWU-133b	236	T	C	TAATTGGCCACTGCCTTATTTATTACAAAACAGAAATGTCTCATGACTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCAGATGACGACAGAATATTTGTTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGGTAAATGAATGTTTCAGTTTTGAATTTAATAGTAACTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTT[T/C]TAAAGATATGATTA
DWU-133a	199	C	T	TAATTGGCCACTGCCTTATTTATTACAAAACAGAAATGTCTCATGACTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCAGATGACTGACAGAATATTTGTTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTGGTAAATGAATGTTTCAGTTTTGAATTTTAATAGTAA[C/T]T [TCCAATTCAGTAAATGGTATCACTCGTTTACCCCTTTAAAGATATGATTA
DWU-36	102	C	T	ATGAGATCCTTTAAATCCTTCCATGAAACGTTTTGTGTGGTGGCACCTCCTACGTCAAACATGAAGTG TGTTCCTTCCTCAGTGCATCTGGGAAGATTTCTACC[C/T]GACCAACAGTTCCTTCAGCTTCCATTCGCC CCTCATTTATCCCTCCAACCCCCAGCCCACAGGTGTTATACAGCTGTTATACAGCTCAGCTTTTGTCTTTTCTGAGGAG AAACAAATAAGACCCATAAAGGGAAAGGATTCATGTGGAATATAAAGAT
DWU-387	169	G	T	GTGTATAAAATGCAACTGTTGATTTCCTCAACACATGGCTCACAAATTCTATCCCAAATCTTTCTGAA GATGAAGAGTTTAGTTTTAAAACTGCACTGCCAACAAGTTCACTTCATATATAAAGCATTATTTTTA CTCTTTTGAGGTGAATATAATTTATATTACAATG[G/T]AAAAGCTTCTTTAATACTAAGTATTTTTCA GGTCTTCACCAAGTATCAAAGTAATAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172			ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAGTATTCTGAACTGTCAAGCTGCCCAGTCAGAT GGGCTGTTGCCATTTAAAATCACTGTAATTAATTAGTTTGATTAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTCATTTGTTCTTGTTCTACAATGAAGAGATGATTCTTCTAGTTTATGGTTAG GCCTTTCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-447	85	A	G	ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAACTGTCAAGCTGCCCAGTCAGAT GGGCTGTTGCCATTTAA[A/G]ATCACTGTAATTAATTAGTTTGATTAGAGCACAAAGCTTAGCTAAT CAACCATTATTTTCATTTGTTCTTAAGAGGATTGANAATCAGTTAGTTAAATGTCTTTCTG TTAGGCCTTTCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-476	63	C	G	GTAAAATTCAGTTTTTCCAGTTCTCTTTGTGCTGCTTCTCAATTAGCGTTTAAGGTGAG[C/G]AT AAATCAACTGTCCATCAGGTGAGGTGTGCTCCATACCCAGCCGGTTCTTCATACACCAGCTATGCA GGAGCTTCTGGGAGATTTTTT

ID	No.				Sequence
DWU-505	67	A	T	---	TCATACTAGGGCAGTATCTCCCTCTAGCTAGTGTGCCCATACAGAAAAATTCTATCACCATACAAAATTTA[A/T]GCAGTATTTATGTTTAAAGCACAGTAGGTCATAACCTGGAAAAGTCTGAATTTATGGGTTCTATGCATGCCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTGAAGATGGATTAACTCTTTGACTTTGAGCTTAAACTTTTAA
DWU-512	131	A	G	---	AAAATCCAGGCATTCGAATCTGTTTTTCATGATTTATAGAGGGTTACACAAAGTGCCACTTATTAAAGAGCTTCCACAGTGAAGATGGAGAAGGTGAACTTGCTTGCTTTGCTTGCACTGAAAATAAATTGCTATCAAGAGCTGCCGTATGGCAGTGAGCAGGTATGTGTTGTTGTTGTTGGTC[A/G]AAACTATGAAACGGTTTTTATTCAAGATGTCTCCAGAGTGAAGATGCCGAG
DWU-525	97	A	C	---	AACTGCATATAGATAATTATCCAGGATGTGTGGCTCATTCTTTTCAGCTTGTTTCTATACTGTTTGTAATATACAGTTTTTGTAACCATATGATTGA[A/C]AAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACACCCAATTTAAAAAATAACATATTCTTGCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAATTCCACCAGGATTAATCTCTAAAATTCTAGTCTCTGATTTGC
DWU-59	94	C	T	---	CATTTCTTGTGAAAGGTAATGGACTCACAAGGGGAAGAAACATGCTGAGAAGTGGAAAGTCTACCGGCCCTTCTTGTGAACGTCACATTGGC[C/T]GAGCCGTGTTCAGTTCCCAGGTGGCAGACTCGTTTTGGTAGTTGTTTAACTTCCAAGGTGGTTTACTTCTGATAGCCGGTGATTTCCCTCCTAGCAGACATGCCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68	C		---	CTTGATCATGGGGTGGAATTTTGTGTATCTGGGCTTCATGGGATGCATAAATTTCCAGTTGGTAAGCAGCAGGTGCCGAGGGTCTGGATCAGAGAAAAAGGCA
WI-19856b	63	C	T	---	CACACTGGCATCTAGGCCTTCGCCTGCCGCATTGCAGAAGGAGGAGGCCAGGTCCCCCTCCTGGAGAA[C/T]GCTGCGTTCCCCAGCCCCACACGGCTTTGCACCACCACAGGCGTGTTGAGGCAGGAGGTGGGTAAGACGTAGCTGTAGACCCAAAGCAACCACCAGCCCTGGGAACCCTGCGGGAGGAGCACTTTAGAACATGGAAAAGTGTGGTCATCCCATCCATTAGACAAGAACACATCCTACACTAATAAAAAGT
WI-18014	40	A	G	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[A/G]GAATGAAAGTGCACCATCAGAGTGTAATTAGGTCTGTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTCTCAAGGGGCAAAGTGGCTTCTA
WI-18036b	97	T	A	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAAACTTCTAGAAATACAAAGAGAACATGATAAAAATCTGATCACAGTGGAAAATTTAATTCTTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATATTAGGGATCTGAAGG
WI-18036a	27	T	C	---	TTCCAATGTAAGAGTCAAGTACCAAGT[T/C]AAACTTCTAGAAATACAAAGAGAACATGATAAAATCTGATCACAGTGGAAAATTTTAATTCTTTCATAATCTTTGACACGGTCAAGTAAGCTAAAGGAAACATATTAGGGATCTGAAGG
WI-18046	72	C	T	---	TGTAAGGTGACTTCTATAAGCTTCCTAAACTGTCAAACTTTCATTTACTGAGATTATTTCAGGCCAATGTGT[C/T][T]TGTGGGTCTGAGATTTGATTATCAGCTGGGTAAGTTAACCTGTTCCTGTTTCA

ID	Pos.	Var.	Sequence
WI-18063	105	G/A	AGGCTTTAAACTGATAACAAATTTGCCTTTAATCACATACAAAAACTCTGCACTTTCATTCCTTCCTTC CCATGTTTTCTGATTTTGATGTAAACTTAAAATTTGT[G/A]TCCTTTAACAATATACTGTAGCTGCA
WI-18078	86	A/T	AGTTGAAAGATCAGAGAGAGGTTATGGTTGGTGAGTAGCTGAAGTTGGTGAGATTCAAACCTGGTCCAGTGTG TTGTTTTTCAGCATCAG[A/T]GTCCACTGACAGTTGATCTCTGCAGTATCTCACATGTGGT
WI-18091	90	T/C	CCAAAGCTCACTCAGTATTAATCATCTGCTAATTCCATCCTTTGTTAATTCCATCAGACACTGTGGT TTTCATCTCTAGAAGTTTGACTT[T/C]GGGCCCTTTTTATACCTTCCATATCTCAACTTGTTAAGC
WI-18119	38	T/C	GCAATCTGTAACAGTTTGGTAGTGGTATTACAGAGGA[T/C]TTGTGTAAAATGGATTGGAGTACTTAC CACTATTCATCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAACAGTTAATTTTGGTTCTT
WI-18142	66	T/G	TTCAAGATAATTACAATTGGAAGGGGACCAATAATTCCACTTTTTAATCGAAAATAATCTATATAC[T/G]CCCAATAAACTCACAGTAAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAGAGGAAAA
WI-18178	68	T/C	GCATAGGGTTGAGGGGTGTACAAGAGGAGAACCAGATTCAGTCCATGCCATGTCAGTCTGGGGG G[T/C]CGGCGGGGATGGACACAGACAGAGATCCACCACAGTGGGGT[C/T]GGGGAGGTGATTATGGCTGGGGAAGATG
WI-18244	35	G/T	TCAATCTGAAAACTTGCTGTAAGCCAGTCAGTGGGGT[G/T]GGGGAGGCTTTCTTGTTAAAAAGTCATTCCAAA GGCACTCACCCGACAGCAGCATCTAGCACCACAGTTGACAGGGACGTTGAGGTGGCAGAGGCTT
WI-18245	115	G/A	ACAGATGTCAGTTGTTTGAATTGGCCCATTAAAGTATGGGGCTTTTCTTGTTAAAAAGTCATTCCAAA AGGCTTGGCCAAGAGTTTGCTATACAACGGAGGGACAGAGAAAACATGA[G/A]CTGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI-18261	26	G/A	GATTTGAAGGGATTGCTTTATTTAAC[G/A]TGAAAAAGCGTGATAGAGGAACTGTTTAAGATAAACAA CTTATAAATACTCCCAATTGTAGAAGTGAAAGATTG
WI-18268	88	C/T	TAGGAGGGAAAAGGAGGTGGGCTGCCTGGGCCCTCAAGACATGAGAAAACGGGGTGGTGGCTTCCAAGC TTCCTTACTTCCCCCATAGATC[T/T]CCTGACAATGTGCTGCAGAAGCCTCCAACCTGGAAC
WI-18299f	107	C/A	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT ATCTATTTGGGGTCTGAGAATTCCACAATTTGAAGAATTC[C/A]TTTGCCAATTATTGACACATATTCTG CAG
WI-18299e	101	A/G	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT ATCTATTTGGGGTCTGAGAATTCCACAATTTGA[A/G]GAATTCTTTTGCCAATTATTGACATATTCTG
WI-18299d	77	G/A	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT ATCTATTTG[G/A]GTCTGAGAATTCCACAATTTGAAGAATTCTTTTGCCAATTATTGACATATTCTG CAG
WI-18299c	67	T/G	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCAATTTTTT T/G]ATCTATTTGGGGTCTGAGAATTCCACAATTTGAAGAATTCTTTTGCCAATTATTGACATATTCTG CAG

WI-18299b	52	G	A	---	TCACAAGTCAATCTCCCATCCAAATGACACAGTTTGTCTAAGATCATTAACTTG[G/A]TTGCCAATTTT TTTATCTATTGGGTCTGAGAATTCCACAATTTTTGCCAATTATTGACATATTCTG CAG
WI-18299a	48	C	T	---	TCACAAGTCAATCTCCCATCCAAATGACACAGTTTGTCTAAGATCATTAA[C/T]TTGGTTTGCCAATTTT TTTATCTATTGGGTCTGAGAATTCTTTGCCAATTATTGACATATTCTG CAG
WI-18307	76	G	A	---	TCAACTTGTACCAAGTTTAGCAGCAAGAGGATACTTCCTTAGAGACTTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72	C	T	---	TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAAACTCCGGGGGGGTGGGGTACTGATT TATC[C/T]TTAGATCCAAATAAAGCATGCAGAGAAGTG
WI-18350	48	T	C	---	ATGAAAGTCACTTCAATCATAAGGGTCAAGAGAAAGAATGTTTTCAGAT[T/C]TAAATCTATGAAAA GGTGTGTATCTGCTTGCAATTTAAGAAACAACACAAGTCA
WI-18395	77	G	C	---	TCTTGACATGATCTGTGAAATAACGTGATTGTGGTTGAATTTCCTGGAAAATTTGAAGAATAAATTG ATTATTCAAG[G/C]TGTGCATTGGTTTATACATATCTCCTCTCTTAATGCAAAGCTATG
WI-18398	62	G	T	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAAAGAAAAGAGAAAACAACTCAAGGGTT[G/T] GATAACATTGCCAGTATAACCATAATTCAAAACAAGCAGCAGAATTTGGGAGGATAATTTGTT
WI-18396	21	C	A	---	CTCGTTGGTATTCTCTCATCC[C/A]TTCCTTCTTTCTTCGCTCTTTCTAAAATTAAAGAAAAGCAATGGAATT TTAAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAACTTATCAACTTGTACAAAGTC AATGAAAA
WI-18409a	20	C	A	---	AAGATGGGAAAGAGGAAATC[C/A]TTTTTTCTTACTAGAGATTTTTTTCCCTTTAATCCTTTTCAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAAGCTCTGGGGCCCCAAGTGCTA
					AAAAAGGAAAAGAAAGGGATGGAGTGAAGGAGAGAGAGAGACAGAGAGGAACAAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCCGAGAAGGAAAACAAGAGAAAAAAAGG TTTATAGGTGGGGAGGAAGGA
WI-18442	62	C	T	---	TTGATGTTAATACTGTCATTCTGGAGATCGGCTAAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCCTCATATTTCCAACCA
WI-18452	38	G	A	---	ATATAAAGCTGGAGACTGGAGGGTGAGGGTGAGGACTGGGACTAGCTGTGTTGAAAGAGAATGTAGC AGTAGTAAAGATGAAAGACTGCAAACA[A/C]GGTTATGGCAATAGAGAGGTGAAAAGAAA AGGCCATATAAA
WI-18489	102	A	C	---	CTGGTGGGGAGGAAACAAAATTGTGGTATATTCATACAATGGAAAACTCTTCAGAAATAAGAAGGAA CAAACCACTGAATCAATCACACAACATGGACAAATCTCAAATCATTATTGCTGATGGAAAGAAACCATTCA
EST5b	93	A	-	---	TAAGAATACACAGTACAT

				Sequence
EST5	93	A	--	CTGGTGGGGAGGAGGAAACAAATTGTGGTATATTCATACAATGGAAAACTCTTCAGAAATAAGAAGGAA CAAACCACTGAATCACACAACATGGACAAATCTCAAATCATTATGCTGATGGAAAGAAACCATTCA TAAGAATACACAGTACAT
EST6	48	C	--	TTAGCTACTTTTCAGAATTGAAGGAGAAAAATGCATTATGTGACTGAACCGACTTTTCTAAAGCTCT GAACAAAAGCTTTTCTTTCCTTTGCAACAGACAAAGCAAAGCCACATTTGCATTAGACAGAT
EST8	158	A	--	GGACAGGACCTCTATTCCCGCCTGGTGCGACGAGCGGCTGATGGACTGAGGCCCCAGGGATACTGGGCC CTCTTCTCAGGGGCGTCTCCAGGACCACGACGATGGGAGATTGGACACTGTGTGCTCTTTGGTGGGGT GATAGCTGTTCCTGAGTTGCAAGCACGACGACGATGGGAGATTGGACACTGTGTGCTTTGGTGGGGT
WI-18740c	104	G	T	TCCTCATTGTTGGGGATGATGAGAAGAAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAGT GAGAACAATCTCATTTACCATCATGTATCCAGTAGTG[G/T]ATAATTCATTTGATGGCTTCTATTT TGGCCA
WI-18740b	96	C	G	TCCTCATTGTTGGGGATGATGAGAAGAAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAGT GAGAACAATCTCATTTACCATCATGTATC[C/G]AGTAGTGGATAATTCATTTGATGGCTTCTATTT TGGCCA
WI-18985a	105	C	T	CCAAAGTCTCCGTTCGCTCATAAAGAAGTTTTGGGATGGGAGAGAATCCAGACCATCTTGGGGCA GCCAGCCCCTGCCTTCATTTTACAGAGGTAGCACAA[C/T]TGATTCCAACACAAACCCCTTCCCC TTTTAAAATGATTTCTGTTCTAATGCATCAAAGGCCTCAGAAAACCATTGTGTGTTTCCTCTT TGAAGCAATGACAAGCACTTACTTCACGGTGGTTTTTGTTTTTCTTAT
WI-18746	114	G	A	GCCAGCAGCTGAAGTCTCTTTTCTTCCTCTCGGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGTGTACTTGACCGTTTTATATACTTTTGTAAATATTCTT[G/A]TCCACATTCTACTTCAGCT TTGGATGTGGTTACCG
WI-19112j	212	G	A	CCGTGTTCACACACACAATGGCAAGCATAGTCGCCTGGTTACGGCCGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAAACACACAGATCAGTAGTGCTATCTCATGACAAGCACAAGAAACCGACGACAAA TCTTTTGCGAGATTTCTTCTAGTGGCTTAGAAAACATGGCTTTAAGAAAACACGGTGATATCTTTGAG GGTGACAAGGC[G/A][T/C]TCTTCAAAACAGTTCCATACCAACTGCTTTGCTTCTAG
WI-19092	232	A	C	TGGTGGCTGGCTAGCTAGTTTCTACAGAACAATAATTTGCCTCTATAGAAGGCTATTCTTAGATCATGT CTCAATGGAAACACTCTCTTTCTTAGCCTTACTTGAATCTTGCCTATAATAAAGTAGAGCAACAACAC ATTGAAAGCTTCTGATCAACGGTCCTGAAATTTCATCTGAATGTCTTTGTATTAAACTGAATTTC TTTTAAGCTAACAAAGATCATAATTTTC[A/C]ATGATTAGCCGTGTAACT
WI-19057i	175	G	A	--	CCCATTTATTATAGGCCAGTGATGTCTCAAAGAGTAGAGGAGCGTCTACTGGTCTTTCAACTCCTTCA GTCTTCTGACGGCCGGACTTTACCGTGACGAAGTGTATTGTCAGGCACCGCCAGCCCACTG TCTTCATGCAGGAACCACAGTGCCAGATCCCCACAGCTC[G/A]TCTTCATCCTTGGTTTTGCCACA

					TGGGACTTCCAACTCAGAGGATGTGGGAATCCAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCAGTCCTCCCCA[C/T]TTCATTCTGCTCAACTCTTCTTGAAGGAGC TGGGCTTCCTGGGCTGGAAGCTGGGTCCTCCCCA[C/T]TTCATTCTGCTCAACTCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGCTAGAGCCTCATCTTTCAGTCAACTGGGA
WI-20103	168	C	T	---	GCCTTACCCATTTTGCACATATACATATGCACCACCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACCATTTATAAATCTTGTAAGGACAAGAAAATGGA[G/A]TTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTTCACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-20441	111	G	A	---	TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACAACATTTAGATGCCTCTTTTGAAAGAACGT TTTAGTCTTTTTAAACTGAGTTAAAAAAAATAACAATGCAATTTTA[A/G]ACACTGTTTTGAAA ACTTAAAAGTGCAGCAATA
WI-19911b	116	A	G	---	GTCCTCAAGGGGGAGAAAACTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAA[A/G]AAAGGGAGTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613c	165	A	G	---	GTCCTCAAGGGGGAGAAAACTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAAC AGCTCCTTAGAAGGCCAATAATAA[A/C]AGTTGGAAAAAAAGGGAGTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613b	156	A	C	---	CAGTAAAAGAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAATA[A/G]TATAACATTAGAAAA GCAAAATTCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGAGTTTTCCCACACTGGAAAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-19984	47	A	G	---	GCCAGTTGGAATATGGCCTATACGAACCAAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTCCTTGGAACTCTGCACCGACTGTCCATGCTGTGTGGGGGACTTACACATTCAAGTTTGACAGI T/C]TGAAAAACCAACTGGAGCTGCTTTCCAAGATGTTCCTTGTCCTTCAAATAGGAATTCCATG TTATTCTTTCTTGCCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-20122	135	T	C	---	GAGTGCCATACCTTCTCCCCAGGCCTTCTGCCCCAAGAGCAGGAGGTGCCT[G/A]AAAGCTGGGAGCGT GGGCTCAGCGCAGGGCGTGGTCACCTCCCATCCCGTAAGACCTCCTTCCCTTCCTCCCAGCAGGCCAAACATG GCCAGAGCTCCTT
WI-18846a	49	G	A	---	
WI-18959	123	G	A	---	AGCAGTGGCCTTATTGCATCCCAAACCACGCCTCTTGACCAGCCTCCTCCCTTGTGGCAACGGC ACAGCTAATTCTACTCACAGTGCTTTAAGTGAAAATGGTCGAGAAAGAGGCACC[G/A]GGAAGCCG TCCTGGCGGCCCTGGCCAGTCCGTGGGACGGGATGGTTCTGGCGTGTTTGAGATTCTCAAAGGAGGCGAGCAT GTCGTGGACACACACAGACTATTTTAGATTTCTTTTGCCTTTTGCAACC

WI-20146	31	T	C	...	TGAGTCTTCTGTAATTCATTGAGCAGTTAGC[T/C]CATTTGAGATAAAGTCAAATGCCAAACACTAG CTCTGTATTAAATCCCATCATTACTGGTAAAGCCTCATTGAATGTGTGAATTCAATACAGGC
WI-18922	74	G	A	...	TAGGAATTGGTTCACGCCTGAGGCAATTAGACACTTGGAAGATGGCATAACCTGTCTCACCTGGAC TTAAGC[G/A]TCTGGCTCTAATTCACAGTGCTCTTTCTCCTCACTGTATCCAGGTTCCCTCCCAGAG GAGCCACCAGTTCTC
WI-18763b	53	A	G	...	TTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA[A/G]TATTTAGAATG TACCATATTTTTGTAAATTATTATGTTTTCTAAACAAATTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18763a	38	A	G	...	TTTCTGTGTTGTGGGGTCAACCGTACAATGGTGTGGGA[A/G]TGACGATGATGTGAATATTTAGAATG TACCATATTTTTGTAAATTATTATGTTTTCTAAACAAATTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18771b	75	G	A	...	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAGATGTTGGG AACAGAA[G/A]AAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57	A	G	...	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG[A/G]AGATGTT GGGAACAGAAGAAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70	T	C	...	GGGAAAAATTTGAGACGCAATACCAATACTTAGGATTTGGTCTTGGTGTTTGTATGAAATTCTGAG GCC[T/C]TGATTTAAATCTTTCATTGTATTGTGATTTCCTTTAGGTATATTGCGCTAAGTGAAACTT GTCA
WI-18742b	51	C	T	...	ACAAAGTCCTGTAGCCCCCTCACCTTTCCTGTTTCACTTTTGCCAATGTA[C/T]ATCGGGTTGGTTT TCTTGTATTATTTAAACGGTTGTGGTTCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94	C	T	...	GTGTGTCCAAAAATGGGGTCTGCTGCTCGCTACCTTGACCCTTCCCTTCCTCTCTCTCTCATCA TCATTCCCAACAACATCCTCTGCCA[C/T]ACACAACAAAACGTAAGTTTCATTGGGCAAAAATTGA GC
WI-19970b	167	G	A	...	TATAAGCCCGAGTCACCAGGACGGCCCTGTCTGGCCACAGCAGGGGCTGCCTGTGGAGCCTGCCCACC GGCCCCCGGCAGTGCAGTCCAGCGGGGAGGAGCCTGCCCGGTTCCTCCTGCCAGTTCCTCACTGCGGGGACC AGCAAAGGCCTTCCACTGGGTTGGTCAAAG[G/A]TAGTCACCTTGGCCTGGTCATCCACAGAGGA TGTTGTTCAAACCAGAAATCTTTAAACGACTGACCTTCCTTAAAAACAGA
WI-19970a	126	T	C	...	TATAAGCCCGAGTCACCAGGACGGCCCTGTCTGGCCACAGCAGGGGCTGCCTGTGGAGCCTGCCCACC GGCCCCCGGCAGTGCAGTCCAGCGGGGAGGAGCCTGCCCGGTTCCTCCTGCCAGTTCCTCAC[T/C]GCGGGG ACCAGCAAAGGCCTTCCACTGGGTTGGTCAAAGGTAGTCACCTTGGCCTGGTCATCCACAGAGGAT GTTGTTCAAACCAGAAATCTTTAAACGACTGACCTTCCTTAAAAACAGA

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WI-19067d	202	T	G	...	TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGC ACATTCCCTCCTGCTCCCCCAGAGACTGCCTCCGCCATCCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGTCCTGGAGAATGTTGTGAGGGGTTATTTTTTAATAGTGTTCATAAAGAAA[T/ G]ACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCATTATC
WI-19067c	153	G	C	...	TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGC ACATTCCCTCCTGCTCCCCCAGAGACTGCCTCCGCCATCCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGTCCTG[G/C]AGAATGTTGTGAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCATTATC
WI-19067b	151	T	C	...	TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCCTGGCTGTGC ACATTCCCTCCTGCTCCCCCAGAGACTGCCTCCGCCATCCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGTCCT[T/C]GGAGAATGTTGTGAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCATTATC
WI-19067a	57	C	G	...	TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCC[C/G]CTGGCTG TGCACATTCCCTCCTGCTCCCCCAGAGACTGCCTCCGCCATCCCACAGATGATGGATCTTCAGTGGGTT CTCTTGGGCTCTAGGTCCTGGAGAATGTTGTGAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATTCTTCTTCTCAAGACGTGGGGGGAAATTATCTCATTATC
WI-19106	247	T	C	...	TTAATCCCAGCCCTACCCCTTGTTAGTTATTTAGGAGACAGTCTCAAGCACTAAAAAGTGGCTAATTC AATTTATGGGGTATAGTGGCCAAATAGCACATCCTCCAACGTTAAAAGACAGTGGATCATGAAAAGT GCTGTTTTGTCCTTTGAGAAAGAAGAAATAATTGTTTGAGCGCAGAGTAAAATAAAGGCTCCTTCATGTGGC GTATTGGGGCCATAGCCTATAATTGGTTAGAACCTCCTATTTTAA[T/C]TGG
WI-18944	147	A	G	...	CAAGGCAAAAATATCAGGAGCTTTTTACCACCTACTAAAAAGTTATTATTGTGAAACAAA AATGCCAGAAGGATAAATATTGATTCCTCACATCTTAACTTAGTATTTTACCTAGCATTTCAAAACCC AAATGGCTAGAAC[A/G]TGTTGTTTAATTAAATTCACAATATAAAGTTCTACAGTTAATTATGTGCATA TTAAAACAATGGCCTGGTTCAATTTCTTCTTCCTTAATAAATTTAAGTTT
WI-18952	232	G	A	...	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGAATGATTGTTCATAATACATAAA GTTCTCTGTGTAATTACAACTAAAATATTATGCCCTCTTCTCACAGTCAAAAGGAACTGGGTGGTTTGGT TTTGTTGCTTTTTAGATTTATTTGTCCCATGTGGGATGAGTTTTTAAATGCCACAAGACATAATTTA AAATAAAACTTTGGGAAAAGGTGTAA[G/A]ACAGTAGCCCATCACAT
WI-18932d	177	C	T	...	CACACCTCATGCTAGCCTCACGAAACTGGAATAAGCCTTGAAAAGAAATTGTCCTTGAAGCTTGTA TCTGATATCAGCACTGAGATTGTAGAACTTGTTGCTGATTTTGACCTTGTATTCAAGTTAACTGTTCCC CTTGGTATTTGTTGTTAATACCCTGTACTATCTTTGAGTTCAA[C/T]CTTTAGTGAGTTGTGGCGTTGGTTCA CTTCGTGGCTGAGGTAAGAACGTGCTTGTGGAAGACAAGTCTGTGGCTTG

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WI-19042	193	A	C	---	TTTGTCAGTGTTGCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGATGGATAAGGGAATAATATACTGCGACAGAGGCCACAGAGAACTTGGTGAGAGTCCAACAGACACAATTTATACTGGTATTAACTATCTCTTCTTTGGACTCTGAAGAGACCACTCAATTGTTTAGATTGTATTAACTATCTCTTCTTTGGACTCTGAAGAGACCACTCAACCA[A/C]GGCTG
WI-18984	208	A	C	---	ATTGGCCCTGTACAGTTTGCTTATTTATAAATTCATTAAAAACACTACAGGTGTTGAATGGTTAAAATGTAGGCCTCCAGTTCATTTCAGTTATTTCGAGTGTGCAGACAGCTATTTCGCACTGTATTAAATGTAACTTATTTAATGAAATCAGAGAGCAGTAGACACAGATGTTGGTGCAATACAAATATTGTGATGCATTTATCTT[A/C]ATAAAATGCTAAATGTCAATTTATCACTGCGCACTGTTTGACT
WI-18851	90	T	A	---	GCTTCAATTGGCGATTGATTCAGTGCCCACAATGTAAACAGGGTTGGTAGTTGTTACTCATTTTGAATATACCTTTTCCTTATTGTATTC[T/A]GTAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76	T	C	---	TCAACTGCAGTGTTGCTTCCCTCCCCCTATAGGGCTGGAATCTGTCTGGGGGAAACTTGCCAACCTTCGTGTCAGACAGAGGC[T/C]GGGGGTAGCCATTGTGCAGTCATGGCCATTGTGCAGTCAGGTGCTGTGT
WI-18821a	69	C	T	---	TCAACTGCAGTGTTGCTTCCCTCCCCCTATAGGGCTGGAATCTGTCTGGGGGAAACTTGCCAACCTTCGTGTCAGA[C/T]AGAGGCCCTCTCTCGGAGGCCGTGCTGTGT
WI-19021a	20	C	G	---	ACTCCTCTGCTGCTGTCCAT[C/G]ACTGTCCTTTGAACCAGGAAAAGTCACAGAGTTAAAGAGAAGCAAATTAAACATCCTGAATCGGGAACAAAGGGTTTATCTAATAAAGTGTCTTCCATCACGTTGCTACCTTACCCACACTTCCCCTCGATTTGCGTGAGGACGTGGCATCCTACGTGGCATAACACATCGTGTGAGCCCATGTATGCTGGGGTAGCGAGTAGCAAGTAGCCCTCCCCTGTC
WI-18908	70	G	C	---	TGGAAATTCCCTTCCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAAGGGTCAGTATGG[G/C]TTAGGGAAAAACATTCCATCCTTGAGTCAAAAATCTCAATCTTTCCCTATCTTTGCCCACCCTCATGTCTGTGTGACT
WI-19037b	155	A	G	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCCTTCTGGTCCTAGCCACGCCGCCCTGTATGACCGCGCAAATATCCCCAAAGCTTTTGGGTCCTCCAAGTCATGCCCGAATTTAGATGCTGGTCATTTCTGGAGAGGGGTCCCCTCCCCTTACGAACACA[A/G]AAACCCAGCCCACACGGGTGGTGGTGGTGAATGGGAGGTGGGTGCCAGCCACTGCTGGGGGGGTGGAGAGCCTTGGTGGTGGTGGTGACACAGTGAATGGGAGGTGG
WI-19037a	47	C	A	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCCTTCTGGTCCTAGCCACACG[C/A]CCTGTATGACCGCGCAAATATCCCCAAAGCTTTGGGTCCTCAAGTCATGCCCGAATTTAGATGCTGGTCATTTCTGGAGAGGGGTCGTCCCCTCCCTTACGAACACAAAAACCCAGCCCACACGGGTGGTGGTGGTGACACAGTGAATGGGAGGTGG
WI-19064	66	T	C	---	TTGAGGAGGTGGGGTGAACTGCTCCTTGGCAGGGATTGTGACACTGCCATTGCTGGGGCTGTGTTCC[T/C]CGCGGGGCTCTTCTGGACCTTGCGACCGTGGATACCAGGCCATGTGCCATGGTATTTGGGTCCTGGGAGGGGTGGGGTGAAATAAGGC

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WI-18972a	112	A	G	---	AGGCCCTGTGTGGCTTATGTCACCCAACAGAGAGGGGTCCTGAGAAGTCTGGCTGCTGCCTGGGATGCCCCCTGCC CCCTCCTGGGAAGGCTCTGCAGAGATGACTGGGCTGGGGAAGCAGA/GTGCTTGCTGGCCACCAGGCACTACGGCTTCCTCTCC TCATTGCAAGTTGTTCTGCCTGAGCACAGACAGTCAGCATGGAATGCTCTTGGCCA AGATGTGCTTTGCCTGAGCACACTGG
WI-19016b	184	C	A	---	GTTTGCAAACCAACATGTGTCTCTTTCAGTCATTCACTGTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTTGTAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCATCTCAAQC/AJCTCAACACTATTGAC TTTTGGGGCTGGATAGTTCTCTGTTGTTGTGGGGGTTTGTCTTGTGCACTGTAG
WI-19016a	161	C	T	---	GTTTGCAAACCAACATGTGTCTCTTTCAGTCATTCACTGTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTTGTAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAAACCTTAGATACATAGCCGA[C/T]TGTATACAGAGGTTTGTCTTGTGCACTGTAG TTTTGGGGCTGGATAGTTCTCTGTTGTTGTGGGGGTTTGTCTTGTGCACTGTAG
WI-20096	21	T	C	---	GGTTTTGGGGGCATTTATTTCQT/CJGATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCCCC ACCCTCATCTCAGAAAACAATCTCTCTCGCCAGACTTG
WI-19591b	156	C	A	---	TGGGGCAATTTAACAAACCAGGCAAAATATCACATATACCTGAATATAAGGTAACTCCAAGCCATG AGTATAAGATTAAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGTGCCC CTTAGGGTGGGGGAGCTCTTCCCCQC/AJCTACCACTCCCCACCCCAAGGCATCATTTTGGGAGAAAAA GTGTCTTCTATCTGGCTAGCTGTGTTATCGTGGATTGCACCTTCTTACACGG
WI-19591a	45	T	A	---	TGGGGCAATTTAACAAACCAGGCAAAATATCACATATACCTGAA[T/A]ATAAGGTAACTCCAAGC CATGAGTAGTATAAGAGGTAAGGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCCCTTAGGGTGGGGGAGCTCTTCCCCACCACCCCAAGGCATCATTTTGGGAGAAAAA GTGTCTTCTATCTGGCTAGCTGTGTTATCGTGGATTGCACCTTCTTACACGG
WI-20310	125	G	A	---	TCCTCCAGCTCTGTCATCCTCGTTGTCTGTGTTCTGTTCACGGCCCCCTCCAGGCCATGGTTTCTTCAT TTAGGTAGGAACAAAAGGCCAAAAGAAACATACAAGCCCAGCTCTCTCGAGAGGCTCCA[G/A]TCAGAA CTGGACCCCTTTAACTACAAAAGGAATCTTGGATGAATTATTTTAGCGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCCTCCCCAATGTCCTCCCCGGGGG
WI-20860	224	G	A	---	CTCTCCCCCTAAGGAGCCTTGGCCTTGCGCCCCATTCAGCAGGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCGTGCCCTTTATCCTGTCTCTCCT CCCCAGTGCTGTCACACTTGGGCAAAGTGGTGGCAGACCCAGCTCTTGTAGACC GGAAGGAAGGGGCGGGTCATT[G/A]GGTGATGGCTTCTGGCTTCTCTGGCTT
WI-19359a	39	T	C	---	GACGTGGACAAAGGAGGAGGTTAAATGAATACTTTGTTTTG[T/C]CATGTTCAAAAAAGAGTATTAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAAGCCATGTTCCAACTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTTCGGGCAATTCCTGGCCTCAAGTGGGAGGCCACGTG GGAACAAGGCCTCAGAAAACAAAGGACACATGCAGCCTCCCTGAGCCAGTTCCT

WI-19766b	93	A	G	---	TGGCCTCAATGACTGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTTCTGTGGTGGGCAGGGCAGG AGATGAACCATAGGAGCAGCCAAAAGTC[A/G]GACAAACAGAAGAAGGCACCAAGCCTGAAACCCTC CGGACAACAGCAGAGTTACCAGCTGCCTGAGGGTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCACCCTCCTACCACCAAGCTCTCCGGCCAGTCATGGACTTAT
WI-19766a	31	G	A	---	TGGCCTCAATGACTGGTACATTGGAGAAGCT[G/A]TGCAGCAGCATCCTTTTCTGTGGTGGGCAGGGC AGGAGGATGAACCATAGGAGCAGCCAAAAGTCAGACAAACAGAAGAAGGCACCAAGCCTGAAACCCTC CGGACAACAGCAGAGTTACCAGCTGCCTGAGGGTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCACCCTCCTACCACCAAGCTCTCCGGCCAGTCATGGACTTAT
WI-20512d	126	C	G	---	CTTCCTCTGTTTGGCTTTGCATTTGTGCGATTTGGAAAAACCACTTGGAAGAAAGGGACTTTCCTGCAA AACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCCTTGACTGA[C/G]AAAGC TTAGAAAGGAACTGAAATTGCTTCTTTGAATATGGATTTTAGGGCGGGGCCGTGGGTGGGCTCACGCCT TATTAATCCCAGGCACGTTGGGGAGGGCCAACGCGGGGGTGGGGATCAACCTGA
WI-20512c	59	T	G	---	CTTCCTCTGTTTGGCTTTGCATTTGTGCGATTTGGAAAAACCACTTGGAAGAAAGGGACT[T/G]TCCTG CAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCCTTGACTGACAAAGC TTAGAAAGGAACTGAAATTGCTTCTTTGAATATGGATTTTAGGGCGGGGCCGTGGGTGGGCTCACGCCT TATTAATCCCAGGCACGTTGGGGAGGGCCAACGCGGGGGTGGGGATCAACCTGA
WI-19599	230	C	G	---	GGGCTTAAAATTCCCCTCTGTTTGGGACTGGTCTCTCCAGTTTACAGCAAAGGATCGCACCCTTTCC ATAACCCCTTCTACATTGGAAAGAGCACACCTTGTATACAGAATGGCTCCGTGAAGTCTTTAAACG GACAAAGGTAAATCACAGCTAACAAACGTGATGTTGGCTCACACGTAACCAAACACCTCTTTTTCA GAACAGAGAGAGCGGTTAAAAGTAAAGGGCA[C/G]TTCCAAGAGTAACACTGCTA
WI-20679	82	T	C	---	TGTTTGAAATAAAAATTTCCATGGTCTTAATTGAACTGTATGTTACTTTCTTTTAGAATATCCTTTTT TTCATTAAAATAAATT[T/C]TCTAAACCACTCTATGTGTTCAACCTTCTGTTTAACACTAAGATATGGGT TTTTGGAAAGGCCACAAGTCACCAGCTCCATGAAGTGGGCGAATTGGTCCTTGTTTTGGAAAGCTCTC CAGGGTGTTTCTCCAGAAA
WI-19909a	29	T	C	---	CCAGAAATAAAGCCTGAATATTCTTTTCT[T/C]TTAAAAATATAATTTTCCTTCTTTTGCTCTTCCAA GTAAATCTTAAAATGAACCTGTTCTAGTCTATTTTAATCTAGGCAATTATAACACTACCTAGGCGGGGG TTTTTTCCTTTATACCTTGTTCTGTACTGTGGAATCAACTAA
WI-20341	221	G	C	---	TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTGCTTAGGGGCATGAGACATTAGGAAG GCCACAATTATGAGTAGTAAATGTGAGAAGGCTACTGCTCCCATTTGTTTAGCAGGA GGCAGGGAAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGTGGTAAATATTGGGTGGTGACGTCATGC ATCCCCCATGCATTGGTTTT[G/C]ATGTCTCCAGTGAGTGAGCTGAGCTCCAGTGCT

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WI-20113	60	T	C	...	TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAAGACCTGAAATACTG[T/C]GGAAACAGTAAAAGCAAATTACCACACAATTAGGAGGAATTATTTCAGACACATAGGATATTTAAAACATCACTCAAATACTGGAGCATGATTCAGCAATAAATTCTATTCGTTATTCATGGATTCATGATTCCGTATTGCTTTAAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGATTCCGTATT
WI-20895	107	G	C	...	TGATGGCAAAGTACAAAGGCTCTGAAAGAACAGAGTAAACAACAGAGAGCAGCGGCCAGTGCAGCGTGTGGCCACTTCCCCACCAGGCAGAACACTTGACTTCATTAAGGCAAA[G/C]CTTACTCTGTTACTTTTTCCTCCCACATAGTTAACCCAAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAATATAACTGGTACTATAGGCAAACAGATGCA
WI-20721	72	T	C	...	CCTGCAATCACAAAAGTGGAACTAGTTGATATTTGAAAATCATACTTGATTTAACCACCTTCAGAAATTCT[A][T/C]AAAACACTAGCAACTTCCTTTATCGAGA
WI-19415c	161	A	G	...	CTGGATTTTAATATTTCTGCCTAATAACCAAATGTAATCAATAAAATTTGGTCAATATCTCCACCTCATTTCTGCTAACATGTTTTGCAAGATTCCCTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAAAGTCATGAGACCCTTAGCTCATTA[A/G]AAGTCCACCTCATGAAGGAGATGATTCAACATCTCAAGCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103	C	T	...	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACTTCTGGCGGGTCGATGAAGAGACTGTTGGTCATGGCGGTGTA[C/T]GTCCTTCTCCAGGCTCATATGGATGTCCTCGAGGTTGCACAGGGAACTGCTCTGCTTGTAGAAGCTTCTCC
WI-19348b	98	G	A	...	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGGTAGCAAGTACGATGGGCCATGCACTTCTGGCGGGTCGATGAAGAGACTGTTGGTCATGGC[G/A]GTGACGTCCTTCTCCAGGCTCATATGGATGTCCTCGAGGTTGCACAGGGAACTGCTCTGCTTGTAGAAGCTTCTCC
WI-19635	98	A	T	...	ATTAGTTCGTGTTGGGCCACATTCAAAGCCATCCACACAAGCTTCTTGTAGGCCATTGTAACACAATGTTAAAAGGTACAGTAAAAAATACAGTATTAT[A/T]ATCTTATTGTGTAGCACGGCTGTGTGAGGCTCATTGTTGAATGAAGCATCCTTAGGCAGCACGTGACTGACTGCATGCAGATATGTGTGCTGAAAGAACTTTGCCTTT
WI-19641a	46	A	G	...	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAG[A/G]TATTATATAGTCTCATGTTTTTAATTTATGAATAAACGTCGATCATTGATTTGATTTGTGATTTGTATTACAGAGATGTCAGGGCTATCTCATTCAGTTATTAATAAAATGGATCAGAGTAGTCAAGAATAAGTGCATAAGTGGTTTAAATTTTAAAAAATACTCAGAATGAGGTAGTATTTTAATTTTAATTCATCCACCTG
WI-19642b	52	C	A	...	ATATAGAGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCTC[C/A]GGGTAAACCAGGACTATTGCATGGCATTCTTTAATACGTATTTGATGGACACAAGTTTTCATGTCTATTA
WI-19673b	180	C	T	...	TCTGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACTTTCTGTGTCATTGCCTTACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTGCATCACCACTGTAAATCTAATAGTGAAAAGGCAAATGATGTCTCAGTATCACTGTGAAAACATTTTC[C/T]CTTGGACCAGCTGAAAGAATCTTGAGGGAGCCTGAAGGCTTCAAGGTCCCACGTCAAAAAACACAGCCC

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WI-19673a	35	G	A	---	TCTGCCATGATCACATTGTGATGAAGAACATGATG[G/A]TCACTAGTAGTAGGTAACTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTGCATCACCACCACTGTAAATCTAAT AGTGAAAAGGCAAATGATGTCTCAGTATCACTGTGAAAACATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCAAAAAACACAGCCC
WI-19724	35	A	G	---	TTTATTTGGGAAACAAAGGATTGTAATTTGGGTAA[A/G]CTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAAACACAGCAGAGTTTTGGTTTTTCTCTT
WI-19307	196	T	C	---	TCCTCCTCCCCAACTAGATGGTATTGATCACTCTGCCCACAAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTTCTTGGATTGCCTTCATGAGAAAATGGTGGCTTGGGAGTGACATTCCTTGCTGT GGTGAACTGCAAAGAAGGAAACCAGGCAATGTATTCCATAGAGACCCTTAAAGAGACCCCG[T/C]TGG AAATGGGCCATGGTCTAATTTGGTGTTGAAATAAACTAACCTCTTTGGCTG
WI-19269	85	A	T	---	CTTCCCTCATCCCCTCTTCCACCACACCCGGAACAAGTGCTCCAGGATTCCCTGCCCACTGGC CATTTTGGAGTGTGTCC[A/T]TTGGGTAGCAATGTGGAAACCACCAGGGCCTTTGTGGAGAAAATGG AGGGGGTTGAGGGAGTCCCAGGAGTCCCAGGCCTTATTTGAGGGGCCTTTGCTGCTCATAGGCGAGCTCG ATCTCCTCATCTGGACAGGTGGAAGCGAATTCTTCCCGGGCGTAGGCA
WI-19946	122	C	T	---	CAATGGACTGAATGAGTGCGTGCTGGGTGGGCACACACCTTCAATACACGTCAAGGTCG CTTCCAGTTTTAGAAAACAGAAATCTGCATCTGAGACGCACAGAGGTTC/T]TCTTCCTG ACCCAGACGCACTCACGCAGGTCCTGGTTTTCAAAACTGCATTAACCTGCGCCAGAGAGTTCAC CGTAGGCATCTTTAATAAACTAACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G	A	---	CACAGCATGGTGTAAATAGCATCAGATTGAATGAAAAGTTTGTTAAATGCAACCATAAATAATTATA ATAAATATACACAAGTAACTTACAGCACACATTTTAGGGCCAAGGTTTGGATCTGTCTGGACCT CAATGT[G/A]CTCTCGGAGAAGCAGCCACGTTAGCAGCAGATACCTTACAGCTTGTCATCTACTCAA GTGATGGCCAACAGAAGCTTCTGAACTCCTCCTGGGGAGGTAGCTGACAAG
WI-19076	40	G	A	---	TTGGTTGGATACTTGCTGGAAAAAAAAAGCAGTTTTAAT[G/A]GTATTCAAAATACCTTTTAAAAA GTATTCTAGCACAAGATTTTCTGTAAACTAGATTAGTTGTAAACTTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATTCCTATTCCAAATCTATCTTGCGCTCCTGAAAAACTGCAGA AAGGCACTTGAAAGCTGTTCTTTAAGATATGGGATTTCTTTTTATTCTT
WI-20218	26	T	C	---	CCACACACTCTGGTTTATAAAGCTA[T/C]AGGACAGACAGAGCAGAGATGGAACTGAAAAACAGGGTAG AAAATAAACATAAATTGGAGGGGAACAGTGGGATGGGAGAAAGAATGACAACAGCCACATGTGCCCCA GTCAAATAACTTTTAGTCCCTGCAGCAGAAGATGCCAACCAAGTCTCTATACTGGCTGGGGATCCTGCC ATGGATGCAGGAGGAAAA
WI-20295g	154	T	G	---	CAACCTTTTTGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTAATATCTCCAGGCTTGATTGGGGAGGGGCTGGGCTCTACCCTTTCTTCTTTCCA TCCAGTCTATTGCCAGA[T/G]CCAGAGAAAGCGCGGGAAGCCCAGCTCTCCAGCATAGCCACTGTGG GTCGGGCTTCACCTTCTCGTCTGCGACTCCTCATGCTCGGGACTTGTCTTTCGGGG

Marker	Pos				Sequence
WI-20361a	192	G	A	---	CTGGGGAGTGCTGACCTAAGTGACATTTTTTTTAATGCCAAATACAGTAATCTCCAAGCTTTTAATGG CTTATGCAAGATGACAGAATATGTGAAATCTGATTGTCCCAGAGTTACACTCTGCACTCCAAAGCTA CAACAGTGCCACAGCTGCCACGCTGAGAGGTTTCCCTATACTTCCTACTACTGTGACAATTTAGC[G/A]ATCCTTC AAATGGGAAAATTCCTAACTACACGAGACAATGGGTCCTACAGTAGGCCCG
WI-20572	75	A	G	---	GAGCCAAACCCAAACAAAAATAAAACAGAACTCTTTTGTAAACTAAGTCATACCTACTTTCTTCT TCAGAATT[A/G]TCAT[A]AAACATCATCTTTACAACATGGAGAAGCGAGGTAGGCCATAATTGTTCA AATTTCATCTTTCTCAAATTTTAAAATTGTTTTAATCCCAAAGGTGCCTATTGAATTCTTCAAAAATA AACTGCCTATCAGGTATCATACCTGCAAATGCTTCTAAATATCTCTTGATTAT
WI-20588	133	G	A	---	CATGACAAAAGACAAAGATCAAAGGAGTAACATAAATTATAAGTTGAATAAAATAGTATACAGCAATC TTCACTTTTTAAGAAAAATGTGAGATCCTTTGTTGGTTTTTATTTCCTTAAGTACAAAAATGCTAAAC[G/A]GGAGCCGAGCTCTTCCGCATTCAGG
WI-20593	79	A	G	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAAACTCCAGTCTTTTTCAGTCTGTTG CTGTACTTCAG[A/G]TTAAAATCTGGGAAATCTGGAATGCATGAGCAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAAGGAACTCAGGATGTGTTAGGAAGGGGGAGTGGATGCCAGGCCTTCACCAGACTAT CCAGAGAAGCCATTCCATGGGGTATTTGGTCTGCATACTGTGAGACACTGAGCT
WI-19765	57	T	C	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATACCTTGTCCTCA[T/C]ATGTATCT TGTCCCTGCTGTCTTTTAGGTTAGCAAGGTGTATGAAATACTTTAAGTTTTGTTGTTTCTTTCCTCGT GGTATCAGTGAAATACTGATCTATTCTCTGGCTAGGTCAATTTACAAAATTGCCATGAACTGAGC AAAAGGCCCACGTGGGATAAAATCACTCACCATGACGCGACCAGTATT
WI-19066i	239	A	G	---	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAAACCTTAAAACCTTCACCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCGTTGGTCACCCTGAGAATTACTTCTCCATATTCCGGATGCTCAATTACAGT ACCATTGCAGGCAAACTTTTTCTTAAACG[A/G]TTTCTTTTA
WI-19066g	184	C	T	---	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAAACCTTAAAACCTTCAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCGTTGGTCACCCTGAGAATTACTTCTCCATATTC[C/T]GGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTTCTTAAACGCCTTCACTAGTTTCTTTTA
WI-19066f	148	T	C	---	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCCATGAAACCTTAAAACCTTCAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCG[T/C]TGGTCACCCTGTGAATTACTTCTCCATATTCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTTCTTAAACGCCTTCACTAGTTTCTTTTA

ID	Pos			Sequence
WI-19066e	147	G	C	---	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGC[G/C]TTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTTCTTTTA
WI-19066c	100	G	A	---	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAAACCATGAAC[C/T]TCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTTCTTTTA
WI-19066b	87	C	T	---	TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA[C/T]TTAAAACCATGAACCTTCAGCTGATCGTCCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATTCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACTAGTTTCTTTTA
WI-19066a	72	C	T	---	TTTACAGCGAGTTTTTCCCGTCTCAATAAGTAATCTAAATAGATTAGGGTGAAAAGAAAATGTG TGTCTAAATAAATCTCCCTTTTGAATGTATATTTGT[G/C]TTAATAAAGGAAGCATTAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTGATTCCATTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCGCCCCCAAAAAATACTGTTTAACAACATATGTTTTAAGA
WI-20660	105	G	C	---	CTGCTGCCAGCTTCTCTCTTGGCCCTCCTGCCCCCAGATGGCGGGTCTCCTGGCAGCCTCCCCTCAGTCTTCC TCCACCCGCCCTCCTTCCTTCCCCAGCCTGCCGCCTGCCATGTGCACCCCTTGGTIC/T]TTCGGCTCCCATCGCC TTGAAAGCTCTGAA
WI-18768	120	C	T	---	TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATGT[A/G]TATTTAACTTCTAGTTGCTCTTGCTTTG GTCTTCTTCCAATGATGCTTACTACAGAAAAGCAAATCAGACACAATTAGAGAGAGCCTTTCCATAAA GTGTAATTTTAATGGCTGCAAAACCGGCAAACTGTGCCCTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGTCTCATCTTGCATCTACCTGCTCC
WI-19087	37	A	G	---	GAAAGCCAGAGATTAGCCCGCCATTCCGCATCTGTCAACCAGGACAGAA[A/T]GCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACTTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAAACA CAGTGATTTGGGAATGCCT
WI-18790	49	A	T	---	AGGAGGGCTGTTCCAGGAGTCCTGCCCAGGAGCTCTG[G/A]GTGGCCAAGCCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGCCCGTGGATCCTGGTCCTAGGCTGGACACAGGATTCAGAAAAGACACCAGGCTGCACA GAAAGAGCCAGAGCGAGATGGCACCTGAGTGTCGGTCACAGCCCTCACTCACTCAAGGCCTCAGGAA
WI-18987	35	G	A	---	AGTCA

ID	Pos				Sequence
WI-18919	26	C	T	---	TGGATGAAAACCACAGGGATTCCGGA[C/T]GCCAGACCCCATTTATACTTCACTTTCTCTACAGTG TTGTTTGTTGTTGTTGGTTTTATTTTTATACTTTGGCCATACCACAGAGCTAGATTGCCCAGGTCT GGGGCTGAATAAA
WI-18741c	64	G	A	---	CTTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38	G	C	---	CTTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCA[G/C]ACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23	T	G	---	CTTTCTGGTCAAGGCTTTGGACA[T/G]CTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170	G	A	---	TCAGAAGCAGACATGGCATCTGTCCTTGCTTGTTGTTGGTTGTTGTACCTTCACGAGAGACCTGAATT TTAGAATTGCCCAGTGCTGCCAGAGTGAGTGAGTGTAATTCTCCTTTCAGGTAAAGATAGGCTATCTC AACACTGCTGAGTGATTCATAAACATATCAACCA[G/A]ATAGCATTAACCCATTTTATTTCCTGTCCTT AGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	46	T	A	---	CCAAGTTGCATCCATGTTGATTTTCTGATGAGACTAGAGTGACAG[T/A]AGTTTCAGAACCCAAAATGT CCTCAGGTAGTTGGAGCATCTCTATGGAGATGGGGATTATGCAGATGGCCTATGGAAAATGCAGCTGC ATAATTAAACACACATTATCAAAGTCCTCTACAATTTATTTATTTCCCGTCTTTCTTTCCCTCTTTCTGCACTGCCATAT ATGGGGAGAGAAATGCCTGCTT
WI-19183	210	G	C	---	CTGTTGAAGGCTTCCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAAAGCACACATTGGATG GCAGCATGGGGTTCTTCTTCCCATTTTATGGGCATGAAATATGTGGTTTAGAATAAGGAACAAGCATTATT CCTTTGCCAACAGCCTCACTCTAAGAGGCTTTTTGCTGAGTCAAGCAAACACTTGCCTGCTCTGCCC CTTGGAG[G/C]TGCATTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214	T	C	---	TTGAAATCCAGTCTCCTGGCCCCCAGCCAGGGTCGTCGTCACCATAGAATGTCTCCTCTACTGGGGTC GTTCTCAGGCTTTTTGTTAGAAACTTGGTCTGAGATGTTCTTCCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAGAGCAATGTTCTTCTTGTATTCTGAAACTGGAAACTACTTAAATGTTCTCATCTGT AAGCATACTTT[C/T]CTCCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198	T	C	---	GTCTCCCCAGAGTGCTCTGCGCACCCCAGCCCCTGTCTGCCTGTAAGGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCCAGGGGGTGCCCTTAGTTTGGACATGCTGGGTAGCAGGACTCCAGGGGGTG CACGGTGAGCAGATGAGGCCCCAAGCTCATCCACCAGGGGCCATCCTTCTCAATACAGCC[T/C]G CCCTTGCCAGTCCCTATTTCAAAATAAAATTAGTGTGTGTCCTTGCCTGTCTGT
WI-19135	20	G	A	---	CAGTTACCCTGCTTTGCCTGC[G/A]AAAGTGTCATCAATTTGTAATTTTAGTATTAACTCTGTAAAAGT GTCTGTAGGTACGTTTTATATTATATATAAGGACAGACCAAAAATCAACCTATCAAAGCTTCAAAAACT TGGGAAAGGGTGGGATTAAGTACAAGCACATTTACTGGCTTACGTAAATGAACTGATTTTATTAACT GCTTTTGCCCATATAAAAATGCTGATATTTACTGGAAACCTAGCCAGCTTCAC

ID	Pos				Sequence
WI-19236	54	G	A	---	TACACAGAGGGTCGCACTTGGACTCTGAGGGTTGGGTGTGGAAGGGGGAAAAGG[G/A]GATGGGAGACCTGCTCCCAGCTCTTCCTGTCAGCCGGTTTACATGGGAACAGGGTTAACATCTGTGTTAGGGGAGGTCACCTTACCCTTTTTCAAGGGCAAAGAACTCGTTGGGAGGATGTCTGTTGTTGTATGTAATACT
WI-19144	222	G	C	---	GTGCCAGTCTTCCAGAAAGCAAGGACTGCCCTTCATTCAGCCTTGCTGACCTCCCAGCCTTTCTAAGGCTCAGCCCCACGGGACTCTGGTGGCTGCCAGCTTGTGAGCTATCTCTATATTCATTCATAGCCAAACAGGAGACCCCTTTGCAGGACGGG[G/C]TGGGAACCAAACACCTTCAGTGCTGGTGCTGGCTCTGCTGGAGCGG
WI-19139b	110	C	A	---	CCCGTCTAAGGGAGGAGAAAGCTAATGTGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGACGGCAGATGCCTGACAGAGAGTGGGTTGGCAGCAGACAACACACTAG[C/A]ATTTCACGGGGTGTGGGCACATGGGTGTGGCACCTGGCGTGTGCAGCATGTGGCCGGTCTCTGTGTGAAGCCACCGTGCTTCTCTTTGGGGGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGTGCGAGGCTTTGAAG
WI-19139a	66	C	T	---	CCCGTCTAAGGGAGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA[C/T]GGCAGATGCCTGACAGAGAGTGGGTTGGCAGCAACAACACACTAGCATTTCACGGGGTGTGGGCACATGGGTGTGGCACCTGGACGTGTGCAGCATGTGCAGCATCTCTGAAATCCTGGCTGTGTGCGAGGCTTTGAAGGGGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGTGCGAGGCTTTGAAG
WI-18910	112	T	C	---	GGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAGAACCTAAACATGAAAGGAAAGGGTGCCTCATCCCAGCAACCTGTCCTTGTGGGTGATGATCACTGTGCTTG[T/C]GGCTCATGGCAGAGCATTCAGTGCCACGGTTTAGG
WI-19235	173	A	G	---	TTCAGGAGGTGGAGTTCGTCGTCACGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACACGAATGTCTCTGTAGCTTCCTTCCACTGCCCCAGTATTGCTCTGTATTTATCAGCGGATGCCCCTCTGTCACTCATGCTGCCTAATTGTTCACAATGGTGGAA[A/G]GCTTCACATGTAATATGATCAGGACCCACCTCCAGTTCTTCTGAAAGTGTGACAGTGTCACGGTTCTGCAGCACTA
WI-19222	179	C	T	---	CGTTTCCCTAACTCACCCAGTTAGTTTGGGATGATTTGATTTCTGTTGTTGTTGTTCCCCCACCAGGAAGTCTTGGAATTGTGAGCCTCTATGTTTCTGTTAGGTGAGTGTGTTGGGTTTTTCACACCTCTTCTGCAGGGACGGCAGCAATCCCTCCTTCCCCCTAAAGGGACTCTGCGGAAC[C/T]TTTCACACCCTCTTCTGCAGGGACGGGCAGGTGTGTGGTACACTGTCGACGTGTCCAGAAGCACTTT
WI-19117	134	A	G	---	AAATAATGCAACGCGCAGGAGGAGGAGAAATGCACTAAGACAAGAAATGAAGAACATTCTCATAGAACATTGATCTGTTTTACAGGAAAACAAACCTGCCTTGAAATTTACACAGTGAGACTGTACATAATTGCATGAAA[A/G]TAGCTATTTTTCCTAAGACATTTTCATTCATGAATATTTCAAGTTTTCATACTGTACACATTTCTTAAAACACATGATACCAGCCAGCAACTGAACTGAAAATGAATGCCGAATTTG

					Sequence
WI-19134c	263	C	T	---	CTCCTGTTCGTGACCTGACACAGGGTGACACAGCCCCTTTCACACTCTGTCCTCCTATCTTCCTGGGTAGATGCCCTGGTGGTGTAGGGCTGAGTACTGAATGGTCTTCCATCCCCAGCAAGGGGGTGCAGCCCAGGGTCAGGCCCTTCAGAGCACTTCATCCACTTGCTGCTCCTCCCCTCTACCCTCGGGGTGGCCACCCTCGGGGTGGGGAAAGGGTTCATCCACTTGCTGCTCCTCCCCTCTACCCTCGGGGTGGCCACCCTCGGGGTGGGGAAAGGG
WI-19134a	162	T	C	---	CTCCTGTTCGTGACCTGACACAGGGTGACACAGCCCCTTTCACACTCTGTCCTCCTATCTTCCTGGGTAGATGCCCTGGTGGTGTAGGGCTGAGTACTGAATGGTCTTCCATCCCCAGCAAGGGGGTGCAGCCCAGGGTCAGGCCCTTCAGAGCCAGGCC[T/C]CACACGGTGGCTAGAGCCAGCTGCACTATCCTTTTCAGAGCACTTCATCCACTTGCTCTCCTCTCCCTCGGGCACCCTGGGTGGGGAA
WI-19224	112	C	T	---	GGTTTCACCAGTCTTTCCCAGGGAACTCCGATGAAGTGTTCCAACAAAATGAGCGAGTGAACCAAGAAGAGGATGACATTAGATCCCAGGAGATACAACAGAGGAGATAATCT[C/T]CAGGATGCCTGTGAAGAAAGATCCCTGGATCCCAGGATGATTATAGGACAAGTTGTTCATAATCCAGCAGGCCAGAAGACTTCCAGGGAAACTCATTCAAGGAGGTGAAAATGATGGATGACTCCTCCAAGATGAAAA
WI-19201	179	T	C	---	GCAGCTCCTAAGGACCACTGGCCATTAGCTCTTGCTTTGATGGCATTCTCTTCCACCTTGTCTTCTCCTTTGCTCTCTGTGTTAGTGTGGCAGGTATGGACAACTCATCCAGTGGAAACACAGCCTCACACTGCCCTTCCGCCCCCCACACTTTGCCTGCAGGTGCACCGAAAGGAC[T/C]TGGGGGATAAAATTCAAAAAAGTGTGATGTGCTGCTCAGAGGTCAGACTCCATGTCTGCCTTGGCCTCAA
WI-19034	45	T	C	---	GAAATGGCTCCACTCAGAGCTCACCCCGGTGATGAGGATAGGGGAA[T/C]ACTTCTATTACATTAAAGGCAACAGCAGTTAGTAGTAAAAAGGTTTTTACAGTGTTTCTGTGTTGAAAGTGCAATATAAATTTTTGCTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTTCAGCATTAAGTTCTGTGTCGAATTGACATTTGCTACTTATAAACTTAGTCCCTAAGTCTTCTTATGCTGTGTCTATATA
WI-19102	25	C	G	---	TGTTCCTGAGTCACGCTGAGGAGAG[C/G]CTTCACTCAGGAGTTCATGCTGAGATGATCATGAGTTCATGCGACGTATATTTCCTTTGGAAACAGAATGAAGCAGAGGAAACTCTTAATACTTAAAATCGTTCTTGATTAGTATCGTGAGTTTGAAAGTTCAAACTCCTGTAAGTTTTTGAACTCAAGGGAGAAGGTATAGTGAATGAGTGTGAGCATCGGCTTTGCAGTGCCATAGAACAGAAATGGG
WI-18548b	65	A	G	---	AAAGGAGGGAGAATCTTTTTACATAAATGCCTTGCATCATCCCTCCAGTCCCCTCACTGGGGAA[A/G]AAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62	G	A	---	AAAGGAGGGAGAATCTNTCAAGTCTTTGTCCAACTTTGGCTGCAAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97	T	C	---	GGCAGCAGCTTTTTAATTTGAACACTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGTTACACCTGAAATCTGCTGAGAGCAGAGCTT[T/C]AAGATCCACATTGCAAAGGCCACTGCTGGCTCACTTCCTCACA
WI-18501	121	C	T	---	CAGAGGGAAAAGTTTATTGAGTCAGCCACACAGAGAACAGAGAAAACAGAGAAGGAGGTTCTGTGTGCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCCTGCGCAGGACAGAGGGGCG[C/T]GGACAGCAGCGCATGCCACAAACATTCA

ID	Pos	Allele 1	Allele 2	Sequence
WI-18017	87	C	A	ACAAAAGAAAATGGAAATAGGTTTGCGAAAACTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCATTAAAAATTATATCTCTTTGCAT CAGAGCTGGTGGGAAAATCAT
WI-18148b	101	A	G	TTATTGCGTTCCTTCGATAACCTCTCTTGGGACTATGAGATCATCACCAGATGTGAAAACGAAAGCA GTGATTTCAGAAACCNTCGATTCTGAATATCCC[A/G]TGGCGGCCATATGCAAAGGAAGATGA
WI-18254	64	T	C	TATACGGATCATGTATTTGTGTGACCACCACTACCACAGTCAATTGTGAGAGCAGTTAAATCAC[T/C]GCCAAAATTCCCTCGTTCCTTGTAGTCAGTCAGTCCTCCCAACCCCAGGNACTTGGCAACCTGTTT TCCGTTCCTAGACATTT
WI-18265b	117	C	A	CAAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAGACGGCCTTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACTGGCTG[C/A]GTTTTCAACCTTTC CTTGGGTGGTTTCTTCAG
WI-18295	40	C	T	ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAAGGTTGATTACT TCCTCTCCAAGGATGATATGTTAATGAATTCCCTTTNCCTTAGCTTCATTCTTCATAATGCCAAA
WI-18459b	64	T	C	GGGCAAGAGACAGAGATTTAATTGAATAAAAACTCCAGGCTGTGACACGGGTGGGAGACACAAA[T/ C]GAGTAATTAACAACATAATATTTTANATGACAGTGCAATTAATTAACGTCCTGGGTAAGCCAGAG GGGGAGGAGGGCGTCTTTCA
WI-22585	56	A	G	TTTATTTAAATTTGCATCCTGAGATAATAATAAAATTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAAGTTCGGAGAGGCAGGTATCCTTCATTTGGCACAGCTGTATATAGATTGA
WI-21155	36	A	G	GGGCTGTGGAGTAACAGAACTTGATGGAAAATTGGC[A/G]TTCTGTGTAGAATTGATTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G	A	GCCTTTGCTCTTTGCTGTCCTCCAGAGGCCTCAGATGGATACGCAGCAACTTCCTTTCTTTTTAT TTTCCTGGCAGGAAGAAGA[G/A]GGATCCAGTCAGCCAGTCAGGATCCAGTTCTGTTGCACAGACAG GGAAACAGGC
WI-19888a	98	C	T	GGCACGGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTATTTGATATGATG AAAATATTTTGGAACTAGAAAGTAGCAGTGA[C/T]TGGACAACGTTGTAAAGATATTAAAATGCCACT GAACTGTTCATTTCATTTAAAAATGTAATTTCACATCATGTTATTTATGTGTTGGAAGTGAACACAG CTTATAATTGTAAATTACATGAGANCATATTTATGTTGGAAGTGAACAAG
WI-21485	82	C	T	TGAGACCATCCTCCTCAACAAAGAATCAGTCAGTTCAGCAACTAATTTCCCACACTGAAGTCTACG CAATTTTCATGCAGA[C/T]TGTGCACACAGTACACAGTGCACAAATCCAGAGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T	C	TCAGAATTGCTTTCCCACTGCCCCAAACCAAAGAATTTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAAGGTACCTTCCTTGGAGGTTGCATGACAGGATTAGTCTTCTCTGTTT/C[T/C]TTGGT GCAAGTTTGAACCAGTGATTATGTACCATTGCATCAGAGCATCTGTTTCCCTGTCGATCCCACTAG

WI-20561b	94	T	C	---	CGTTGCTTATTTAAGAGATGGCTGTTTATAAGTAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATTG TACTTCAGATGAAAAATCCTTACATG[T/C]GGAATCAATGTCTTTTAAAATTTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20561a	25	A	G	---	CGTTGCTTATTTAAGAGATGGCTGTTT[A/G]TAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTA TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAAATTTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20116e	69	T	A	---	GCTTTCATTTCTGTCACCCACCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT A[T/A]ATAAATCTATATCATTATCATACACAAACACATTCTACCAGCACTGTGAAGACACACAGA CTAGGCTTACTAGGCTTGGGGCCTCTCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116c	59	T	A	---	GCTTTCATTTCTGTCACCCACCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGT[T/A]TAGAA CATATATAAATCTATATCATTATCATACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCTCTCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116a	22	C	G	---	GCTTTCATTTCTGTCACCCAC[C/G]CTGTCGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAAATCTATATCATTATCATACACAAACACATTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGGCCTCTCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20466b	133	G	A	---	AAAGATTGCAGTCCTGGGACACAGTTTGGAAAACACTATTTATAAGGTTGCACATATTACAAACAG NTCCCAAATGGTGAAACTGGTATTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGC[G/A]TGTGAACTAATGTTAAAAAGTTAGAGCTTGTCTCAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTATCCCTTTCAGGTTCGATT
WI-21444	39	A	G	---	CTGGGCAGCAAGTAACCATTTAAAGAAATACTCTCAAC[A/G]AGTTCTTTTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAAAATACTTATTGGAACTAATTCTTTGTATTTATTCGAGGAAGAAGAATCT ATAAGATTGACTTACTCATTGTTGACTGGTTTTTGAAGCCTTACTGGGG
WI-21034b	148	T	C	---	AGAATGGACAATGATGCAGATGATTTTGTGAGCATTTGATGAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACTAATCTGTTTCTGTAGAATTACTGGTCATGG GAGATTGGATAGA[T/C]GCCTAACCTATCTCAATTTAAGTAATGTGAGCAA
WI-22091c	205	G	A	---	GGCGTGTATTTGATGCAATGTCCAACCAGTCAAGCTATCATTGAAATCCAAATATTTCCCAGTAGAG ACATGCAGAGCAAATGTCAATGTCAGCTTTTAAGTGTATATTCCCCCCTTAAGTGACTCATAATTTC ATTACTTGTCTCTGTAGCTTTTAAAAGTTGTAGCATTAAGTGGTATTTACTTGAGGGCA ACA[G/A]A[A]ATTACGGCTTAACAACACATCAAATCATGAGGGCTCAGGGATTG

Marker	Pos				Sequence
WI-21805a	45	A	T	---	CAACTGCTCTGAGGTCTTCACTAGCTGATTGATTATATCCTATATT[A/T]AAAAAAATCTATATAGTCTGCAGTCTTTGACATACTTCTCAAGGGTGGATATGTGGTGGAATGCAGACTCCATCAATATGTGTGGTTTTGTTTGCTTTTGTAGCTTAACTGCTGTTTAGNAAATCCAGAGAATATGATTGAGGCCAGAGTTACATTGGTTCATAAAATTCGAACAGTTGAAGGCTGTGTTTTGTTAATTGCTG
WI-21778b	155	T	C	---	AAAAATCCATAATTATTGAAACCCAAGTTACAGAGAAAGTTCGTAACTTTTTTATTGAATTATTGACTCTGCCCGCGGTGTCGTTCGTCGCTTCAACTCCAGTCTGTCAATGCCCCTGTGTAGGTGGGGTCCCCAGGTCTGGGCTTCTGAGGTCCT[T/C]GGTGAGAAGGAGGCAGGTGGT
WI-20907	241	A	C	---	TGAGTCAGTGGTCAGATGGGCAGTTGCGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCCTCTCAAATGATCTAGAGCTCATCCTTGGGCGGTACATGAGGGGCAGTTGTTGTTCTTAGTACCCATTTAGCCCATGGCTCTTCAAGCAATTCACACTGGGAAAAACACACCCTCACAAGATGCCTATCCATTTGAGTTCATACAGGTTTTAGTAGCTAGAAACTAAAAAACATTTTA[A/C]AATTATCTA
WI-21449b	222	C	T	---	AACAGCAGCAGTCACTTCCAAAAATGCAAAAAAATTACAATTTTAGAATAAAATTATAATGTTTATAATGCGGGTCAGAAGANTTGAAGGTACAACAGAATCAAATCACGCACACTGGAGCGGCTGGAGAAGCCAAAGCCCACTGGTCAGGGGTCCAAGCTGACAAGAAGTCCCAACCTGAGAGAGGTCTCCACACCCAAATCATACCCCTCAGCTTCCCA[C/T]TTGACAGAGCCAGTGTCCTCTGGGTTAG
WI-21558a	157	G	A	---	GCTTACAAGGAAGGCCTGTGGACAGGCGGAGNTGGGTGGAACCGACTCCAGCCTGGAAAAACCTGCCCTCCCATCCCCCCTTAGCGCCTTCTTGGCCTTCCGGGCTGATTTCTTCGACAGCAGTTCTGGCCAGGGCCAAGGAGCTGTGTGGTGGGGGCCAGTAT[G/A]AGCCAGGGGACTCCCTCCCACAGATGAGGGCCTAGGCGCTGCAAAAGGGCCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178	G	A	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGGGCCGTGGCTAGCAGAGCTCATGGNGACCAGTCCTGGGCCTGACCAATGGGTGATTACATTTAAAAACCAAACAAAACAAAATACCAAGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG[G/A]AATTTCATGAAAATTTCCCCTAAACCATAACAAAACTGTCCTCCTTACCCCAAAGTGCTGGAGAAAG
WI-22187a	110	C	A	---	TTTGCTGTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGGGCCGTAGCAGAGCTCATGGNGACCAGTCCTGGGCCTGACCAATGGGTGATTACATTTAAAAACCAAA[C/A]CAAAACAAAATACCAAGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG[G/A]AATTTCATGGAAAATTTCCCCTAAACCATAACAAAACTGTCCTCCTTACCCCAAAGTGCTGGAGAAAG
WI-21609b	146	G	A	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAAACGTGCAGTCGTTCACAAGCTGTAAAAACAAGCCCAAACCCAAGACATCACAAGAGGCAAGAGCAGTGGCAGTGGAAGGGAGCCTGTAAAGGATGTTTCAAAG[G/A]AGGGGTCCCGGCTATGTGGCCCACTGATGTGGCACANTGGCAGACANTGGCCAAAGAGGAGTTGGAGTTTCGGTCTGGGAAGTGGCAGAGCTGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

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WI-21609a	42	C	T	...	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAAA[C/T]GTGCAGTCCGTTCACAAGCTGT AAAAACAAGCCCAAACCCAAGACATCACAAGAGGCAAGAGCCAAGAGCCAGTGGCAGTGAGGAGCCTGTA AAGGATGTTTCAAAGGAAGTGGCCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI-22512a	104	T	G	...	ACATTCCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAAATCCCTTGGTGCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGGTCCTTTGTGATCTG[T/G]ACCTCACCCATGTCTCCCACCTNAGTTCC CACATTTCCCCCACGTCTCAAGGGCAGGCAGCTACACTTGACTGCA
WI-21028b	139	A	G	...	ATCGGCAAGCTACAGCCTTAAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAAGGGTCGTGATTGAGCAATCTAGGGGATATGTGACAGGGG TTTC[A/G]TGCACTGGTACAGAACACAACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAAT CTACGG
WI-21028a	121	A	C	...	ATCGGCAAGCTACAGCCTTAAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAAGGGTCGTGATTGAGCAATCTAGGGG[A/C]TATGTGACAG GGGTTTCATGCACTGGTACAGAACACAACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAATC TACGG
WI-18829d	58	A	G	...	ACAACATGCCTGTTCACAGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG[A/G]TTTCA TCATACAAGACAAGCACAAAAGCACCACCCCATGCCTCCTCTGAGGAACATTGGACCATGCACCCTTGAAA AA
WI-18829b	35	T	A	...	ACAACATGCCTGTTCACAGGGGGAAAAATCCTAGG[T/A]AATAACTTATGTGTACTTCTTGATTTCA TCATACAAGACAAGCACAAAAGCACCACCCCATGCCTCCTCTGAGGAACATTGGACCATGCACCCTTGAAA AA
WI-20964	87	G	A	...	AGCCAACTCAAGGCCAAAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAAGGA GCACAGGTAGTCCACAGAATA[G/A]GACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAATTAA AAGAATACTAAGATTAGATGAACAACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAAGAGGAAC AGATGTTAACAAAACAAATTAAGGCTGCTGGGAACCTGAGTCCATGTTAAGCTTG
WI-20059a	59	T	A	...	CTCTGAACTAAAGGGCCGTGAAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCA[T/A]ACAT TGGCTGGAATGAGGTGGTCAGGAAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAAATAATTACAAAGACTGACACTCTTTACCTTACCATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCCTTAGGT
WI-22130b	165	C	T	...	TGTTTTGAGGGCTGTGTAGCAGACTACATAATAGAGCGGTGAAAGCGGCTGCCTTCCCCTCTCCTGACAC CAGCAAGGGGAGGGGAGGCACCCATCCACCGGCCCTGCTTGCT[C/T]GTGTTTAATCCAGGTTAAGCTAACTAGGAA GCCAACGGAANAGGACCCCGCGCTTACATGTCTCATGCAGTCCCTGTCCCTGTGATGGGAATGAC ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTGTCCCTGTGATGGGAATGAC

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WI-21661	117	G	C	---	GCTTAGTGTCTCCACCCTTTAAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGT CTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAAATAAAATA[G/C]TTAGTGCACAGTC ACACAAAACTACCTTCTAAGGAAAACTGTCCAGTGAAGCCGTTAAATTGTGTCTTTCAGCTATGAAG GA
WI-21980a	25	T	C	---	TCAGTTTAAACACATTCATCCAAGGA[T/C]AGATTAATTAATGTCAGGTGAGCATAAAAGGGGAGATTA TAAACCAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTAATTTCAT GGGTGAAGCCCCTGGGATAAAG
WI-21636	71	A	G	---	TGCTTGTATTAAATGTGGTGTTTACATTATCCTATTTCACAGATGGAAACAGAAAAATACCAGCTTTTT AAA[A/G]TAGCAATATCTATTATTATAATAAATATTGAAATAACACCATAATATATCACTAAGGA AGTAATCTAATTGTGTTGATTTGTTGCAGAGGGAGAAAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGGTGAGAAACTAGGAAGGGACAGGGATTTC
WI-22457a	112	G	A	---	TTGCTATAATTCCTTAAAAATGCAAAAGAGTACATCCACAGCAGAGTATAGCCAATCACTCATTAGA CAAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACTAAAG GAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGGAAACAGTAATGCAGATTAATACCTGGGGCC AAAACCCACTGAACTCACCCCAGCTGAAAAACACTGAAGGATACTGGGTAAGGA
WI-21524b	97	C	T	---	GCCGTGAGGGTAGCGTATATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGCGTCATACTTAT AATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTCTGCAAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCCACTATGACAATGAGTTGTTGATTGTTTGGAGTTGCGGTGTC CTGTCAGAAAGATTTCTTGACTTTCTCCAAGTTACTTCCTTCCAGGGGATG
WI-21524a	35	A	C	---	GCCGTGAGGGGTTAGCGTATAATGAAAAGGTGTAATA[A/C]GCCTGATGTACGACCTTCGCGTCATACT TATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTCTGCAAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCCACTATGACAATGAGTTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTTCTTGACTTTCTCCAAGTTACTTCCTTCCAGGGGATG
WI-22652a	32	G	T	---	TTACCTTCCAAACCAGGCCACTTTGGAGAAAG[G/T]AAGAGAATGCTATTAATCAAATAAGCCAAGAC AATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACACCATCCATTCCTGCCACAGAACC TTTGCACATGCTGCCCTCCGCCACTCCGCCACTCCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTT CTTTAGGG
WI-21703d	197	A	G	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTCGGGCAGGGCTC TGCATCCCCTTTCCTCAGCACAGCACCACCATCTTCACCCTCCTGGGAAAGCAGCATTGGAGCCTACACCA CTTGTGCTTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTCTGGAGTCTGGGGAA[A/G]G TGGGCAGCAGCAGCACAGCTAGGGGCAGTAGGGGCAAGGACTTAAGGGAACTTGTGGGGAAGAG

ID	Pos				Sequence
WI-21703c	134	A	G	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGCTGGGCAGGGCTC TGCATCCCCTTTCCTCAGCACCAGCACCATCTTCACCCTCCTGGGAAAGCAGCATTGGAGCCTACACC[A/G]CTTGTGCTTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAAAG TGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGGAACTTGTGGGGGAAGAG
WI-22663c	139	G	A	---	CCCTTGTCAGTCTGTGCCTCGGCTTCTCACTGCACTGGCGAGGTGAGCGGCGCTCGCTAATCTTATTC CCAGTCTCGGTGAACATGGCTCGAGTCTCTCCCGGCTCAGTGTTGGGTTTGCACTGGTGCACTTACAG GC[G/A]GAAGAGCTTCCTCATTTGCTGAGGGGCTTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22663b	55	C	T	---	CCCTTGTCAGTCTGTGCCTCGGCTTCTCACTGCACTGGCGAGGTGAGCCGGCGCGCTC[C/T]GCTAATCTTA TTCCCAGTCTCGGTGAACATGGCTCGAGTCTCTCCCGGCTCAGTGTTGCACTGGTGCACTTAC AGGCGGAAGAGCTTCCTCATTTGCTGAGGGGCTTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22663a	38	C	T	---	CCCTTGTCAGTCTGTGCCTCGGCTTCTCACTGCACTGG[C/T]GAGGTGAGCCGGCGCTCGCTAATCTTA TTCCCAGTCTCGGTGAACATGGGCTCGAGTCTCTCCCGGCTCAGTGTTGCACTGGTGCACTTAC AGGCGGAAGAGCTTCCTCATTTGCTGAGGGGCTTTTCCTGAATCCGTGTTGAATGTGGGT
WI-22668	99	A	G	---	TCTTTTATCCTGCTGCCTGCCTGAGTATTCTGGGAATCCTACAAGGATTTGAGGGAGCCCTTGGGATT CCAACCTAACAAATTAGTTTCTGTAATATT[A/G]TTCTAGTCCATTTAGATTGTGTAAATGATCTAA ATGGNGTAACCATTTAATATCAAAAGTATAACAGCATTAAGTCAGCTTTGAAGAAACTTTTATT
WI-22631a	52	T	C	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTTCAGTTCTGA[T/C]AGCACCATTTT CAAGTTTAGGCAAGGTATTTAACCTCTCCAGGCTCATTTTCTCTTTTGTAAAATTGTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTTT
WI-20258	157	G	T	---	AATCCACACTTTCACGGAGGGGACCACAGCCTGCCATGTCGTCCCAGGCTACACAGCAGCGGCGGCTAC TCTGCTGGTTGGTTGGTGGCAGGTGGAGGATGGTGACGGCGCATTGGAAAACCGTAAGGCATGACAACG GGAGGCGGCCGGCCGGGGTGTTCAG[G/T]CGCGTTGACGGCAGGTGCATGGGCCTCTACAGA AGGAGGAGGCGCAATTCACAGCGTCTTGACGTAGTTTCCGGGGAAAGTACC
WI-22714	212	C	A	---	ACTACACACATATGCTGATTTTCAAACAGTAAAAATAACATTTTACATTTGTAGAGAAAATCTAGGGTCT ACTAAATAATCTAGTACTTGTTTCCACTCTCTCCTAACTCTGACAGGAGTGTTGTGGGAAACGAAGT CTGAAAAGGATTCAAAGGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA[C/A]A[A]TGAGTAGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734a	44	G	A	---	TGGGGCTACTTTAGATGGGATGGGCATGGCGTCAGGGTCTGGGAAGGCCT[G/A]TCTTAGAAGACATTACCCA AATGATGAGAGGCAGCCAGTCGTCGAAGCCCATAGTTTGGATGGCGAGACTTTTCCGGCGAGAGAAAT AGCAAGTGCAAAGGGCCCTGAGGGGAGAAATGAACTTGGGCTTGTCCTACAGGGTGAAAGGCGGCCGGGT NTGGCTGAGGTTTAGTGGATG

WI-22724	117	A	G	---	TGATATGATGTCTGAGATTTGCTTCCAAATATGCCTAGGAAGGGAAGAAGTGTTTAGAGATATAGGA CAAATCAAGATTGTCAAAATGTATAGTAAGTAACTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTGGGAATT
WI-22750	48	G	A	---	TGTAACCTGTGTTTTCCTGAAAGTTGAGGGAAAGCTGAGCGAGCTAAT[G/A]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTCTGACCATTCTGACTGTGCT
WI-22775a	60	A	G	---	TGCTGTTCTTTAGTTCATGACGTTATCACAATGTGCTACTGTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGAAAATAAACTCCCTAAGGGCAGCAATAATTTCTGTCTTTGAATCCTTCATTCAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAACTGAGGTATGTAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143	C	T	---	CTTTAGCTAATGAAACTGGCTATGTGGACTATGATGAGACCAAGAAAGCTACCCAAGTCCTGAGGGAG CCTAGTCCTCCTAAATGCAGACAATGTACCCATGACACAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAGAGAGTAGGTATAAGAACCAGGGAGAGTGGGGGTCCAAAT ATC
WI-21016	207	G	A	---	TCTCTCGTGTCTTGAGCCCTCATCCCCACCCCTCCAGCCCTCATGCCCACCACGTGTCCCACATT CCCCATCCTCCCCGTGTCTGCTCCCCATCTCCAAGTCCAATTCCAAGGCCACGAGCCCTGGCAGCTTTCTG GGAGCAGCAGCATGAAAAGGAGGGGAGTGGCAGAGATGGCAGATGGGGGTGGAGGTGGGGTCCAGCCAGTGCGCGCTGTGGGTC CT[G/A]TTGGGCGTGGTGATGTGGGGCCAATCCTGAGGCCAGAGGTTCA
WI-21031	31	C	T	---	TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCCATTTGTCTCCAACGGTGGCACA TCTTCATCTTGTTGTATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAAACACACACA
WI-21314	122	A	T	---	CCATATCCAGTCTTCTTGAAGCTTCTATTGACTTTAGGGTTCAGTTATTATATCCTTTATCACTAT GACTTTCATTTGATTTTTTATTTGTTTCTTCCATTTCTCTGTCAAACTTTTC[A/T]TTTTGTTTATAA ACTGTTTCTAAACTTCACTTAATTCTCTATTTNCTGTAGTTCCCTGAACTTCTTTAGAGG
WI-21186	95	G	A	---	AGCGAGCATCAGAATCACCTAGAGGGTTGACTAAAACAGACTTCTGGACCCAACCCCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGGCCTTAC[G/A]AATTAGTATTTCGAAGACCTTCTCAAGTGTTGCAG ATGCTGCTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAAATGTTCTCTCCTTTCTTTTAAA GGAGAGACAGGAATTCCAGAGAGAAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94	A	G	---	CCACGATAACTATAAAAGCAGAAAATTAGCTTTGAAAATCAAATAACATATTTAGTAACACACATT CATTTTTATAAACACACATAAAGACACC[A/G]GGNTCTCAGTAATGCTCTAGTCAAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCATTTGCATCACCTAGGGGAATTGCTAAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39	T C	---	TTTTCCCCACATACCAATGCACCTGTTGTATAAACTATT[T/C]GTGGGGTAAGCCCTTCTTTGGAGAC CAGTGACATAGACATGATTCCCATTATATTATTAACAAATAATTATTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTTATTGAGAAAGGAGAAGTCAGCATAGTTTATTTCCATGTAATAAAAGCTT AACACA
WI-19937d	186	G A	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185	C T	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCCTCAGCAAGT[C/T]GTCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227	C T	---	GAAAAACGGGGTGCTAAACAAAGAAAAGTCTCAGATCCCCACTGAAAATCTGTTCAGTTCCACAGGCTC TCTCCAGAAAAATGCATATGTACCAATTGCATGTACAAATTCAGAGCCTTCAAATACATTCTGGGG TCCAATCACATACTTCAGGTTCAGACTCCCAAATATTCCTACTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGTATTTC[C/T]TTCTACTGAATCTTGGGTGGGAG
WI-21122a	42	C T	---	TCACTTTGATCATATCCCCTGTAAAGCTAAAGTTATTCA[C/T]TTAACAGGAACTCTGTTTTTCC TTATTCAAATGTCACAGCCGTTACTGGTCTACATATTGCTAGCAGGAGGACAACTGGAAATACT AACAAAATACTGGAATTCACATTACAGAACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTTGTGGGGTTGCT
WI-21254	53	A G	---	CAGTTTTGGTACAGGAGGCCCATGAATGTGGGCGGGAACTATTCCACAGGAG[A/G]CAAGGAGAAG CTGTTCTCTGG
WI-21054	23	G T	---	AAGGAAACTGCATGGGTACAAAT[G/T]TCCAATTCATACTTAACAAGGTGGGGAAACGGGTCATTCT TGGCCTGCTCCAGAACAAGGGGCGGAGTCTATGCACTCCTG
WI-21059b	181	T C	---	GGGACCAGGGGTAACACCATTAGCAATATCCGTTATCTTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCTTCCCGGCTTGCGTCGTCATTTCTCATTTC[T/C]ATTGTAGCCAGGGCAAAA AATCCTGGGGAAGAGACATACTTCACTGAAGTCATTCTCTATTC[T/C]ATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63	C T	---	GGGACCAGGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATTCTTTCCCACTGAGCCTGG[C/T]TT GAACTACAGCTGCCAGCATTTCCCGGCTTGCATTTCCCAGCTTCGTCACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAAGACATACTTCACTGAAGTCATTTCTATTGTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGCGGTGACTATCCTTGCCTATC

ID	Pos			Sequence
WI-20442	37	T	C	TCCACGTGAAGGAAGAAGAAAAAAAAAAANGGGGGGGGGGCTTT[T/C]TAAGGTGGCACAATTTTAAGAAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAAACAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43	T	C	GTGACAAGAGGTGAAGCAAGGGACAAGGGGCAGCAAGGGGCAGTCT[T/C]CTCGGCCGCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T	C	ATCAGAAACTGCAATCTGCACATGAAAAGACCTGGGGGGAATGCCTACATCTGGAATT[T/C]CATTAC ATCAACGTTAAATTTGTCCGACCAGTTCTTCATTGCTGATCACTTTGATAATGACAGATCCAACAT GAAACTCCTGAAGCAAATGAATATTTACCTTGTGCTTTCATGCAAATTTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCAGATCTAAGGAATCTAAGGAATTGTGACAGGGATCTTCT
WI-21149a	167	G	A	AGGACCTGCTCTCACACGTTCCCTCACCCCCACCAGCTTTTGGCAAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTTTTTTTTAACAATGACCTTATTTATCTTTAACTTAACTTGAGTCTTATATA CAGACCTGCCCAACTGGAAAGCTTTACAC[G/A]TGCTTCAGAATGCGGCAGTATTGCACAATGGTT TGGGGCAGGTTCTGTGGTTAAACATGGGATGGAACCCCAGGCTCTACCTG
WI-21376b	188	A	G	GGTGTCAACTTGGAAATAATGGTTAAAAACAGGATAAGCATTAAGGAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTGTTTTCTCTCTTTATCCCGCAAGTGGAGTTTCATGTCCTCGGGTGAAACCA GACAGTGTGAATCTGTTCCAGCCCAAATCTGCAGCATTAGGGATGAGTTCTC[A/G]GAAGTGATTCT GAACTGAGCACGCACTCATGTCTGCATGGGGAACTCTGGGGAGGAAGAGCCT
WI-21382d	125	C	G	CCATTGCAGTCCAGAGATGAGAAACTGACCAGAGGCAAATCATGAACACAGAAACGGGAGTCAAGAGA AGGGGTTTCTAAGATGGAGAAGTGGGGCGGGGTTTGGATCCAGTGGGATNTGGCTTCCC[C/G]AGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCAGCACCAGTCCTGATGGGGAGCAGAAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAGGGTCCGAGGAGAGCTGCTCCATAGTCTCGCAC
WI-21437a	201	G	A	TCCCTGAGGTTGGAGTCCTAGCATAGCTCCCCTCCCCTCAAAGAGGGACAAGGGGTCAGGGGCAGAGC AAAAATCCAGTCTGCTTCAACCACGGAGACTGCCTTGGGATGGAAAGTTTCTGGAGCTCCCTCCATT CTATTCCTGTGGGGCAGGAAACATGCCCCCTGNCTGCCCTGGGGGTAAATGGCAGGGGTCACCTTTACCAGGGGC[G /A]CAGGCATAGTGTGCCCCTGNCTGCCCTGGGGGCCACCCTGGGAACAGT
WI-21202b	156	A	C	CAAAATAGAAATTCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTATGAACATGTATTTTATAAAAATGGTCACAATATATTTTAAGTTAACTGATTTTATTGAGGGG AGGAGGAGGAGGAGAGTTGACCAA[A/C]GTCTACATGCATAGACAGTCTACACTGCATAGACAGTCTCAAACATG A
WI-21202a	61	T	C	CAAAATAGAAATTCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATG[T/C]TGA TCTGTTTATGAACATGTATTTTATAAAAATGGTCACAATATATTTTAAGTTAACTGATTTATTGA GGGGAGGAGGAGGAGGAGAGTTGACCAAAGTCTACATGCATAGACAGTCTCAAAGCGTATCTCAAACATG A

Identifier	Position	Allele 1	Allele 2		Sequence
WI-21627b	153	A	G	---	GCATGAAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA[A/G]TCCAATAAATAGGGTTTAAAAATGTGTTGCTTA GACAGTATACTACTCTACAATAAATAAGGGTTTAAAAATGTGTTGCTTA
WI-21627a	106	A	G	---	GCATGAAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTC[A/G]TTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAGTCATCTAATATTAAACCATATTTACATAATTTGTAGG GACAGTATACTACTCTACAATAAATAAGGGTTTAAAAATGTGTTGCTTA
WI-21399a	75	C	T	---	GGATTTGAGTCCCAACTTGATCTCAAATTCACTTCTTGCATGTAAACAAGCTCATTCCCTCTAAAGTT TCAGTTT[C/T]TTCACCAGTAAAGGAAAAGGTTGGACCAGACATGTTGGACCGTAATTGCTTGGTAA CTGCCCTTCTGCATTTGTCTCTGAGGTTGTGTGTCCCTAGGACTAGGTAGGATCTCTCTTGCTTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATACTTGT
WI-20329a	68	G	A	---	CGATGTCTGCTAAGATAGGAGGTTAATTCTTTACATGGTGAGTGGGTCACAGAGACAAGACATCAAT C[G/A]TCTGTTAGCAGCGAGAGAGACACTTAAGTTGCCCCAGAGTACAAATCCCATCTCTATGAGAC AGCAGTGCTGGCTTCTTAAAAACCAATCAAAAAGAAAAGATTTAGAGGTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGACGCCCTTGAAGGGAAAGGCCTCACT
WI-21249	155	T	C	---	TTCTGGCATTCAAATGTACATGTAAAATCCAATTCAACAGATCAAAATTGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACTTTTAAGAAACATTATAAAGGTAATT AAAACTCTAGGTGTATACTTA[T/C]ATGGAACTAGTTATTTCCNATTAACTACTGTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTTAAGGAATTATAAAACATTGAGA
WI-21504	147	C	T	---	TGACACAGCATCAATTTCATGAATACTTTGAAAGGGCCATTAGAAAAAATAAGAGCCAATTGGGTC ATTTGAGAAAACATTTTCAGCACAGCAATTACAGTGGGGGCACGGGCCGTTCGGCCTCCAGCTGGGTTTTCCC AGATGCAACAAT[C/T]GCGGTTCTGGCCTTCTGCCTTTGGGGGATGGCCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115	G	A	---	CTGCACCAGGGGAGGACAGCTGCTGCGGCAGGGACTAATAAACCCTTCCACCTGGCCATGGTGGTGTT CTCTATGGACCGGAGGCCCTGAAACGGGGCAGGGAGGGGCCAGGAGAAC[G/A]CACTAGCTTGGGGGTG GGCACCACCAGCTTCAGACCCCTT
WI-21475c	181	A	G	---	TAGCCCCTTCTCTGCCAACATCTGGCAATNTGAGGCTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCCTCCAAACCCCAGGCCTTCTCACTTGCTTACTAAGCACACAG CAGTCTGAAGCTTGGGACCTGGGCAGTGCGTCTCTTGGAGAAGGCA[A/G]AAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCTTCCGGTTCCTCCACCCTATTTCCTCCCCTGAAG

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WI-21475b	117	A	T	---	TAGCCCTTCTGCCAACATCTGGCAATNGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCCAGGCTTCTC[A/T]CTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGGACCTGGGCAGTGCGTCTTGGAGAAGGCAAAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCTTCCCGTTCTCCACCCTATTTCCTCCCCTGAAG
WI-20893d	207	A	G	---	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGCTGCAGGG CTGTCTTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTGTCACGTAAGTTCATCACCGCACTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAAACCTGCCATTTCTTCTCTTTTACAATGCAGT TTC[A/G]ACATAAACATTGGTAGAGTAAACAACAACAAACCACAAGCCTAAATG
WI-20893c	179	T	C	---	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGCTGCAGGG CTGTCTTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTGTCACGTAAGTTCATCACCGCACTCC AGCGTCAGGCCAAACCTTTCCGTGGACCTGGGNAAACCTGCCAT/C[TTTCTTCTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAAACAACAAACCACAAGCCTAAATG
WI-19941c	71	C	G	---	GAGCTCAAGGGAAGACCCTTACCCAGATAGGGACTAACTGGAGGGGTGGAAGGAAACAAGGTGAAA GGTAT[C/G]GGTCCTGGTGAGACAAAGCAGGGGGCCTGAGAACACAGAGCAAGGTGGGTTTGGAG GGAGCACAGCAGGGGTGCAGGAGGAGCATTNTGGAAGGAGAACCAAAGGACAGAGAGACAAAGCG AAACTGGGTACAGCAGGAGCATTNTGGAAGGAGAACCAAAGGACAGAGAGACAAAGCG
WI-21552b	166	C	A	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCTCCTTCACCTCAAGCATTTATCCCATAGTGTTACAAAGAA TCCAAGTATACTCTTGATTATTAAAAATGTA[C/A]AATTAAATTTATTATTGAATTTAGTTACCCC ATTGTGCTATCAAATATTCAATCTTATTCATTCTTTGTAACTATTTATTTGTA
WI-21552a	66	G	A	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTT[G /A]TAATAATTACTTCAGAGTAAATGCGATCTCTCCTTCACCTCAAGCATTTATCCCATAGTGTTACAAAG AATCCAAGTATACTCTTGATTATTTAAAAATGTACAATTAAATTTATTATTGAATTTAGTTACCCCA TTGTGCTATCAAATATTCAATCTTATTCATTCTTTGTAACTATTTATTTGTA
WI-21512	54	C	G	---	TCCTCGTACTTCATGCTCCCCTCGCCCCAGAACCTTACAAAAAATATTTCTGT[C/G]TAGAGAGGGA AAGAGCTGGTGCCTGCTCGTGGAGGCAACGTCCAGGTCCGGGAAAGGCACTCGGTCGTGTCTGTC TCAGTCGATGGGAGGTCTCCACTCGCCCCACACAGCAGCCTCGGGGCCAGAGATGAGAATATGCTGTAA TCCAGTACAGGGGGTGCGTCGTGGGGTCCCCAACAGCTCTCTTGGGGG
WI-21513b	192	G	A	---	CACATAGTTTCTCAAGAAGAGAGGATGAACTGAAAACTCCTCTAAGGCAGGACAAAGCAACTTTCCATT ATTCTTAGTTTAGACCCAGAATCTTAATTTTATATTCTCCTTTAATAACTGTCAAAATACACCAAATA CTTAGAGGAAAAATATTCACAGTATACCAAAACATTTTAAGATAAAGAGGCAGTGTAA[G/A]AGTAG TATTCTCTACATACCACCAGTATACAATGATGCCTTCCTGCAGGTTTAGGAAC

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WI-21514b	133	C	T	...	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAAGGAGCACATTACCAATGGAGC[C /T]ACAGGACTCCAAAGACCTCAGAAAGCATTTAAGGGTGATTGTCAAGGGTCATAAGGAACT ANTTTAAGGCTCAGATGGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-21514a	100	A	G	...	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAGTATCTCAACATTACAAACCCCA[A/G]TCTTCAAGGAAAGGAGCACATTACCATGGA GCCACAGGACTCCAAAGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCGAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGGTTAAGGGTCATAAGGAACT
WI-22020	27	C	G	...	ATGAAACATGTTGCAGTGCGGATGAAT[C/G]TATCATGGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATTCTACCTGTATGAGGGTACTT
WI-19576a	113	A	G	...	TTCATCGGTTCTTAATACAGTACAATCCTTTGTTGAACAAAGTCACACTGGCAATGATTATTTACA GATCCAAAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATTC[A/G]TCAGTTCAGTTGATTAGT CACAGAANTTAAACATCTGCCCAGATACTACACAATTTGGTAAAACTACAGCTTCTCTCCACGGGGGA G
WI-21695a	141	A	C	...	ATACACAGGCCACAATTGCAGGATGGAAAGGCAGTGGGCCACTTGGAAGTGACTACACACATGGCAATA AGCAGCCTATCTCTTTACCAAGCACTAAGCCTACACTGTGGGGCATGTGATGGTAGGCCAGACCCTTCCAA GGGAATA[A/C]TACTACACTAAGCCTCACTGTGTGTTCAGANTTCTAAGGCCCAGCAT AGTGGGAGGAAATGTGATGACTTCACTGTTGTATTATGAGGAACTCACTATACTAGGAAGCAACTTATGAGTG
WI-21574a	235	C	T	...	AAACCCAGAATTTAGGTACTTTGTATTATGAGGAACTCACTATACTAGGAAGCAACTTATGAGTG TGTAAATATTGATCTAGCAGCAACTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGGCAGGCAGGGCCAGGGAACTTACTGCCTACTTCCT[C/T]GTGTCAGGTGGGA
WI-21644c	151	T	A	...	TGACTGCCAAGATTAGGCCCCAACTTAGGAGCCCATANTATTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTCACCATANTATTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGA[T/A]TTCAATCAAGATCCATGGAATGATGCAGTTTAACATGTGTTCTCAGC TTGCCTACTGACCACCTTTCCTTTCCTTTTCTAAATATGGCAACAGCAGCAAGTC
WI-21614b	55	G	A	...	TGTCTTTAAACCTCAAAAGTCCAAATAAACATATAGACATTTGANTATAGCTATC[G/A]TTTAACA AACCTCATTATGATCACTGTTGCAAATTTCAGTCACCTAAAATACGGAACCATGACTATTAATAAACA TTTACTGTGTGTGGGTTTGTTGGGACTCAAATGGTATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTGGGCAGTTGGCTGTGTGTGTGGG
WI-21615b	151	C	T	...	GACCGGAGAAAAACTGCAAGGCATATGATGATGTTGTCGAAGTATCACATGACTATTCAAGCTTATAGA GAAACTTGCAAAAAGTACAAAGATGGCTATTTTAAATTTCATACATATTAAGATAAGGATGGACT CTTTCACTGAGTATTAT[C/T]AGGACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCCC TATTCTATATTGGGCCAAAGGGAAAAAGGTAGGATGGGTACTGTGGAAACGGA

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WI-21981	61	T	A	---	TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCTTGAAGAAAAAAAA[T/A]GT CTCCCTTATGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAACATGCATGGGATAGA CACTCGTTCTCTACAGATCCGTTGCTTGGGAATTACAGGAACAATAAAAGGATATAATGGATGGGTT ATTACTTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAGGTTAAATTTGG
WI-21660	120	C	T	---	TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAACACGCCTCTCCACTGCT TACTGTGTGTACCAAGAAGCAGAAAGCAGCTCACCCAAGCCTAACCTGGCC[C/T]TGTCTTTTCAG GCTTCTCAGGATGCCCACAGCACATACTGGGGAACTGGGATGCAGGAGAAGCCAGGGTCTGTCTTC AGGAGGGTCACAGC
WI-19105c	211	C	T	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAATATTTGTGGTCCATGTGGTTGAGTCTGTTAAGAAGGA CACTAAGGCACACATGCCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTCCTT GTCTGTAGGTTCCAGGGCGTGGGCACAGAGGTGAGGGCAGAATNTTGGGGGTCCCAGTGGATCTCCCC ACAACTTC[C/T]TCCAGGGGCAGGATTTCCACCCCAGGGCCCAGGGTCCCCG
WI-19105a	33	T	C	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAATATT[T/C]CGTGGTCCATGTGGTTTGAGTCTGTTAAGAA GGACACTAAGGCACATGCCTGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTC CTTGTCTGTAGGTTTCCAGGGGGCAGGATTTCCACCCCAGGGCCCAGGGTCCCCG
WI-21760c	81	C	A	---	CAAACCTAGTCACTCTACTGATGCAAATGATTGGACAGGTGTCTTCCTAGCTTTACAATAAGNGAGG GACCTCTGACTGCA[C/A]CCTCGTCTGTCTCCAGTTTCAGGGCA
WI-21760a	35	A	G	---	CAAACCTAGTCACTCTACTGATGCAAATGATTGG[A/G]GGTGTCTTCCTAGCTTTACAATAAGNGG AGGGACCCTCGACTGCACCCCTCTGTCTCCAGTTTCAGGGCA
WI-21569b	198	T	C	---	TCTGCCATATTGTTCCCAGCACCACTATTACTGTTATTATTCTCTTGAGGAAAACCAGGNATTAAG AAATCTGGTTGAATTTCCATGATGCCTAACTCTATGGTTAAAATCCTTTCCTTACCAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTTGCAGAAAITTATCTCTAC[T/C] AGAGACAATTCATAGTTCATAATCTTCAGGGTTGTGCTTTACTTGGGGGGC
WI-20934a	72	T	G	---	CCAACACATGCAACATAGTCTTCATTCTTAAAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA GAGAA[T/G]TCTAAGACAAATGGTCAAATTGTGGTCTTGCCACTAGTGGTAATTCCAGCAGAC AAACAGCATGAGAAAAGGCCGGGACAGTAATAAATACGTGCCCATTGCAATGAGTTACCCAATC AAGCCCTTTACCTCCTTAAGATGGCAGATTAGAAGACCCTNTTCCCCAGGAGA
WI-21561	55	T	G	---	TTTCCATTTATTCAGCCGGGCGGCCCATCAGAGAACAATAGCATCTATACCTTCGAAACC[T/G]CCTCTTAAC CTCTCCCAGGCAAAGAAGGAAAAAGTATTAAGATATAAGAGGCTTGAAATATAATGATGATAAATGGTAGCCTTTCTGGA TTTAGAAAGTGCTTATTAAGTATAAGACCCTNTTGTTTAAAAAGATTTTTGGATGCATTGTCCCCA AATAATTTTTGTAATCTGTTTAAAAAGATTTTTTGTAATCTGTT---

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WI-21961c	200	T	G	AGCTTTGCTTGAAAAATTTGGTACTACTACCTTTATTATTATTACTTTTATTTTTCCGTAAGTTATTGGGGTACAGGAGGAGGTATTGGTGGTTATATAAGTTCTTAGTGGCGATTGTGTGATTTTGGTGCACCCATTACCCAGGAGTATACACTGCACCATACTCGGTCTTTATCCCTCGGCCCCT[T/G]CTCCCACTTTTCCCCTCAAGTCCCAAAAGTCCATTGTATCCATTCTTATGC
WI-21961b	73	G	A	AGCTTTGCTTGAAAAATTTGGTACTACTACCTTTATTATTATTACTTTTATTTTCC[G/A]TAAGTTATTGGGGTACAGGAGGAGGTATTGGTGGTTATATAAGTTCTTAGTGGCGATTGTGTGATTTTGGTGCACCCATTACCCAGGAGTATACACTGCACCATACTCGGTCTTTATCCCTCGCCCCCTCTCCCACTTTTCCCCTCAAGTCCCAAAAGTCCATTGTATCATTCTTATGC
WI-21956	26	T	G	CCCACTTGGGTCTCTTCAAGTGAAT[T/G]TCCTTTCGTTCCTGTTCCTGTTCTGTTTTCTGCTTCATGCCCCTCAGTCGAATTCTTCTTCTGAGGCGGCAAGGACTGAAGTTGCTGTGTGGACCTGTAGGGGTTCGACGCGGTAACTCAGGGTAACTCCTATCTCTTCCCACCGGTAACAGAGAGGGGGTTACATTATGGGGGTCCAGGTT
WI-21966	148	G	A	CAAACATACATCATTATGGCTGCCTTTATTTAAGAAATGTTTACTGAGAAATCTGTACTGTAACAACATATTTTTGTTAGAAGCATGAGTGAGAGTGTGTGTGTGTCCTGCGCGGCCATGGCCACTGAGGGGATTGCAATGGG[G/A]AAACAGGATAAAAAACTTGGTCCGAAATCTTTGCTTATTAACCTTGGCCCCTGCTCCTCCTCACAATGTTTCTCACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146	G	C	TATACTGGTTTTTGGTTACATGGATGAATTGTCTAATGGTGAAGTCTGAGATTTAGTGTACCCATCACCTGAGTAGTGTACATTGTACCCAACTTGTAGGCTTTTATCCCTAACTTCCACCCTCCCAT TTTGAGTCTG[G/C]CATAGTCCATTATATCACTCTGTATGCCTTTGCATACCCATAGCTTAACTCCC
WI-211139a	165	T	C	GCTCTAGTGAAGAAATTCAGGAGACGCGGTCTTCTTCAGAGCAGAGAGGGCTTGGTTCAAGTCCCTGTTCTGCCACTTACTAACTGCATGACCTTGAGCAAGCCCACTTAATTCTCTGCTCCTCTGTGAAATGGGTACAATGTGGGTCAGCAGTAAAGGAACTAATACAT[T/C]GTACAGCACTTCAGCACAAAGCCTGGGCACACAG
WI-20317b	217	G	T	CACTGCATGGAAATACACACAGGTAACATTTTAAACAGTGGGGACAAAATTTTAAGTACGTGGCCAGCTGTTGGTTGTCTTGTGTGGTCATTAAAGACAATGTTAAGANTCAGGAGTACTTAAGTGCTAGTGGTTACAAATTTGTTCTCTTCAGTTTTCATTAAGTAAATTCTAATGATGATATACATATTACTGCAGATAAAACCATCATCAGAAA[G/T]TATTAAATTAATTGCATATTTGAGGCTACTCT
WI-22082e	179	G	A	CAGGACTTGGTTTGCTTGCTGTCGTGCCCAACTGCACATAAATGTCCCTTTTGTTTGTTGTGTTGCGTTTTTGCATAAGAAATATGTCACATAAATCCCTTTTTGCATAAGAAATATGTCCAGAGGGTCTTGCTTATCCGGATGACGGAGGGTACACGGGGCGGCGTCCGCTCAGTTCCGCGCAAGGACGTATTC[G/A]CTGAACTGGGACGAGTCTACTCCTCCCCCCACAGGAGCCCCACGATTTCAAATCCTCTTTGCTGCAACCTCT

WI-				Sequence
WI-22082b	67	C	T	...	CAGGACTTGGTTTGCTGTCCCAACTGCACATAAATGTCCCTTTTTGTTTGTTGAGTTATTGGTTGTGTGTG[C/T]GTTTTCCTTTTTGCATAAGAAATAGTGTCCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGGAGGGTACACGGGGCGGTCCGCTCAGTTCCGCCGAAGGACGTATTCGCTGAACTGGGACGAGTCTACTCCTCCCCCACAGGAGCCCACGGATTTCAAATCCTCTTTGCTGCAACCTCT
WI-20993	139	A	G	...	AACACAAACTCCATGCTCTTCAAGGATTCCCACACCCAGATACTAGAAGACATATTAAAATTTACAGCAATTAAAACAGTGTAGTTGGTACAATAACACATATAGCAATGATACAAATTACAAATTAGGGGGAAAAAAACCCTGGGCTTCT[A/G]TAACAAGTGAGTATACATTAAAGACACAGTATTGCAGAATGGCTTCAGGATTAATTTGATTAATTTAGAGAGAGCCTATTTCAGGTCTTCCTAGCTCATCCACACATCACC
WI-21723b	125	A	G	...	AAGCGGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATATTTCTGAAGATAACAATTATGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCCCAACAACAGCATGATAAATAATTCAACTATGTAGAAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATCATT
WI-21723a	82	G	A	...	AAGCGGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATATTTCTGAAGATAACAATTATGGACTTTAAAGCTC[G/A]ACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCCCAACAACAGCATGATAAATAATTCAACTATGTAGAAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATCATT
WI-22132	99	T	G	...	CAACAGATGCTTGAGCGCCAAAAAGCAAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTCAACCTTTAATCTGACTTGCCTTTACTATCCTT[T/G]CCCCATTCTTCTCTAATCTCTTTTGCCTTACAATATATTACCTTCTAGTTGTCACCTCTAGTTAATGTCCTGCCCCAAACAATACTAACCCATTGAAGGATAACTATGGAAACCTTTAAATGGGACAGTGGG
WI-21006a	106	A	G	...	TGACAGATCACACACCACATTTGTTGTTGTAACTTTTTCTCCTTCAAGAGTCACCTTAAGCCAGAAGATTCTCTTAAAGAACACATACACAC[A/G]AGAGGCAAGTACAAAAATGTAACCCCACCAAAGTGCATGTGAATGAAAGTGCAAAAAAGGCTTCATTTGCAAACTCTGAGGATCATTCTCTCTGCTTCAGGAAAATAAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138	C	G	...	CTGAGGCCTGCTCTCTAACTTCATNTGACGGAGCGAGTTTCCTGGCTTGGAAATAACTGAAAAGATTCATTTTCTCTTGTGTACAAAGGATTCAAAATATTTTCACATCTTCCTTCTGCCAGTTAAACGTGCCGTGGCTTC[C/G]CAATACACACCCAAGCGTAACTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAGATGGTA
WI-21079c	166	G	A	...	AATGAAAATGCCACCCAGAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTGTGCGCAAAATCAAGTTGTTTTAATACCAGTGTGCAGCTTGATTCCTCCATGAAATTAAAGCTGTGTTGTTGCTCACTTGTTTACATAACTCAGGCCCACCCTGAAATATCTGCTAGTGGG[G/A]AATTTACAACCCACTGACCATCTCAGCTCAAAGCCAGAGTGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAAT

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WI-21079a	50	G	A	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGT[G/A]CGCAAAATCAAGT TGTTTTAATACCAGTGTGCAGCTTGATTCCTCCATGAAATTAAAGCTGTGTTGCTCACTTGTTTACA TAACTCAGGCACCCTGAGAATATCTGCTAGTCAGGTGGGGAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAAT
WI-22129a	45	T	G	---	TCTGTAGATTTAGCCATGCCATATATTTAACTTTAAGGAAAAG[T/G]TTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCAATAAGTTAGCTCTAACAGTTAACATTGAAGTCTTATACCTTATATTA AATGTTTAGCAATCTCTACTACATTTCAAATATAAATATTGGTTGCAAATTCCAGNAAAGGGCA TTAACCAAACATGGGACTGATCCTGGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79	A	G	---	TGGAGTTAAGTGGGGCTCTGCTATTTCCCCAAGAAGGACTCGGAAGATGTTGATTCCCAGGGCAGAGT GAGGGGCAGGACA[A/G]GGATGAGGCTCTTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGGACTGCCAGGTTGGGGAGCCTCACCCAGAGAGCTCATTGACCCCACACCCACCACTCACC CAGCACACAGGCACACGCAGGGCACAGGGCACACGNTGCACTCACCACGC
WI-18916b	42	C	T	---	AATGGCATCCCTGTCGATACCAAACATCTTCAGCAGCTCAGC[C/T]GGCTTCCCACTTCTTGGTACCC GGTTAACTGCCAGGNGGGTGACAGTGATGCCAGGCTCGCCCACTACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-18916a	35	G	C	---	AATGGCATCCCTGTCGATACCAAACATCTTCAGCA[G/C]CTCAGCGGCGCTTCCCACTTCTTGGTACCC GGTTAACTGCCAGGNGGGTGACAGTGATGCCAGGCTCGCCCACTACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-19828c	200	A	G	---	TTCCCTTCTCCCCAAGAAGTGGGCAGAAAGCTTGTTAACCTCCTTTACAGATGAAGAAAACAA GATCAGAGGTGCTAAGTGCTGTAGCCTAGTGCCAGGNCTTCTGGCCCCAATTCTGGGTTCTCCCCAAG CCCATGCTCTTCCCACTTTCACAATCTTTACTTCTCTCTGACCCTCACCACCACCAAAATT[A/G] [C]TTTTAATTCTGGAAAAGAAAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47	C	T	---	CACAAGAGTCTGTACAACCTTAGGGACACAGCCCCTGGCCCTC[C/T]AGCTGCGATGCCACCCTC ATATCCCACCCCCATCCCCAGCCTCCTGCCCCGACACCCCAGGCTCCCCTGCTCTGGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCCTTGATCCAACCACAGCATCT
WI-19860	51	C	G	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGATGTTTCCAAAGATG[C/G]CTGCATCAGTAT CTCCCATCCCACATAATTTCTGTTGATTTGCCATTCACCCATAAAATGGTGGGATCTACCTCCCCT CCTTGCAAATTTGAGCTGGNCCTCTGATCCTGTCTAAGGATCTGAAGCC
WI-19889b	80	C	T	---	ACCCAGCTCCTCTTACCCTCTGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAAACTGCAGGGCAAG AGGAGTGAGGGG[C/T]TACAGCATTTATTTCCCTCTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTAGTTCCTTGCCCACAGTCGTAACTATTGC

WI-19891c	172	C	G	...	TGTTGGTCTGAGAATTCACAGCTTACTACAAGGAAGCTGAGAATTGCTTGGTGCCCCTCCCCCCCG ACTCCTCTGCTGCTGGGAAACGTGGCTTTGNCTCCCAGACACGTGTCAGATGCCAGCTCTCCTCAGCGG AGCTCCCGATCCCTCAATTTGCCATCTGTCTGACTC[C/G]CGTCTTCCCCGGGGCCGTGGGGGCGTGCTTGT CAGGCAGGCGGCGGGGAGGAAGGAAGGAGGAGATCCAGGGTCTGTCTG
WI-20155a	81	C	T	...	GCACCTGTAGGGGGTGTAGCTTCCATGTTCTCCAAGCACGGGCTGTACATTACCCTTAGGCTGACCAT TCCCTTGCGGGCGGGG[C/T]GCAAAACTGCTTTGAGGAAATNTCCCAGGAGGAATAAACTAGAAGACGC ACCTGCTATTTCACCATACTATGGAGAATACAGTCAATGAGTGGTGGCAGAAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAAGTCTCTCTTCTGTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91	T	G	...	AGCCATACACAATGCATTGCAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGCGTCAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCA[T/G]ACACCAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGGGAAGGATGCT GGGTGATCTTGTTCCCCCGCAGAGGGCCTGGGAGGCAGGGNGGGGTGGTGGGAA
WI-20270a	53	G	A	...	AGCCATACACAATGCATTGCAAAGAAACAAAGCAGCTGTACAGGAGTGGGGACGC[G/A]TCAGTGTAC AATACATTCATGTCCAGGATAAGGAGCATACACCAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGGGAAGGATGCT GGGTGATCTTGTTCCCCCGCAGAGGGCCTGGGAGGCAGGGNGGGGTGGTGGGAA
WI-20622	130	T	C	...	CCACTTTCAATATTTTACAAAAATGCTCACGCAGCAAATATGAAAAGCTTCAACACTTTCCCTTTGTA ACTTGCTGCAATAAATGCAACTTTAACAAACATACAAAATTTCTTCTGTATCTTAAAAGTTGAA[T/C] TACTAATTTTATGATGTTACTCATATTTTATTCATATACTTTAATGACATCATTGCCAATACACATA CATTATTTCTNTAACTTTATTTTTACAATAAGCCAACATCTGTCATGCAG
WI-20768b	190	C	T	...	TTCCCACTCAAAACTCCCACCCCAACCTTCCTGGAAGGCAGGCGTAACAGGACCTCCTGCCTGCCTGC TCACGACTGATTACTTTCAATCCCAGCTGCAATGCAAAGTCAGCACACACTACTGCTGGGA[C/T]CAGGGACTC CAGGAGAGGTCTATTTCTGGGCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTCC GTAATTCGCCTTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTCC
WI-20768a	71	C	T	...	TTCCCACTCAAAACTCCCACCCCAACCTTCCTGGAAGGCAGGCGTAACAGGACCTCCTGCCTGCCTGC TCA[C/T]GACTGATTACTTTCAATCCCAGCTGCAATGCAAAGTCAGCACACACTACTGCTGGGA GNTCAGCACACACTACTGCTGGGACGNTCACCAGGAAGNTCAGCACACATACTGCTGGGACGGACTC GTAATTCGCCTTGGTCCAACTCCTTCTATGGGGTTTAGCTGCCCTCATTCC
WI-21909	153	A	T	...	TGTTTGCTTTGTGCCAGGTACTCTACTGCTTTACATAAATTATCTCATTCATTGTCACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGTGCCACCTAAAATAAGGATATTGTTGGTCATCTTTAAAGAAA TGTCTTAACATACCAAAAG[A/T]AGTGGAATCAATAGAATAAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAATAATATAGGGATACCACCTAAAATTTATATTTCTATGTATGGAAAG

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WI-22202	128	A	G	---	TGTTGCTTGGTTGTTGTTGCTTTCTGGAAACATATTGGAAACACTGTTTTTCATAAGCTGTGTCCTGACAGTGGCACAATCCCATCCATCTTCAGGCCTTTAATAAGGTCATTATGAAATCTGAATTCT[A/G]TTAATACTCTGGTGCATTCATTCATCTGCAAAAGCAACTGGCACAACCACTCCTTGCCGGTGCAGCTCTCGGAGAACATCTAATATTGAGTCTAGTTCTGTGCGGAACTTCTCCAGCTCAC
WI-22189	70	C	T	---	CCAAGGATGAAATTTCCACATTTATTTNCTTTTATGTGAATAGAAAATGGCAGTGAAGTGTCCTATGAA[C/T]GAGGCGAGGAATGGCGTACCAGCGTGCCGGTACCAGCAGGTTGTGTGCTTCCAAAGTACACTATGTGTGGTGGAGACAAAGGGT
WI-22283	109	T	C	---	GGGGAGGCATCATAGAAAAAAACCCTCAGCCAGAAGTTAGGACATTGTGATTCTCAGCCACTAACGAGCTGTATGACCTTGGTCACTAGGCCTCTGCAGGCCTCTGGTTG[T/C]TTCATTTGCAAAATAAAACCCAGACCGGGTCATCTTTCAGTTCCCTTCCCAGCTCTCTATTATTTATGATTCTTATGATTTATGAGCCATGTATGATTATCAGTCTCCCCTGATGACTCACTCAACTCCAATGATGCAAAGTGTATGATTTATCAGTCTCCCCTGATGACTCACTCAACTCCAATGATGCAAAG
WI-22290a	136	C	T	---	GACGTCATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTTATGGGCCTCTAAGCACCGGCCAGTAGTGGGGAATGCCACATGCAATGGGTGAGTGGGGATCTGGGGGGGTCAGGACCTTGCTTT[C/T]TTCCAATCTCTCCTTNATTCTCTCTCCCTATTCCCCTCCTTTCCCCAAATGTCTAAGGTCCCAATTCCCAGAACCCTCCCAG
WI-22292	53	A	G	---	CCAGTGGAAGGGTTACAGCCATAGTGAGGTTCCCCCATTGCTCAGTACCAGA[A/G]TTTGAGTACGGTCGTTTAAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186	C	T	---	ACCTTGCACACCTGCCATCCGGTGCCATCTCCTGGCTGGCCACATCTATACCCCACTCTGGCTCTGAAAGGCTTGTCAACCAAAAATGGGCAGCTGGGGCTAAGGCATATTTAAACAAAGGCTCCAAAGGACCCCTTTCACTTGGGTCTGCTAGCCATCCAGCCTCTCTCTCAGCCAAAGGCAGGATTGGTGGT[C/T]CTTGTGTTTCTGAACAGGGCCCAGGGGCCCAAGGCATGCCAATGCCATCCATCGCAGCACTCAACCCT
WI-22395b	127	A	G	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAATTTCTATACAGAAATGGTTCTTTCTTCTTGAATATTTTGTAGGGATGGATGATGAATTGAAAGTGAATTAAAGTCAAGATAAAGGGGCAACTCTTTAAT[A/G]AAGGAAATGTTACCAAATCCATAGTGAAGAGTAGAATATGTTCTTTAGAGTAGNTAGAAGAGTCCCCAGGCTCCT
WI-22405	90	A	C	---	TTTATGGCTCCTGAGTGCCTTCACCCAGCTACACTTTACCTTGTATCTATAAAAGTGTAATTTAGAGTAAATACATTGGCTGTAAAGTCG[A/C]GATCAGGTGCTCTCCACCAAAAGCAAAACAAAACTGCTGAAATGTGGCAAGGTTCTCAGTG
WI-22419b	67	T	C	---	CCCTTCTGGACAGTTTGCTTTATGTTGTTCAGACAATCAAGGNTCGCCTTCGCCAGGCACAGCCCAGTGC[T/C]TGGAGCATGGCATCAGCAGCAGGCTCCCCCGGCCTTGAAGCATGCGTGTGCACGAT
WI-21342d	59	T	C	---	ATTTTCCCTTTCTGTGTTTCGTATTTCCCCTTTTGTCAGTAAATNAGCAATACACTGA[T/C]TGGAAATCTGCATGAAATAACATTAAACAAGTTCATAACACACCCATATCAGATGTATAAAGCAAGAGGTTGAAAAAATATCCCCTAACCGAATGCAAATTAGGTATCCCTCAAATTGCACATTCTCCTCCTAGTTT

WI-21763b	154	A	G	---	CATACCCTTTAGGTGCCCACATTGATCTTAGTTAACAGTCTTGTGTAGTTCCCTCTTAGGCTTCAAGA TAATTGTGATTTCATCGCACCCCAGATACTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACT GCTCTCCCACAGCTGATT[A/G]CAGACATTGCCTGTGCTCTTCCTACCCCAGCTGTGTCTAGTGCACTT GA
WI-21763a	135	T	C	---	CATACCCTTTAGGTGCCCACATTGATCTTAGTTAACAGTCTTGTGTAGTTCCCTCTTAGGCTTCAAGA TAATTGTGATTTCATCGCACCCCAGATACTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCAC[T/C]GCTCTCCCACAGCTGATTACAGACATTGCCTGTGCTCTTCCTACCCCAGCTGTGTCTAGTGCACTT GA
WI-22440	64	A	C	---	CAGTCCATTTGAGTCCCCAGTCGCGAGGGTGCATTCTTCCTTATCTTGCTTAAGCCACTTGGGTA[A/C] TCCATTCCAGCTCTGCCACCCTTCTCCAGTTTTCTCATGTCAGAAGTCCCTGGAGGGAGGAGGCTTTCTGG AAAT
WI-22449	74	T	C	---	CAATGAATGTTGTGGCATATGATTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTAC TTCTTT[T/C]GAAAAAATACACAATGGGAACTGACA
WI-21965a	112	A	G	---	CAGGTTCCACCAGAGCCTTTATTTCAGCCACTCAGGACCCTGGCTTTCTGCTCCAAGGCACTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGGACCTCCCCCACAGCC[A/G]CCCCCACAGGGTTCTCTGTT TCCCAAGTCCTGATGGATTCAGGCAAGACCTTCACCCACTACCTGCTGGAGGAGGGGTC ATGAGGCAGCCTGGTGGTGCCCAGCTCCAGCTGTGACACACTGCCAATGTGC
WI-21687c	115	C	G	---	CACCTGGCAGTTGAGTCAGATTGTGAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACACATGGTTTCCTAGTCAGAAAGTCTCATGGACTTTCTTCCTCTAAG[C/G]TGTTCTTATGATCAGAC CACCTCCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149	T	C	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAAGAATTTCACAACTATTGACTATACAGAG TCTTCAATTCCAAAAACAGTTAATAGTAACTTGGTGGCACATACAACAATGCATTGAATACTCTGTAT TATTCAGTAACTAAAT[T/C]AGGNTCCTGCATCATTCTCTTCACA
WI-22250b	132	C	T	---	ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACTGTAGTGGGTTATTATGGGGTCTCCTGGCCTGTGTTATG[C/T] GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89	G	A	---	ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACT[G/A]TAGTGGGTTATTATGGGGTCTCCTGGCCTGTGTTATGC GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192	G	C	---	GCAGGCCATCCTCCTCTCCAACACCTCCCAGGCCACCCTGGGCGCCCAGAGCACCCATGCCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCCCTGCCCCCAGGGGGATGAGGCCCCAGCCCCCAGAACCTG[G/C]AGTGCTTC TTTGAGCGGGGGCGGCCCGTGCTCTCAGCGTGCTGCTCGGGGAGGTCTCTGGGGGAGGTGAGGAAGGAGGT

Name	Num				Sequence
UTR-04932-2a	149	C	T	---	GCAGCCATCCTCCTCTCCAACACCTCCCAGGCCACCCTGGGGCCACCCTCATGCCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCCTGCCCGCCAGCCAGGGGGATGAGGCCCCAGCCCCAGGTTCTCGGCTTCTCAGGACGTCCCAGCAAGTGGA GCCCAGAGAGGTTTG[C/T]TGGGGACTCCCGTGCCTGCTCAGCTGCTCCTGGGAGGTGAGGAAGGAGGT TTTGACCGGGGCCCCGGTCCCGTGCCTGCTCAGCTGCTCCTGGGAGGTGAGGAAGGAGGT
stFIBBb	412	G	C	---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGGGAGCATGAGCCCTTTCCCACGGCCCTTGCCACTGGTCTCCTGGCCCTCTCTCTGATCATGCCCAGG TTTGCACCAGCCTCGAGTCTCCATGTTGTAGTACATTCTCCAAGATGCAGCCCAGGAGCCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCCTTAGAACCTTCCATGGTT
stFIBBa	341	T	C	---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGGGAGCATGAGCCCTTTCCCACGGCCCTTGCCACTGGTCTCCTGGCCCTCTCTCTGATCATGCCCAGG TTTGCACCAGCCTCGAGTCTCCATGTTGTAGTACATTCTCCAAGATGCAGCCCAGGAGCCCTCTCTGA AGGACCAGTCTGGTTACGATGGTCTGAGCTTCCTTAGAACCTTCCATGGTT
stIGLV2	61	T	C	---	GTCACAAGAGGCAGCGCTCTCGGGACGTCTCCACCATGGCCTGGGCTCTGCTCCTCAC[T/C]CTC CTCACTCAGGACACAGGTGACGCCCTCCAGGGAAGGGGTCTTGGGACCTCTGGGCTCTGATCCTTGGTC TCCTGCTCCTCCAGGCTCAAGCTCCACCGGGCCCCAGCCACTCACTGGCATGT
stSG10017c	70	T	C	---	GTTCAGGCTCATCTTGAACTCCTGGTGTCAAGCGATCCTCCCACCTCGACTCTCCGACCTCCCAGGGTGCTGGGAT TA[T/C]AGGCCATGAGCCCCACCTGGACACAAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG10017a	33	G	A	---	GTTCAGGCTCATCTTGAACTCCTGGTGTCAAGC[G/A]ATCCTCCCACCTCGACTCTCCCAGGGTGCTGG GATTATAGGCCATGAGCCCCACCTGGACACAAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG10023	63	A	T	---	TAATGATAATTAGGGCCATTCTTCCCACACGAAGATGACACAATTGACCCAATATCATTGAGGC[A/T] AACAGTTTGGGCGTGTTTTTCCAGTAGTAGTGATGACAGTGA
stSG10096	36	G	C	---	GTGGAGAAAGATCGTCTTTCCTCCCCCATGACC[G/C]GCCTTCCCGCGGCACCTGTGCGTTTCC ACCCCGAGACGCGGCCTTTGTAGGGACCCACTCGCCCCACTCCGCTGCGCTGGGTTCCGCCCTCCTAG GGCTCGAGTGTTTAAG
stSG10118	107	C	A	---	TAGGCTTAAACCTGGAATCTACAAGCCAAAGTCCCTCCCTGCCTGAGGGCAGTACCCTCCATTGGGC ACAGTCCAGACCCAAGTCAAAGATGCCCATTCCTTGCG[C/A]CTCAGCCCTGCAGTTCCTTCCATTTCC ACCAGCCGTGCCTTGTTGGTTTTCCTCCCAGTGAG
stSG10120	89	T	C	---	TAGTAGGTAAGAAAAGCAAAGGAGGATTGCTTATGCGATGACTGTTTACAGTGGTGTCAGACTATGC CGTGTTCACGAACACTTAATAT[T/C][T/G]TTGTTGTAATCTGATTTATCCTCGTCTTACAAATG
stSG10178	42	C	T	---	TTGAAGCAATATTGTCTAGCACTCTGCTGGACATTAAGTCCG[C/T]GGGAGGAGAAGTGAACAGGAA TCGAATTCTTGTCTTTAACTGCCCTTAGTTAGGGAGATGTTAAAATACTTGGC

ID	Pos	Allele 1	Allele 2		Sequence
stSG1019 3	136	G	A	---	GGAACAATACTACCTAAGGACAAAATACTATTATTAAAAAAAAAGTCTTCTCAGTGTATATTGTGTAA CACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTTCTGTAGTGCCATCTATACAAACTTTTAC TT[G/A]TTTGAAAACTGAGATTTAAGTTGCAAACT
stSG1020 2c	143	G	T	---	AAGCTAACTTAGGTGAATGGTGCCACTCAAAGGTCTTCCGAGGGAAGCTCAGTCCTGGCTTGCGAG AGTCAGCCTTGGTCACCTCATAACGGGGCTCAAGGCGTCAAGGAAGCAGTCCCACTGCTTCT CGCTGTCA[G/T]CAAGACCACAAGGCAGATGCCCACTCGTGTCCTCTTCCTTGTCTACTTTCT
stSG1020 9b	75	A	G	---	TCTTTTCTCTTTCACTCTCAGTCACCATGATTCAAATAAACTAATTCTCCTTAAGATCCCACTTTAT TTTTTA[A/G]CTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34	C	T	---	TCTTTTCTCTTTCACTCTCAGTCACCATGATT[C/T]AAATAAACTAATTCTCCTTAAGATCCCACT TTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29	T	C	---	TACTAGACATGCAAAATGAGAAGATTACA[T/C]GTGAATATTTAAAGAAGTTATATTGTTTGACAT AATATGCATTGTACCCGGGCATAATAAAGTTAAAAGCCAGTTATTCTGA
stSG1025 2	108	A	C	---	ATAGGTTTCAGGAACAAAATCATTAAATAAATGAAAAATGAGAAGAATTCTTATTTTTGGACCAATTTT AGGCACTTAAGAGTTTCTTTCTTCCCTTGATCA[A/C]AGTGAAGATATGATGAGGGAATTC AGAAATTTCTCTTCTTG
EST10915 0	123	A	C	---	CTGTATTAATTAAGAAGGCACTATTAATGAGGGACGGAAAAATCTACCTGTACACAAAATTCTGTAC TTTAACAGCATCTTCAAAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAG[A/C]ATTTTAA GAACTGAGTTATTTGGAC
EST11023 1	166	T	A	---	TTTTTGTTAAACCAACCACCCTGAAAGTTTCCACATGTGAAAATATAGATACAACAGTGAACAAAAT ATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAAACAGCAGGGC AATTAGTCAATTCAAATTAAAAAAAATAGTACATGTTA[T/A]GTGTAATAAAATTAAATTACAAAGGCTTT TCCACTCGTGGATTGATTCCTTTTTTTGGAGGAGGGAGTAATCCTGG
EST14096 8	71	G	C	---	GGGATGTATATTACAGATAACAACAACTCACAAATATACCATCAGAACATCAGACATTGAAAACTAAGGCCATTCT GTGA[G/C]TTATTTTAAAACTTGGTGTTTTGCACATAATGATCTTAAAAAAAAATGAATTACCAAA ACCAAGATCTCTCTAAAATGAAAATTAATGCAGGTACAGGATAACTTTAGGCTGTATATCTAATC TGAAG
EST22113 6c	125	C	A	---	TGCAAATTGTGAGAAGGCAGGAGGGCAGCAGGGGCCAACCCTGGGACCTCATCTCTGTCTAGAATGTGAGGTCG CAGGGGATGCTTAAGTCTTCCTCTGGCAGAGACCGAGGTGCAGAGATGATTCTTCTCA[C/A]CCCTTC TCTCAGGGTCGTGGAG
EST22555 7	60	G	A	---	TCAAGCATGTGTAAGGCACTACTGCCCCGCCAGACCCTTCTAACTTCTGCACACTGGAAGGT[G/A]AAA CCTGGGAGGAGAAGAGACACTCCCCTCCCTAGCTTCTGGGCACCCTCCAAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAGGACAAAAGACAAAGACCAGGGCTCAGAG

ID	Position	Allele 1	Allele 2		Sequence
EST22917 6	74	C	T	...	GTAAACCTTGCAAACGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTTGGGCTCTCAATGCA ATAGAAA[C/T]TGACATGGGCCAAAGACTTCCCAGACAAAGCACGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65	A	G	...	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACCTTAACCCTGTCCTACTCA[A/ G]TGTGGTTTGCTAGCCTCACTCGCACACAGGAAGCTTGGAGGCTCCAAGTCACTCTCCA
EST36745 3	56	A	G	...	GAGGGGGAACTTCAAAGAGGATTCCAACAGTGAAGCAGAATCATGGGCAAAAGTC[A/G]CTATGG GGCCAGACTGAGGTTGGACCACACAGCCAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCACGCACGGAGTAGCCAT
STS-R37410c	201	A	T	...	TGTGACCATACCAAACCTATGCAATAAAGAGAAAAAAATCCTCACTTAAAAAAACAAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAGTTCATAGCATTTTGGA ATTTATGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGTATG T[A/T]TATTGTGAGTGGTGCTCTAGTGGCCAAT
STS-R37410b	139	G	T	...	TGTGACCATACCAAACCTATGCAATAAAGAGAAAAAAATCCTCACTTAAAAAAACAAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAGTTCATAGCATTTTGGA ATTTAT[A/T]GTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS-R37410a	48	C	T	...	TGTGACCATACCAAACCTATGCAATAAAGAGAAAAAAATCCTCA[C/T]TTAAAAAAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAGTTCATAGCATTT GGAATTTATGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS-R42778	74	C	T	...	TATCGTGGGAAGTTCCAACCTCATATGCTGCTTTTCTACTTGCTAATATTGGATGCTTCTTGCCA GGCTCTC[C/T]TTTAAATTGTGCTGTGTAACCTGTCGTGGGACTGAGGAGGCG AGGTAGCACGACACTGTGAGTGCACTAA
UTR-04350	125	C	G	...	CAATCTGAAAGAGATGCATAGCCGGATTGGTGCTTCAGCAGCGTGTGGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTAGTGGGGTTCCTCCCGGGATGGTGAAAATGTTCCGGACCTAGATA[C/G]TGACGA AGGTAGCACGACACTGTGAGTGCACTAA
stSG1026 6	55	T	C	...	GAAATAAACTAAAACTGCAAAGCAAATCACTGTTAATAAGAATTGTTCTTCGTT[T/C]GACAGTTG AAGTGGGTGTGAGATGGGCATAGCCAATGAACAGTGTCCTCAGAATGCGGGGCAAA CTCCTCTGTGAAAATGTAT
stSG1028 2	70	T	G	...	GTATAATTCAGCATAAGCCAAAGCCTTTTAAAATAACCAATACTATCATTTTATGAAATCTTTACA AGA[T/G]AAGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCAATTTAAGAGTTGACTATC
stSG1031 0	128	C	A	...	CACTTTAGATATGAGGAAAATGGTTTAATGGACAACAAAGGAGTCAGCCACGTTGGAACCAACATAG TTTCATACCACCGTTGAAACCATGTGTTTGATATGCAAATAACAAGCAAATAATTTTCACT[C/A]TTG TCAATGCCAATGCATTGAAATGCAAGGCCCAGAAAATGAGAAAAATGAGAGAAAGGATAACAAACTTTGTATAAAAAGGTA AGAATTTCTGTGTG

ID	Pos			Sequence
stSG1033 1b	116	T	C	TTTAAAGCTACACATGTCTGCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTCGGGCTCCAACCTGTCTGCCTAGGAAGGCCTAGACCTCAAACACCAACCACCTCCA[T/C]GCATTTCTCTTTGGCTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTTCTGCGCTCCCACCTGTTCATCTGACTTAGGACCCTCC
stSG1033 1a	107	A	T	TTTAAAGCTACACATGTCTGCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTCGGGCTCCAACCTGTCTGCCTAGGAAGGCCTAGACCTCAAACACCA[A/T]CACCTCCAGCTCATTTCTCTTTGGCTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTTCTGGGCTCCCACCTGTTCATCTGACTTAGGACCCTCC
stSG1243 b	225	G	A	ATTGGCAAATGGGAAAATGACACCAATCATTGATTACAGAAAATGGTTTTATAAATCCTCTCTGAAATTATGTTCAGGCCCAGCAATGGCTATGCCTGCAACACCAGCCTGGGCAACATAGTAAGACCCCATCTCTGTTTTTTTTAAAAAAGAAATTCTGTTC[G/A]AAGTATTTCAGACCAAAAGGAGGT
stSG1345 b	60	G	A	AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTGAACTAGTTTGCTTCTTCTTAC[G/A]GCTTCACATTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA
stSG1345 a	54	T	C	AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTGAACTAGTTTGCT[T/G]CTTACGCGCTTCACATTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA
				TTAATGTCATCCAGGGAGGGGCCAGGGGTTCCCATGAAGAGGGGAGACTTGGTATTTGT[T/G]TCAATCATTAAGAATGGGTGGGATTCACCACTTTGAACTGAACCTCGGGGGGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCCGACAAAGGGTTGTTGAACTGAACTGGTATGTCCCTTCTCGTCGCCAGCAGCTTCAGTCCCTTCTCGTCG
stSG1385 b	117	T	G	TCGTCTCCTTTCCAGTGCTTCTGCCAGAAGCATCCCCATGATGTGTGACCGCACAGCACTTTGTGTCT[T/C]GCTTGAGCACTTGCCACTCTGGCTGGTCAAGGCTCAAGGCTCAAGATGGC
stSG139	69	T	C	GATCTGGTTCCACAACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCAAGGCTCTCTCCATGTGGCAAACAAGATGGCTGGCTCCTCCACTTCCAGTTTGGCTTCTGTCTCCAT[T/C]AGTCTCTCTCCATGTGGCAAACAAGAGATGTCTCACTCCCATACTGGTGGTCCCAGGTTCACGTCATCTCCTCAGCTTGGAAATCCTGGAAATCCTGGAAGAAGTCCAATACCTGGGAAG
stSG1427	103	T	C	CCCTGGGAGTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTTAGGTCC[A/G]CTCCCTTGCGATGAAATGTGGGAGGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACCGCA
stSG1471	50	A	G	CAAAACCAAAAATCCTTCCCAACGATATATTACTATTTAGTCTAAGT[T/C]TTAATTCAAAGGTTGAGAATGACGAATTCAAGAAATTCTTCATACATAAATTGCTTTCCTTAGTTCTGCAGATGGGTA
stSG1483	44	T	C	CACACCCACAAGTTTCATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCAGTGTGCA[C/G]AATGTGGAGGATGTCTGTTGCAGCTGTGTAGTTACTAATGCAGTAGTTACTAATGCAGGAAAACCCAATGCAAAGAGGAA
stSG1696	67	C	G	AATGCCTGA

Marker	Position			Sequence
stSG1847 b	95	G	A	TTGCAGAGCAACAAATGGAAGCTTTAAAACCTCTTCAACACAAATGCTACCCCTAAAAATGAAAGAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTTCCAATGTGAAAACCAAATTAAAAATAACTTGATCACTGTGCT TCAAACACAACTG
stSG1847 a	49	C	A	TTGCAGAGCAACAAATGGAAGCTTTAAAACCTCTTCAACACAAATGCTACC[C/A]CTAAAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTTCCAATGTGÁAAACCAAATTAAAAATAACTTGATCACTGTGC TTCAAACACACTG
stSG1897 a	83	A	G	CTTAATGCCCCTTCCTCCTCTCTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACTA[A/G]GCCCACCACCTTCCTCCCCGGGTCTCCCCAAGATGACT
stSG2022 a	86	T	C	TGTCTTGAGGTTTCAAATCTGAGATATCTATGGCAAGTTTATAAAAGTACATTGATCAAGGTACAA TTTTTAACATTAATATACA[T/C]ATTCCATAATCTCATCTATTAACATTAACACAGGCCTTTGTTGT TGTTATTTTTCTCCCTACAATATTCCTGACTCTGTGAGGGACAGTGGGCCTCAGTTGGGGGGTTGAC T
stSG2076	104	C	G	AAACGTTGTCCCAAAATTGTGTTCAGTTCACAAGTATAAAATAAGACTTCTGAAAAAGTTACA ATTAGTTATAAAACACTTAAGAATATATTTGACATTC[C/G]ACATCACAGTGGGGCATTT
stSG2108 c	71	A	G	TTGAGCAAACAATGATTCGCGAATTGGGCAGCTCCAACCAAAAATGATTGAGGGGCTCCACAGAGA GAGC[A/G]TAAGGGGAAGAGACTTTTATAGGACAACTGTGAGAAGTAAAGCAAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTCTATCTTATTGGTCTATGTGTAGTTCTGTAGTTATGTAATTGTAAG TTTGTTGGGCTGTGTCTGA
stSG2108 a	49	T	C	TTGAGCAAACAATGATTCGCGAATTGGGCAGCTCCAACCAAAAATGATT[T/C]GAGGGGCTCCACAG AGAGAGCAATAAGGGGAAGAGACTTTTATAGGACAACTGTGAGAAGTAAAGCAAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTCTATTCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTTGGGCTGTGTCTGA
stSG2141 b	173	A	G	TTATTCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCACTGGCATGGCGATGGTGCAGGTGGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[A/G]AAGTTCCCTATTATATTTAAGGC AGTTTTCAGAGAGCACTGGCATTCTTGTTTGCTCTG
stSG2141 a	113	C	T	TTATTCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTATTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCACTGG[C/T]ATGGCGATGGTGCAGGTG GGTGCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGAAAGTTCCCTATTATATTTAAGGC AGTTTTCAGAGAGCACTGGCATTCTTGTTTGCTCTG

stSG2148	50	A	G	---	TGGGAAACAACCGGCTATAGTCTGAGTCATATTTTTTAGACCGGTGATTTC[A/G]AAAGAAAAACAATAAATGTGGATTAGAAAGGAAACAATCCATTACTGTATTTCGATACTGTATTTCGATGATTGTTCCACAGAGAGCTCATCAC
stSG2175	68	C	T	---	CTCAATGAGGACTCCATCAGCCAAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGTGCT[C/T]GCCGCGTGACTCAGCTAATGCTACCGGGGTTGGAGCGCACACCGAGCCCAGCCACCTTTTCCATACCTGGGCACCGAGAGGGAGAGGGAGTGGAAGGACCA
stSG2189	41	C	T	---	CAAGTGGTGAAAGCTGGGATTTGAGCCTGATATTCACACTA[C/T]CTACACATTCCCTCCAGTATAATAGGAACTCATCGCTACCTTTGAGCACTTAGTGTTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTCCAGCTTTGCGAAC
stSG2200	49	T	C	---	TGTTGATGACCATAGAGGATGCAAAGCTCCGGGCTGGTTCTGTATGATG[T/C]TTTATATTTATGTATAATGTCTTACCTGATGATACCAACATATTACTAGCCTTATAGATGAGGATGGCAGCTTGGCTGGTCAAT
stSG2243	85	G	T	---	CATTTTCTGCCTCCTGCTTCCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAAGATGGTCAGTAGAAAAG[G/T]AGAGCATCTCCTCAGCCCTGGAAGACAGTGTGGGAGCTTCAGCT
stSG2257	65	A	C	---	TCAGTGATTGTAGGAGCTGGCTAAGTCACTGGCGCTATCTGTGAGGCAGGCTATCAGAGGGCAG[A/C][C/T]CTGTCAGGAACTCTCGCCAAGCACTGGGCCTGCTGCTTCCTCCAGCCAGAATTCTTCCT
stSG2306	67	A	G	---	GTCATCAGCGTAGAGGTCACTGGTATAAACAAACAGTAGCTATATGATATTTTACA[A/G]TATGCTCCCATTGGGTTTTCCAAACTGATACAACCATGAGGTGAACACTTTCACTGTTTCACAGTTCCTCCAGAGA
stSG2334	70	T	G	---	GAAAACTACCCACCACAGCATCATCGTGTTAAAAGAAGAGAGGATGAAAGAAAAAATCCCGCAAAAAACAAAAAA[T/G]TGTGCAGTGGAGGGGCTGTGGGAGGGGTGAATG
stSG2339	63	T	C	---	AGAGCAGAAGAATGGTGAATCAACAGACCTCAAATTGTCTTGACTGCAGAAGTAACTGCTGTCAC[T/C]GTTCTCAGAGTCAACCATTACGGTGACTGGCTGTGCTTCCTATTCATCA
stSG2465	76	C	T	---	CAAGACTAAGAAGCCGCACCACCCGAGTGGTCCCACTCAAAAAGAGATTTCTGATTCTACCTCAAAATGCAGAAACCA[C/T]TACAGATTAAAGAGAAACAACACACACACTTTGAGAAACTCGCCCCTCCTCATCTTCAAAGTGTGGGGTATGCA
stSG2549	140	T	G	---	TTGCAGGCTTGTATTCCACAATAACAAAGTCATGTATAGAGAATGTGAAATGATACTTGAAAACCAAGATATATAAAATATTGAAGTCATTTATGCCTTTGATGACTGGGTTAAATATGCAAAGCAGCTAAAGGAATAT[T/C][T/C]ACCACCACCACCCCCTTTTTAACT
stSG2577 b	123	T	G	---	AATTGCCAAATGGAAAATTCCCAGAGGGATTTTTAGACCAACTTTGCCCTGTTGCATTCCCAGTTTGGTCCCAATATAGGCCTTCTGCAAGAAGAGATCAATGCCGAACTGTGAAAGCA[T/G]GAACAATCCCGGCCCAGATTAATTATT

stSG2577 a	121	C	T	---	AATTGCCAAATGGAAAATTCCCAGAGAGGATTTTTAGACCAACTTTGCCCTGTTGCATTCCCAGTTTGGT CCCAATATAGGCCTTCTCTGCAAGAAGAGAGATCAATGCCGAACCGAACTGTGAAAG[C/T]ATGAACAATC CCGGCCCAGATTAATTATT
stSG2700	58	G	A	---	ATCTCCTGACTGCTTAGTGGGGAAAGGAATCAATTATTTATGAACTGTCCGGCCCC[G/A]AGTCAC TCAGCGTTGCGGGAAAATAAACCACTGGTCCCAGAGCAGAGGAAGGCTACTTGAGCGGGACACCA
stSG2724 b	101	T	G	---	AAACAAGCTTTGTCATTTCCACTACATTTGTGTCTTTATATTAATATTTGCAAATGCTATAAT TTAATACTTATATTCCAATTGCTTGCATAATCA[T/G]TTTTTTAATCCTGGGGTGTTGAAAGAAC
stSG2776 a	65	G	A	---	GTGGCCGATCTTTACTTTTCCAGAAAAAGGCGGTAAATAAAAACCTGTAGAAAGTCTCGAATATGC[G/ A]ATTGGCCCTTTGGAGTTAGGCCCAGGAACTTCAAACAAGGGACACTGCTGGCCAACCACAAAA ATATCCACTAATTCCCGAATATAGTAACCCTGTCTTGTCCGAATG
stSG2791 b	109	G	T	---	AAGGAAAGGTGGAGGGAAGAAGGGAAGAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATACTTCTGAACGGTAAACTAGCAATTTAATAAATATT[G/T]GGGTCCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 a	100	A	G	---	AAGGAAAGGTGGAGGGAAGAAGGGAAGAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTATACTTCTGAACGGTAAACTAGCAATTTA[A/G]TAAATATTGGGGTCCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2826	85	C	T	---	CCGCAATTTCAACACACATTCTATGAAAACTAAGGGTGGATCATGTACAAACAAAAAACAAGC TCCCTCCCTCCCAAAACAAA[C/T]GAACAAAATAAAGAAAATAAAGAAATGCCCAGGTTTA ATTTTTTCC
stSG2850	88	G	A	---	ATGGGTGCATTGTAAAGGCAAATTAAATACTTTTCAGGCAGGGGCTGGCAAATTTAATGAGCTGA TGTGTCCCAAGGAGGAGACGGCC[G/A]GGCTCACCATCCCATCAAATACTCCTCCCAT
stSG3031	71	T	C	---	ATACTCACGGGGGCTGAAGGGCAATGTGAAGAGTGACTCGAAGTCCTGGCATTTCTGTGGTGTCAGC AAA[T/C]GCCCCTTTATTTATTTAAATGATTCCAGACATCTGGGCAGCATAGCT
stSG3058	81	G	A	---	GTCCCAACTCCTCTCCTTAGAGAAAAACTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAAGTCAAAC[G/A]TGAAGAAGCATCAAAGCAAAAACTGGCTGAGGC
stSG3092	94	T	G	---	CAGCATCTTCCAGAACATTCCTAGAACTGAACCATTCTTGTCACTATTGAAAAACAAAGCCAAGTTC CAAATCCAAAATAATAATAAATGAACGTGC[T/G]GATAAACATTCTTTATGGTTCCAGCCCTACTTT AGTT
stSG3230	95	A	G	---	AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTAGTCAATTGTCAATTGGGAGTC[A/G]GTGGGGTGCTAAGTGTCTGTGAACTGAAGTAG
stSG3245	160	G	C	---	ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGAGCAAGCAGCCCTGCTCCCAGGGGCCC CAGGTATGTGTAGAGGCCCAGTGGGGGTGGCCACTTGGTGTTTCTACCACCCCCTGCCATCCAGTCTG GCCCCAGTCGTACCTCACCTGGGGAGGTTG[G/C]TTGTACTTGGCTTAAGTACTTCATGCTTTAT

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stSG3265	42	T	C	---	AGGTGAAATGAGTTACTAAATGTAGCATTTATTTATAAGGAA[T/C]GCATTGTTGTGAATAGTTTCTCAG TTTCATTATGGAAAGATGATGATTCAGCCCACATTCAGTGTGTATGTTTCTAAATAACACAATCGAC AGGAACTGTCTGTTCAGCTGAATTTCTTGGGCTTTATGTGGCAGTGTGGTAAAAA ATCTGTCTGTCAGCTGAATTTCTGTCTGTC
stSG3269 b	141	C	T	---	TGTACTTACTGTGTCATCCTATCCTTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACTAGG AGTGAAGGGAGGAGGAGTCCTCCCAAAGTTACCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA[C/T]TGTAGATCCCCAAGTCCCTGACACATTTTCTTCTAAGAAACT
stSG3269 a	24	A	G	---	TGTACTTACTGTGTCATCCTATCC[A/G]TTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACT AGGAGTGAAGGGAGGAGGAGTCCTCCAAAGTACCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAAACT
stSG3284	130	C	T	---	TTAACTCAAGAACTTTCAGTTACACAGGAAGAGATTTATCTAATAATTAAAATGACTAAATTACAAAAAGC ATAAAATGTTTGAAGCCATTTTAAAGTTGTTTGAAATCCATATTAGCACTCAGACTTCCCCCA[C/T] TCCCTAACTTTTGTTAATTGCTGTAATGGGACATTTGTTTGTTTGATCTTACCC
stSG3292	99	A	T	---	GTCTCAAGTGAATCTGTAAATACATTTTTAAGTCTGACTTCAAATCGGTACATGAGGCTTAGACATA CACATCATTGGACAAGTGACTTAAATATCTAA[A/T]TTACAAATCAAATAGCATTTTCCTAACTTCAA
stSG3323	26	C	A	---	TAAAATGTCATATCTTTAGCTCTCCACT[C/A]CCAGTGTATCCATTTTCCCCAGCCGTAGAGCTTTTCTG TTTCTGTAGATTTGCCTGTCCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACACATCCATGCTGTAGACATGCTGCTTCATTCGTTTAA
stSG3369	69	C	T	---	GATCCCCAGTAGTATTTTTCTAAATTGAACTTGTTTGTTGTGGAAATAAAAATCTGAGGACCACTCAGAG GG[C/T]ATAAGGGAACCCTCTTTGTTCTTAGTTCATAAGGACTTCT
stSG3398	125	G	T	---	CAAGACTGTAAGAACGTAGGCCTTGTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCCAGGACTCAGG CTTCAGCTTCACAATCCCGGAGGAAAGGAAATGACACATTTCCAAACTGTCAACCTTTGTAGC[G/T]CTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
stSG3416 a	43	A	G	---	TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG[A/G]CTCACTGTAGCCTGGACCTCC TGGGGTTCAAGTGATCCTTCCACCTCCAGCCAACTGAGTAGCTGGCCTGCGAGGACAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3424	173	T	A	---	GTAAAGACAAGGTTTTGCTATGTTGACCAGGCTGTCTTGAACTCCTTGGCTTCAAGGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTGAGCCACTGCCCCCGCCGACTTTAAACTGAAT GTTGAAAATCATTCTGCTCTTTGCTGGGTAACACTGA[T/A]CAAGTTGCTTAACCTTTGTGAAACCAC TTTCCTTATCTGTAACAAAATGGACAAACAGAACTTTTTCCTTTCCTCTC
stSG3436	88	T	A	---	GTTCATGTTAAAGATTAGGAAAAGCTGTGGATGTGAGGGTCAGGTGATGTGATGGGAGGCCTCACAGA ATGAGTGGCAGAGAGAGGGCCCC[T/A]GAAATAGCTTACTCTGTTTCCTATC

ID	No.			Sequence
stSG3463	103	C	T	GATACAGAGATAGTGTGGTATGGATGGATGATGAAGGACAGTAGTATGAAGGACAAATAATACAAAATATATTTTATTG AAATAAACAAAGATCATACACAGTCCAATGGGTCAC[C/T]TGGAACAAACTTGCTTGACTATATTA CTGA
stSG3491 b	71	G	A	CAAGATACTTCATTGTCTCTAAGTAGTGCAGTGCTGGCAAATATTTCTCACGAACAAGGACGATTTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTACCTCCAAATAGCCTGCAATTAGCAGTCTGA ACAATCTTCTAATCTTTACTGGCACCTGTGGATTTCTATTAAACTCATTTATACTATTTTC[T]GTGATG ACAGAAAATAAGTTAAC
stSG3523	33	C	T	TAGCCATCTTACTCTAGTTCTTTTGGGTTTTA[C/T]GCATATATGTGTGTACAAACACACACACC CCTAATTCCTCAAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
stSG3536	213	A	G	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAAACCAAATACAGAATGGCTTC TGTGATACTGGCCTTGCTGAAACGCATCTCACTGTCATTCTATTGTTTATATTGTTAAAATGAGCTTG TGCACCATTAG[A/G]TCCTGCTGGGGTTCTCAGTCCTTGCCATGAAGTATG
stSG3583	112	G	A	GAAAAAGCTTAAACATACGATCCATGTGCAAACCCAAAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCTCAACACCTAC
stSG3586 a	60	G	C	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAAATCAGGTGTGGTGTG[G/C]ACG CCTGTAGTCCCTACTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGGCCATTGAGCACTCCAGCTTGAGACTGTTTCAAAA
stSG3589	101	T	C	ATATAGTGCTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAGGCAAAAAAAGT GTATATACCACCCTGGCACAAAAACCCCAATGA[T/C]CCTATTTCCAAGAATGTATCCAGATGAAA GTATCCAACAACAAAAAGCTATATACAC
stSG3590 a	70	A	T	GAGAGATGAGCTATTATTCTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAAAA AAA[A/T]TTTCTGATGTCTCTTGACCCTGTAGGAAAACATTCAGTTCTACACT
stSG3619	78	A	C	CAGTGAGACTTCTCATTTATAGCAAATACATTTTGCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCATTT[A/C]AACAAACTTCCAGAGAAAACTGGGCTCTATATTTAAG
stSG3644	40	T	C	ACATATGTAACTGCCATTAGTAGCCATATTTAGGATGAGA[T/C]GGATTGAGAGGCATGAACCAAGG ATGCGTAATAATCATTATGAAATAATAAGTTATCTGGGGAAACGGCCATTTGTCCAACATTTACTAA GTGCCTACTA
stSG3646 c	70	G	A	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGTCTTACT GGT[G/A]ATATTAACTTTGATACTTGGTGTCTGCTAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55	A	G	---	CTCATAATTAGAGATTGAGATTGTGCATTTGGCAAGAAGAATATATGATGATAACAATA[A/G]TATGTCTTACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTTCTCCATTGTAGAGTCATTCTTCTCTTTGTA
stSG3646 a	43	A	T	---	CTCATAATTAGAGATTGAGATTGTGCATTTGGCAAGAAGAATATATG[A/T]TGATAACAATAATATGTCTTACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAATTTTCTCCATTGTAGAGTCATTCTTCTCTTTGTA
stSG3693 b	85	A	C	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCCTGGACTCACGAAATATCCTACGAGGC[A/C]TCGCCCCTCCGAGACTGACGATTATTAACCACCCACACGGAAAAAGG
stSG3693 a	30	C	T	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCC[C/T]TCTGAAAGCCGATGACCATCCAACCCTGGACTCACCTGAAATATCCTACGAGGCATCGCCCCTCCGAGACTGACGATTATTAACCACCCACACGGAAAAAGG
stSG3698 b	145	G	A	---	TCTTGCCCTTTGTTACCCCTAGAGAGATGGCACCCAATCCCCAGGGGTTGCTCTCTGACTTCCACCATTCACTGACTTTATTGCCAGAGGAGCTCCCAGGAATCCACAGTTCTGGAAGAGAGGGGGCTCTAAGTCTTTATTGGG[G/A]AGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51	C	G	---	TCTTGCCCTTTGTTGTTACCCCTAGAGAGATGGCACCCAATCCCCAGGGGTTG[C/G]TCTCTGACTTCCACCATTCACTGACTTTATTGCCAGAGGAGCTCCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCTTTATTGGGGAGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107	C	T	---	ACCAGCCTCATGTGCAGAGGGGTTCCTGCTGGATCCCCAACTGGAGCCATCCCTGGGCCTAGACTTCTGTCTCCCTCACTCTCTAAATGAGTGCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAAGTGGCTATGCTGGTGCT
stSG3725	104	G	A	---	GCCAAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAAATCAAATATATTATTACCAGCCAACAGCAAACAGCCC[G/A]AGCAGGAATCGGCACACATAGTCATAAATAACATCAGGGGTAAATAACGGCACATTTA
stSG3751	128	G	A	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTCATACCTTTTTAGAAAGATGATTTTGAGGGCTTCAGTATTTAAAGGGGGAAAGCAGGCTGGAGGGGAAAGAGAGGATATGGTCCC[G/A]TTGCTGACTCCCATGTGTTGCAAGAG
stSG3787	49	T	A	---	TTCTGTGCAAAAGAATCCACATCACCATCATTGTTTGGTAGCAGAGGATCTCTTA[T/A]AAAGTTCCCTAAGACACTGAGGGCATAAAACCAAACAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCCT
stSG3880 b	115	G	C	---	GACAAGAGGGAAGAGAGATGCGCCAGAGACCAGGCTGGGGTCCCTGAGTGCCAGGCGCCACCACACGTCCTCCTGGGTCAAGGCTGGGCGAGCAGGTCTA[G/C]GGCCACGGAGGATGCAGGGGCTGGGAAGGGGACCCAAAGGGAGTGCATTTCTGCCCT

stSG3880 a	36	G C	---	GACAAGAGGGAAGAGAGATGCGGCCAGAGACCAGGGCTG[G/C]GGCCAGCTGGGGGTCCCTGAGTGCCAGG CGCCACCACAGTCCTGTGGGTCAAGGCCCCTCCTCTGGGGAGCAGGTCTAGGGCACGGAGGGGATGCCAG GGCTGGGGAGGGGGACCCCACCTCGGGGACCCAAAGGAGTCCATTTCTGCCCT
stSG3895	44	A G	---	AATCAGCCATTGTACACAATTGCAGCTATGTATTGTTAGTGTTGT[A/G]TTTTTTTCCATTAACTAA TACATGCCCTCACTAGATATATTCAATTAGTGTTATCACCATGGAACAAGATGCTGATTCGTCAACTG AAAAT
stSG3902	104	T C	---	TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCGACTCTGGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTCACCTAAATGTGAACTGCTTCTTTTC[T/C]TCAGCTCAATAGCTTAACATCTAATTC ATGTTTGCTCCCTTTGCTGGACAAT
stSG3935	50	G A	---	GGGGTGTCTGACGGACGACAGGCACACCCAGTTCAACAAGCAATTTGTCC[G/A]CTAGTGTGCAGGC TCCTCCCCCAGTTCCCACAGGCTGAGTACTATGGGGTCACAACCTTCCTGGACGT
stSG40	25	A G	---	GAGGAAGAGGGTTGAAGAAGTGCTGA[A/G]AAATATATTTAAGATTTCCTTGGGGAGAAATCTCGTGC CCAAACCTGGTGATGGGATCCCTTACTATTTAGAATAAGGAACAAAATAAACCCTTGTGTATGTATCA CCCAA
stSG4009	32	A G	---	GTGTGGGCTGTCTGATGATGAATGGCGCGCTC[A/G]TACTCTTTACGGTCTTCTTACACTTTTATGCTCCT ATGAATTCTCTGATGGGCTTAAGGGCTGAACCATATCTGAAGGTTTCCCACACTGCTTACA
stSG4033	123	T C	---	AGAAGCCTTGGGGACAATGGCAGTGCCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTGCAACCAAAGAACCTAATGTTTCAAGCATAAAGGTACTTT[T/C]TGTGAAC AGGTGGGCAACAC
stSG4038 a	29	G A	---	GCTGAGAGCAGCGTGTACAGCCACGCCCTGT[G/A]CGCAGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCCTCAGTCAGGAGGTTCAGGCTCCCGGAGAGCACCTGAGGGGTTCCATCACT
stSG406	53	T C	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAAAA[T/C]GGTTTTAGTT TTGCTGAAGACTGGCCTTATTAATGGACAGCAGCTTTCCTAACAAGAGATTATTAACTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55	G T	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGTATTAG[G/T]ATAAAAAA GTTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAATCAAG CCTTTGGACTAACCCCAGGGCATTGCCCTTCATCCTGG
stSG4095 a	27	A C	---	ATCTGGGCTGAATTAGTCAAGCAGGTC[A/C]GATACTATTGTCTGCTAGATGTATTAGGATAAAAAA GTTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAATCAAG CCTTTGGACTAACCCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65	G A	---	TGCATGTTCCACATCTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[G/ A]CTTTTTCCCCTGCAGAGAGCCCACAGTTAAACACGTTCCAGCACCATTAATCCACCGAGCT

Marker	Pos			Sequence
stSG4128	54	A	G	CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCT[A/G]TATATTATTT TACTTCTTCTGAAAATGCCACATAATTTGCAATAAATGATTCACTCTCCTTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAAATGTTCCAGAGGG
stSG4209 b	128	G	A	CACGAAACAGATGCAGCCTACACAGTGCTGTAGGACCGAGGCTCACAAACATCCACATGGCACAAGC AGGGGCCGGCCACTCCAGGCAAACGAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTCG[G/A]GC AGGGGGGGACCCACGGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65	G	A	CACGAAACAGATGCAGCCTACACAGTGCTGTAGGACCGAGGCTCACAAACATCCACATGGCACAA[G /A]CAGGGGCCGGCCACTCCAGGCAAACGAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTCGGC AGGGGGACCCACGGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31	G	A	CATTACCCAGAAGCCCATGGAGGACGCCAGAGC[G/A]CACGCGCCGGGACTCCCGCGATGGCTGGGGGG GCTATGGCGTCTGACAAGAGGATGAGCGAGGGCCGGGCCTGCCTCCTCCCCCCAGGGGCAGACGTGAC TGGGGGACCCATGGCCGGAAGGAATGGACCGGTCATG
stSG4301	81	T	G	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGAGGGTAGTGGCTCCCACACTTTCCAT TTAAGCAAATAAATT[T/G]AGCTTCTGAGTAGTTGTTCCCAGTTCACCCAACATTTTG
stSG4331 b	71	T	G	CTCACAAAGGCCAACACAGAAAAAGATACAATTCATTCACTATATTTTAGTTTTTATGACAC AGAG[T/G]TGTTTCAAACAAGTTAAGTCACCTGAAGAGCATGTTAAAAGTTTAAGTTATCACTT GGAGACAGAATTCTTGGCCTCGCCCTTGTCATTCTGTTTGATGGGGTGTGC
stSG4340	76	G	A	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGGAGAGAATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109	A	C	TTCCCAACCATTGAGTGACAGAGC[T/C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG AAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGCA[A/C]CCTTCACAACTAGAAACGACTC AGCGACTTTTTCTGTGAGCAAATGTCGAGG
stSG4361 a	24	T	C	TTCCCAACCATTGAGTGACAGAGC[T/C]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAATTAGG CACAAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAACTAGAAACGACTC AGCGACTTTTTCTGTGAGCAAATGTCGAGG
stSG4376	73	A	G	TTTCACTGCTACTGGTTCGGTGTTCGGTCTGCGGCTCTGCAAGTCCTGCAAGAAGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC AACAG[A/G]CTGGAACTGCGGCTCTGCAAGAAGAATGACAACATACGATTTTCTT[T/C]TCAGTCTTGTAGT
stSG4381	50	T	C	GAAGGCCACAAACACTCCATAGCCAGAGAATGACAACATACGATTTTCTT[T/C]TCAGTCTTGTAGT ATCCACAGTAGTGATGTCTGTCCATGTCCAGAACACCCATTAAATTCCATGCC
stSG4410	79	A;G		ACCAATGGTTCTCTGCTATGTGCATCCGATATTTTTGCCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAAACACCGC[A/G]TGACAACGAACCCAGTGGAACTCAGCGTGAAACTCAGGGTGCGCAGGAGGGTGGCTTGT CAGCTGGGT

stSG443	65	C	T	---		AGCAGATCAGTCAGCCACTTGTCTTCTCTCTTCTTAGGGAGGAGGCTAGGCAGTGAACACATCA[C/T]GTATGCAATGAGAGAAAATAACCAACTGGTAGGATGGGGAGGGGAGGCAGGGAATAGGCAC AAATGGAATTCTATCCTGGCTGTCCTTCTCAGGTC
stSG4430 a	54	A	G	---		ATGCACATTAAATGAATGGCCTAACTACTGGGAACTTTAGTAGTTCTATAAGGT[A/G]ATTAACATA GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATGAGGCATCAAGAGGGCCATTT
stSG4448	99	G	A	---		CCTCCCTTCCCTTCCCTTCCCCTTCCAGTCTTTTCCCATACTGTTCCCCGCCCCCGCCCCCACCCCCAGGCTCT CGCCTAGCCCGCCCTGCCCTCTGGGGTCACTGC[G/A]TGGGGTTAGGCCCCCAAAAAA
stSG4449	92	T	C	---		ATTAGCCATTCATCTTGCAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT TAACTTTGGACAACTTAAAACTTA[T/C]TAGTGACATTGCTGTCTAATAATCAAATACTTCATCATA GGCTGAACATAATTATTAAAAGAGCAAAGTTACCCCTCCC
stSG4467	42	C	A	---		CAGACATGAGGATGGCCCCTGTCTCTCTCGGACAGAGCCCTCA[C/A]AGATGATGTCCATGTTTGTGT GAATGAAACTCAAACACTCTTCAGTTTTAGAGTCATTTTCTGGTATCGAGCGACCACCACCGAGGAG CACACACCCTGCTTCCAAGGCTGCCTTCTGCCACACAGT
stSG4475	21	A	C	---		ACATGTCATTCCTGACCAGG[A/C]TATTAAATAGTTTATTTAGAAGAAAATGAGTTGAAGTGAGCGA TTAAGAGACACAAACTGGACTTTGTTTCTTTACTGTAGCACCCAGGTTCATG
stSG4477	32	A	G	---		GTAACATTCTGGGGGTGGGGGTGAGACAAACA[A/G]ATGAACCAATAATTAATTACAATTATACATT TCAAGGAGACTTTAATCTAGGTTAATGTGAAACGCAGCCATCAATGGTTGTGTCAGGAAAAGGGAGA TGAAGTCTTGCTCTGGGGCAACGTTTGGCCTCATTGCAGTCAGACTTGGC
stSG4531	79	C	T	---		TGAACTCAGAGCTGGGTGGGGAGCTGCAGGCAGGGAGGCTGGGGCGCCAGGCGCCGGGGA CAGCAGGCGGCTCG[C/T]GCCACGTCCTGGCGTTGGTAGAAGAGGACATAGGCTGCCTTGGACTCGATCT GATTCTCATTGACAGGGGAGACGCGTGTTGTCATCAA
stSG4550 b	86	G	A	---		TGCATTAAGGAATGATACGGCCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT AAAAGAGACAGTGGGCACC[G/A]CAATTGGAGGGGAAGGCGGGGGAGGTTTTAGAGAAC
stSG4550 a	85	C	G	---		TGCATTAAGGAATGATACGGCCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT AAAAGAGACAGTGGGCAC[C/G]GCAATTGGAGGGGAAGGCGGGGGAGGTTTTAGAGAAC
stSG4590	47	A	G	---		AATCAGGCACAAGCTCGGGGAGAGAAGCCAACAAAAGCTCTTCTGCCAC[A/G]ATGGGAGGGAGGACAC CATTGAAAAAGGCATCGTTCCTTCCATGCAGCGAGCCCTGGCTCCCACAGGCCATGTGGTCTCCTTG
stSG4623	22	T	C	---		AATCTGTATCACCCAGCCGCTGG[T/C]CAATGTACTAGTAGCTTTCCACAGGGATTTTTATACTTATTC CTATAAGGTTTATCATGAATAAAAAGCTCACAACTCTTTCAGCCATTGCAGATTCACATTTATCT TAATATTCCTGTTCAAGATGCTCTGGAG
stSG4843	102	A	C	---		TAAAAAAAACAACCCCCCAAAAAAACACCCAGAAGTTTTATGTTTCAGATTTAAAG GTATTTCTTTCTTAGCTTCTAAATTTTGAGTCAT[A/C]ATCAGAAAGTCTTCCCTACTCCAAGGTGA GAAAGGA

stSG4850 a	38	C	T	---	GGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC[C/T]GTGCACTTGCAGGCCACGTCAGGAG AGCCAGCGGTGCCTGTCGTGGGGAGGGTTTCCAAGGTGCTCCGTGAAAGAGCATGGGCAAGGTTGTCTGACAC TTGGTGGGATTCTTGGGTCCC
stSG4879	86	A	G	---	AACTCTGAAGGGGTGACCTCAACCCAGCCCTTGTTCTTGTGTGAGGTCCTTGCTTTTGCAGAATGGCCTG CCCTTGGGGACTGGAGCAG[A/G]CTTGGGTGAGCTCTAGGTGAGCTGTGGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104	G	A	---	ACTCGACTGGCTCGCTTGCTGCTGAGCGGCGCTGGGAGCTGCGGCTGACCACTCGCTCTTCAG AGACTCGCGGCCGGGGTGACCACGACTACGCTGCC[G/A]GTGGGAAAGCAGAAGCAGGACC
stSG4896	112	C	T	---	AAACAAATCAAACCCAATCCCCAGCAGTCTATGTACAGGGCCACTCCCTGCCTCTCTGCCATAGAGA GGTTGGGGGGGCAGCTGAGGAGTGGTGGGGGCTGGGGCACCTTTTCT[C/T]CAGCCACAGGCCCCTGAGG AATTAATTGACTG
stSG4932	22	G	A	---	ACAGTGCCGATGGTTACACAAT[G/A]TTGTAAATGTATTTAATCCCACTTACGAATGATTAAAATGA TAAATCTTATGTTTATTTCATCACTACCAAAAGGCTGTGGGTGCAGGGGTGCTGGTTTCTGGTCCT
stSG4950	24	A	G	---	TCATGACTCCCAGGAAAGGTCCT[A/G]TTCTTAGCTTCCTCCTCCCTACTTTCCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATTAGTAGGCATTGCTCCTGCTCCCCTACCCCTACACTTCAAGG
stSG4957	136	G	A	---	AGATACGGGCAAAACACTGGGATGCCTTCCTGCAACTTAAGAGGTCTCCGAGTTATATTCTGGGTT GGGAAACACTGACCCAGCCAGCCCTTATTCCTTCCAAGGACTCTAGTCATTGGCAAGGAGGATTCATGAGCC CC[G/A]GTGGACACAGATGGGGGCCCCTGCTCTATATTCAAC
stSG4961	91	C	T	---	GAAGGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCACAGAGCTTTGTCTTAG AGGAGTAGATGAAAAGGAAAGTA[C/T]AGAGAGGGCATTCAGGCCAGTCAGCAACACAGACAA
stSG4967	72	A	G	---	ACTGTGGCCTCTCTCAGCAGATTCAGGGGGTCGTGCAGGGCTGGTTACCACCAAACTCAGTAGGAGTGCAA GGGCTA[A/G]TACCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTCTCCCTTTTCTTGCTGTGC AACCTTG
stSG4997	22	T	C	---	CAAAGGAGAGTAGGAGCCCCAA[T/C]TTTAATGGTTTCCTCTCCCCTCATGCTATTTGATCCAAAAA CTATATACAATTTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGGAGGCAAGAA GGGGATAGGGAGGAATGGTGATCCAAAT
stSG6312	37	C	T	---	ACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAAACA[C/T]TATGCCATGCGGGAAATAAAATGCTT ATCCAGTGGAGCGCTCCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107	G	A	---	GCTCTCGGTCAAGCAAATTCTCCAGGACAAGGACAAGCAAGAGCAGTAAACACACATGTATGACCCTTA CAAGTGCTTTAAGATTTTAAAAATGTAGTGTGATGTTTTGTCCAC[G/A]ATAGTTCAGGCAATTAAGAATAT GCAACCCAGAGAATTTCTGTGAAAAACATTTTGCTCTTTGGCCTGGTGTGGACAAAGGGGTGGCCAA ATGGGATTGAGTGATGAGCAGACATG

stSG6362	88	G	C	---	TGTGAAATGTACACTCAGGTCTAACAAATACCTATTATTTCTCTGGTTAAGAAGGTTTAGCAGGAGCCTCCAATGAGCCACTGTATGTA[G/C]AGAAAAGGGAAGGAGCAGGAGGAGGAGGAGAACAGAGATCTGCACAGAAT
stSG8010	62	G	T	---	CACATCTGTGTTTCTGGAGCAAAGGGAAACCACAGAGAGGCCAGGAGTTTGGGTGTGCACTGG[G/T]TGTCTTCAACTGGGTGGAAACCAAACTGAGTCCTTGAAGTCTCGCTCCTGAGGCTGCAGAAGAATAGATGGCTT
stSG8022	53	G	A	---	AGCTCCTGACTCCCTGTTCAGTGACGTCATGTTGGTGAGCCTGAAATGACCCAC[G/A]GTGGGGAGTTATTTACACCATGGAAACTGGAAAACTCTACAAATCAATGCGTTTATTTCTTTATTTTCAGAGAGGGCCAGGTTTATCAGCACACGCTGTATCTCC
stSG8032	67	G	C	---	TGATTGTTAGGGATAAGTGGGCATTGTTGTTTACAAATTACTTCCAAAGAATTCAGAAAATTGTGTGT[G/C]TGGGAGGGCAGGGTAGCAAGATAAAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA
stSG8064 b	46	C	A	---	AGCTGGCTCTTCCTCTGTGCGGTTGTTCGGGGAGGCTTCACGTCCTCG[C/A]CCGTGGTCCCTGGGTGGCCTGCAGGACCAGGGGGTGGGAAACAATGCCAGGGAGAATTCCTGTCACATCAAACAGGGAACA
stSG8064 a	23	G	C	---	AGCTGGCTCTTCCTCTGTGCGGT[G/C]TTCGGGGAGGCTTCACGTCCTCGCCCGTGGTCCCTGGGTGGCCTGCAGGACCAGGGGGTGGGAAACAATGCCAGGGAGAATTCCTGTCACATCAAACAGGGAACA
stSG8072	59	A	G	---	CACCATCATCACGAGTAGGCTGAGGAGCAGGAGGGGTGGGTCTTGCTGTGTCTTAGGG[A/G]TGGCAGAGGAGGAAGTCCGAGTATTAGTGGCCGCATGCAGTTCAAGCCTGTGCTGTTCAAAA
stSG8100	40	A	G	---	ATACACCCACACACCCCACTCAACCTTGTATCAAATTCCA[A/G]AAGTGTAACTAAAGTATAAGAATATCATGACTAGTTAAAAGATAGCAAATACCATAAGGTACAAGTTCAAGTATTAGTATAACAAGTATCTGAGTAACAAATGTCCTTGGAAATGGG
stSG8102	138	T	C	---	AAGGCTCCTTGAAAGCATGGTTATTTGTTCATTAACTTGTTCTCAGCTATACTGAAGTATGATTGACAAATAAAACTTGCATATATTTGAGATGTACAGTGTGATGATACAATGTATACAAATGTGAAAATGA[T/C]TGTCATAATCATAATCAATAATTGGTATATTGGTTTAGGAAATGTGATGGT
stSG8105	110	A	G	---	CAGTGGTTCTCAAACTCCAGCGTACACGAGGATGGTCTTGTGTCTTGTTAATACACAGATGACTAGGCCCACCTGCGGAGTTCCTGTTGGATCTAGGCCTGGAGTCTGGAGAATATTC[A/G]TTTCTAACAAGTTCCCAGGTGACCCCTGAGCGTCTTGGGACTGGGGAACATGCTTTGAG
stSG8130 b	96	T	C	---	GTGTGTACATCATTGGGAATGGAGGGAAATAAAATGACTGGATGGTCGTCCTGCTTTTAAGTTTCAAATTGACATTCCAGACAAGCGGTGCCTGAGCC[T/C]GTGCCTGTCTTCAGCACAGTTCC
stSG8130 a	36	C	G	---	GTGTGTACATCATTGGGAATGGAGGGAAATAAATGA[C/G]TGGATGGTCGTCCTGCTTTTAAGTTTCAAATTGACATTCCAGACAAGCGGTGCCTGAGCCTGTGCCTGTCTTCAGCACAGTTCC
stSG8145 b	124	T	A	---	TTGTGGACTTCAAATTCTTTCCTTCAGATTTTAAAATGACATTATGCATTATGACATTATGCGAACACAAATCTAAGAAACTAAGAAATGAATGAGATGT[T/A]CTGAAATCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCCTCTCGTCCTGTGTAAGG

ID	Pos	Allele	Allele	Sequence
stSG8145a	97	C	T	TTGTGGACTTCAAATTCTTCCTTCAGATTTTAAAATGACATTATGCATGTACATATTTTAAAATTT AGACACATTTAGAGAACAACAAATTGTGAA[C/T]ACAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCCTCTGTCCTGTGAAGG
stSG8150	36	A	G	ATTGTTCTTGCAATTGCTTGGATTTTTCAGAATAGTTA[A/G]ATAAAATAATAACGGAATCCTAGGCAT TCGTGTTTTCTATGTTTTAACAGGATTTTCGCTATTAAATACCATGCAGGAAATT GGGAAAT
stSG8340	30	C	T	AGAGGATTATGGGAGAGAGCTGGGCAGGATC[C/T]CAACATTATGACCCTGAACCTCCAGAACTGGAT TCACTAGAAGGAGAGAGAGAAAAACGCTCATCAAAA
stSG8466	111	G	A	TGTGTATTGGGTGACTGTAGCCTAAGGATAAATGAAATAAATAGACAGCAATGTTATAAGCAGTGGGA GGAGTGAACTGGGAATACTTGGTTACAAGGTATTTGCACTACCT[G/A]TGAAGCAGCACAGCATTAT TTGAAAG
ESTD-ACE				GATCAAGCAGTGCACACGGGTCACGATGGACCAGCTCTCCACAGTGCACCAGTGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCCCGTCTCCCGTGGGGCCAACCCGGCTTCCATGA GGCCATTGGGGACGTGCTGCGGCCTCTCGGTCTCCACTCCTGAACATCTGCACAAAATCGGCCTGC
ESTD-ADA				ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCCTGGGAATTCCAGGGTCACTGTTCCTCCTGTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAGTGGGACTGTGAGGACATGGAGGCCTCGGCACTGCGAGCTGCAGACCC GCAGACCAACTCCTGAGCTTTCTGGGCCTCTGAGTCTTGTCCTC
ESTD-AK-168				GGGGAGTGACAGCTAGAGCACCAGGGGGCTCTGTGTTCTCACGAGGACAGGCCTTCTGCTC ATTCTGG
ESTD-ALB				AATCCCAGCCACTTTAGGAGGCTGAGGCAGGCAGATCGAGGCAGGCATATCACCAGAGGTCAGGAGTTTGAGACCAGTCTGA CCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGTGCATGCCTGT AATCCCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCGGAGGTTGTGGTGAGCCGAGAT GGCACCATTGCACTCCAGCCTGGGCAACAAGAGTAAAACTCTGTCTC
ESTD-ANT1				TCTCCTGTCATTCCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGGCAATTAACCAAGTAATTCA TGGACTGCCCAACTGCGAAACAGAAGGGCGCAGTGGAGCGCAGGAGTATTATGCTACGGGTTACCTT TTTTTATGGGAGGACCGAACTGAGCCTCAGATGATCCTGT
ESTD-APOA2				CCAGGTGTTGTGGCCACGTGCCTGTAATCCCAGCTACTCGGGGGACTACTCGGGGAGGCTGAGGCAGGAGAATCTTTGAAC CGGGGGAGGCGGAGGTTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTAGGTGACAGAGCAAG ACTCC
ESTD-ARSB				GGAAGAAAATGGAGCCTGTGGGAAGGAGGCGTCCGAGGGGGTGGGCTTTGTTGGCCAAGCCCCTTGCTGA AGCAGAAGGGGCGTGAAGAACCGGGAGCTCATCCAGGAGCTCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACACAGCCTCTGGATGGCCTTCGACGTGTGGAAAACCATCAGTGAA GGAAGCCCATCCCCCAGAATTGAGCTGCTGCATAATATTGACCCAAAC

Name	Sequence
ESTD-AT3a	AGACCTCAGTTTCCTCTCTTCTGTGTAAAAGGGGAAGTTTGTTCTTGGATCTCCATGGGCCCAGCCAGCACTG GTGCCCCTGTGAGTCTGTATCCAGGTAGAGGAGATGGGACCAGGTGGAGAGGAATTTGAAAGGGCATTG GAATTCAGAGACAAAGAGACAGATATTAAGAGCTGGGGAAATGTGG
ESTD-B3AR	GGCTGCCAGGGGTTCCGTGGGAGGCGCGGCCCTAGCGGGGGCCCCTGCGGCGCTGGCGGGGTGCTGGCCACC GTGGGGAGGCAACCTGCTGCTGCCTGGGTCATCGTGGCCATCCCGACTCCGAGGACTCCAGACCAACGT GTTCGTGACTTCGCTGGCCTGGCCGGACGTGGTCGATGGGGACTCCTGGTGGTCGGCGGCGGCCCACCTT GGCGC
ESTD-BA511	GGGCAACATAGTGAAACCCCATCTCTACAAAAATACAAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGGAGGCTGCAG TGAGCCCAAGATGGTGCCACTGCA
ESTD-BCL2	AGCTGGATTATAACTCCTCTTCTTCTCTGGGGGGCCGTGTGGGGTGGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCCGTTGCTTTCCTCTGGGAAGGATGGCCGCACGCTGGGAGAACAGGGTACGACAACCGGGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTCGCAGAGGGCTACGAGTGCGGGGAGATGTGG GCGCGCGCGCCCCCGGGGCGCCCCCGACCGGGCCATCTTCCTCTCCCA
ESTD-BCR	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCGGAGACTCATCATCTGCGCAAGA GACCAAAGAGGGTCAGCTTCTGTTGTCCCGGGAAAGGCAGGCAGGTGACAAGCTAACTCTGCTTCAAA ATCAACCATCCGGTGGACACTGTGTGCTGCCATCTGCCTGGCACA
ESTD-BRCA1a	AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGTCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAAGGGTTTGCAAACTGAAACTGTAGAGAGTAGCAGTATTCACTGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAA CCAAATAAAT
ESTD-BRCA1b	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGGAAATGAGAACAATTGAGAACATTCCAAGCAACAATTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAATGTT TTTAAAGAAGCCAGCTCAAGCAATAATTAATGAAGTTCCAGTACTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD-BRCA1c	ATGCATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAAATAAAGGAAGATAC TAGTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAGGTTCCAGAAAGGAGAG CTTAGCAGGAGTCCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	ACACAGGTGCTGGCCACTGGGGCTGGGGATCCTCCTCCCCTAATTTGCTCCGGGAAGCACATTCATCAA
ESTD-C6	CCCAGTCAGTTTGGGGGACAGCAGCCATGGCCGCACTGCGACTCCTGCTAGTCCTCGGTAGCCTTTCAACCATGCCATTCCATCTAA GCTCTGCAAAAT

ID	Sequence
ESTD-C7	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	GGCAAGTTTTATTGATAGAGGAGGAAATCAAATAATGGCAATGAGGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAATGGGCAGTGCCAACCCATAGGCGGGATACAAAAGAC AGGCAAGGAAGGGGGTAGAACCATCAAAGAGGAATAGGCTGGTGACCCAAAGCAAGGAGGAGACCTAG TAACATAATTGTGCTTCATTATGGTCCTTTCCCGGCCTTCTCTCTCACACAC
ESTD-CB23	TAGAACCATCAAAGAGGAATAGGCTGGTGTGACCCAAAGCAAGGAGGAGACCTAGTAACATAATTGTGC TTCATTATGGTCCTTTCCCGGCCTTCTCTCTCACACATACACAGAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTTCCAGAGGACCTGAAAACGTGTTCCCACCCGA GGTCGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAA
ESTD-CB24	ACCAGGACCAGACAGCTCTCAGAGCAACCCTAGCCCCATTACCTCTTCCCTTTCCAGAGGACCTGAA AAACGTGTTCCCACCCGAGGTCGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAAG GCCACACTGGTATGCCTGGCCACAGGCTTCTACCCGGACCACGTCTGAGCTGAGCTGGTGGGTGAATGG GAAGGAGGTGCACAGTGGGGTCACAGACACCCGCACAGACCCCGCAGCCCCTCAAGGAG
ESTD-CB25	GTTTTCTTTCAGACTGTGGCTTCACCTCCGGTAAGTGAGTCTCTCCTTTTCTCTATCTTTCGCCGTC TCTGCTCTCGAACCAGGGCATGGAGAATCCACGGACACAGGGCGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTACCTACATGTCTCTGTTCTGTGTCAACGAGTCTTACCAGCAAGGGGTCCTGTCTGCCACC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGTATGCCGTG
ESTD-CB27	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGGCCTGGTTGCATTTCAGGAGTGTGTGGAGTTGGAGTTCATCACTGACCTATCTTCTGA TTTAGGGAAAGCAGCATTCCCTTGGACATCGAAGTGACAGCCCCTCTTTCTCTCCACCCAATGCTGCT TTCTCCTGTTCATCCTGATGGAAGTCCTCAAAACACCATTTCCATACC
ESTD-COL2A1c	AGAATGTATATAGTCCTCCAAACTGCCAACTCTCCATTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGTCTCTTTCCGTCACTTTCAGGGTGTTCAAGGTGGAAAAGGT GAACAGGGTCCCGCTGGTCCTCCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCTTTG GTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1d	TGAGAGAACACCTAGTCCTCCATCCTTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGCTGGGACCTGGAACACTGGACTTCTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTAATGGCAAAGATACAAATACAATACAATTTTATTTGACCAAACACTATCATGGAACAGC ATT
ESTD-CPT2	GCCGCAATGCCCGGGAGTTTCTCCAATGTGTGGAGAAGACATGTTTGATGCCTTAGAA GGCAAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCCTCATCCATGAAAAC TGGGAGGCCGGGGCCATAGTGCCTGTAATCCCAGCATTTTGAGAGGCTGAGGCGGGTGGGATCAC TTGAGGGTCAGGAGTTTGAGACCAACCTGGCCAACAT

Identifier			Sequence
ESTD-CTLA-4	--	:	ATGGCTTGCCTTGGATTTCAGCGGCGGCACAAGGCTCAGCTGGCTACCAGGACCTGGCCTGCAC TCTCCTGTTTTTCTTCTTCTCTCATCCGTGTCTTCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAAAGCCAC
ESTD-CYP2D6	--	:	CAGGCCAGCAGGTGGTCGAGGTGGTCACCATCCCGGCAGAGAACAGGTCAGCGACCACCACTATGCACAGGT TCTCATCATTGAAGCTGCTCTCAGGGTTCCCCTTGAGCCTGAGCCTGAGAGCCGAGAGCATACTCGG
ESTD-D11S1873	--		AAAAAAACATTTTAACACCTTTCAATCATATACACCATAAATTTCCATTTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAATTACTTGCAATCTAAAATGTCATAACTGATTAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAAATTATGCCCATAT CTGCATGTC
ESTD-D17S33	--	:	CATCCCCAAGCCCATCCTCTTAGCCACTGGCATTTTTGCCGCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCCTTGTAGTCCATGGAAAGGCTCCTCTGGGGGCGGGTG GGGTTGTGTGGCTATGTGGTGGTCTTGTTGTGTGAGACGGGGGCTTTGGTTTCAGTTGCACTATTGCGTTATT GCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCTC
ESTD-D18S8	--	:	TTTGAGACCACCCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAAATTAGCTGGGTGT GGTGGTACATGCCTATCGTAATCCCAGCTACATCGGGAGGCTACATCGGGAGGCAGGAGAATTGCTTGAACCCA GGAGGCAGAGCTTGCAGTGAGCCAAGATCACACCACTGCACTCCAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD-D3S11	--	:	AACTGATTAGAACCTGAAAATACATATTTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTTGCATCATTAAAAAAATCCAATAAAGTACACTGTAATAAAGAATATCATTGT TTATTCAAACTATTTATCACTTATTTATTGGTAAGCCATACTAAAATTCTAAAGCATGTTTCTGAAAAG TTTA
ESTD-D3S12	--	:	AGGTTCCACATTATTGCTGTGATGTTTGCTGAGTGTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACCTTGAGACGTACTTTTCAAAACTCTCTACAGCCGTTGTTGTTGTTATTAATTCAAGGTTGA ACATAAAGTA
ESTD-D3S2	--	:	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTCCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCC AGAAGTGAAACATACTGCTCCTAGAAGCCAGAGTCATACTGGATGTTCTTCGGTTCTTCGGTTCTTCCGCGATGG CAGGTATGAAATAATAATATAATCTGCCTTTATTTGGAAGGATGCCGGTATGT
ESTD-D4S338	--	:	TTTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAAATGTATTT CTTAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGGACTGCAGAATAAAATGTTATTT TAGCTGTCAGAAAAACAAATAACTATACTTCTGCATATGTTCATCAGAGCCCTTGGGTGACCAGGTGTATT GCCAATAAGCAGCAGTAATATTTGTTTTTCATGCAGTAG
ESTD-D4S95	--	:	CTTTCATGCACGATAGGCTTTCTCTACTAATCACACAGAATTTTGAGAAGAGCAAAACAACTTTCAAGG ATAATGGGGCAATCACTTCTTTCTTCTTTAGAGTCTACCGG

ESTD-D7S399	::	:::	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCCACCTCCATAGAT AACTGCTAGAGAACCCAGTCTCCTACATCATCCTTTCACAAACATTTTCATCCATGGACTCCATACTAG AATATTTGAAGAAACAAACAAACATGACAAACATTTTC
ESTD-DM	::	:::	GTGGGGACACCGAGGGCTCCAGGCTGGGCGCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGGCCCTGGGACCTCACTGTCCTGGGGAGGAGGAGGAGGAGTGGGGAGGGAGACA GAATGCTGATTATCTGGTGGAGAACCAGAACTTCTGGCCTGTGGGGCAGCTGCTTCCAAGACC TCCTGATTTGAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DRD1	::	:::	TCCCCAGCCCTATCGGTCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC ACAAAACGGTCAGCACCCAACCTGAACTCGCAGATGAATCCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTCTGGGGGCTCGCTATTAAGAAACTAAGGTAC
ESTD-DRD2	::	:::	TCTGCCCTTTGGTGCAGGAGGCTGCCCGGCGAGCCCAGGAGCTGGAGATGCTCTCCAGCACCA GCCCACCCGAGAGGACCCGGTACAGCAGCCCCATCCCACCACCAGCTGACTCTCCCCGACCCG TCCCACCACGGTCTCCACAGCACTCCCGACAGCCCCGCCAAACCCAGAGAAGAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD-DRD3	::	:::	AAGACGATGGCCAGGATGAGCGCGCAGGATAGTAGTAGGCATGTGTGGGCGGCCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAGGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCCAGAGGGAGGTGCGTGATGCCAAGGGGCTTCCTGTGAGGAGA
ESTD-ERBB2	::	:::	TCTTTCAGGATCCGGATCCGGCCTGGTTGGGCATCCTGCGGCTCCGCTAGGGTGTCAGCCGGCTGTGG GGTGAGGGGGGTGGTGGGTCAGTGCCCGGCCGGGTGCAGAACCCCACGCGGCCTGGGAGGACTTCACCC CGCCCTCACCTCCGTTTCCTGCGACGAGTCTCCGCATCGTGTACT
ESTD-ETS2	::	:::	ACTCACAGTGCTTTTAAGTGAAAATGTGCGAGAAAGAGGCACCAGGAAAGCCGTCCTGGCGCCTGGCA GTCCGTGGGACGGGATGGTTCTGGCGTGTTTGAGATTCTCAAAGGAGCGAGCATGTCGTGGACACACAC AGACTATTTTAGATTTTCTTTGCCTTTGCAACCAGGAACAGCAAATGCAAAAACTCTTTGAGAGG GTAGGAGGGGTGGGAAGGAAACAACCATGTCATTCAGGAAGTTAGTTTG
ESTD-F2	::	:::	GATAAGTACACTGAGGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAAATGGCCTCCAAGGCCTCCAAGGCCCGTAGGGGGGATCGTAGGGGTGAGGAATGGCCC AGCCCAGTCCCCGGCGCCGGTCCCGGTGCCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGGAGGATGGGGC TGGATGGAG
ESTD-F9	::	:::	AGATCCTGATGATTTTTTCCTATTTTTTCTAAATGTTTACAGTTTGAAGTTTATGCCCA TGCTCCATTTTGAGTTAATATTTGTGTAAAGTATGATGTTTAAGTCAAACTTCATTTTTTTTCCATA GGTATGTCCAATTTATCCAGCACACAATTTGTTAAAACAAAAAC

ESTD-GCDH	--	CGCAGACCGGTCAGTGTGGGGTCGGGAGTGTGAGGAAGGAGGAGGAACTGGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGCGCACCGTGTGTTCTGCTGCCCCTGTTCAGTCGTGCTGCGCCAGTCGA GTGTAAGGGACCTCTGGTCGGCACCGTGTGTTCTGCTGCCCCTGTTCAGTCGTGCTGCGCCAGTCGA CTCTGTCCCGGAAATTCCGAGAGCT
ESTD-GCK	--	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGCCCCTCTCAGGAACACAGTGTAAGCCCTGGCAGGAGAATCCCCCACCCCACCCTGGCTGG AGCAGGAAATGCCGAGCGGCGCCTGAGCCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAAGCTGTCCCCAGGTCACAG
ESTD-GNAT2	--	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCACAGGCATCATTG AAACCAAGTTTTCCGTCAAAGACTTGAATTTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-GPPK2L	--	AGTCTTCATCTGCGGGTGTGTCCAGGTAGAATCCCTTTCACCGCCGAGAACTGCTCTCGATATC
ESTD-HRAS	--	CTGGGCTCGCCCCGCAGCAGCTGCTGCCCACCTGGCACCTGCGCGCGCCAGGCTCACCTCTATAGTGGGGTCG TATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD-HSD3B1	--	TTGGAAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCCCCACATTCTGGCCTTG AGGGCCCTGCAGGACCCCAAGAAGGCCCAAGCATCCGAGGACAGTTGTACTATATCTCAGATGACA CGCCCTCACCAAAGCTATGATAACCTTAATTACACCCTGAGCAAAGAGTTCGGGCCTTCGGGCCTTCGATTCC AGATGGAGCTTTCCTTTATCCCTGATGTATTGGGATTGGCTTCCTGCTG
ESTD-HT2	--	GGGCTAAAATTTCCGAGCAACTTGCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGAGATGTGTTACAGTTGTCAGAGAGAATAAAAAGGATAACCTGGGGTTTTCTGTGC TTTGCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGGACGAGCA AAGCGCAGTCGTGAAGTTTCAAACAAGACACACTT
ESTD-HT4	--	ACCAACGAGCGCGCGATACAGACACTCTTAAGTTTTGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGGTGCCTTCTATCTCGCAAGAATGCGTACTTATTTGAATAGTAGAGGTAA ACCACACGCCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	AACACACAAGCCCAGCGGAATTGAACTCGCGACCCCTGGTTTACAAGACCAGTGCTCTAACCCCT GAGCTATGGAGCCCCTGCGTCTGCTGTTCTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCACCGGGCAATAGGATGGTGAGTACGGTAAAAATTCCAGGATAATTCTCTACAAAATGAAA ACATTTTCGTGCTCTGTAAATCCCTGAAAGGTTCT
ESTD-IGFBP1	--	ACCCAGTGGAGCCCCGGCTCATTGCACGGTGTCTTGGCAGGAGGTGCCCTGCCCTGGGAGGAAGGAAGATGTTC CAGGGCACACATAGCTTAGTGGGAGACTC

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ESTD-IGHV4-6	TTTACTATTTCAATGGATACAGAGAATTGTGGGAGTCACTATATTCCTATGAACAAAAAATTCAGATTTCAGTGTTAAGTAATGTTGCCTACATTGTGTGCTACATTCGAGAAAGCAATATGGAAAGATGAGTATCTATGGATACGAACTGAAAGTGGTGGGTGCACGGACATAATGATTCAGAAAGCAATATAATACTAATAAACGGAGTTGAATATAAAACCCAATGTAAAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	CAAAGTAAGCACCCAATAAAATGTTAGCTATTACTATCATTATTATTTATTTTTATTTTTTTGAGATGGAGTCTGGCTCTGTCACCCAGGCTGGCACAATCTCGGCTCACTGCAAGCTCTGCCTCCTGGGTTCATGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCACCCGCCACTGTTCCCGGCCTAATTTTTGTATTTTTAGTAGAGACGGGAGTTCACCGT
ESTD-IL1B	CCACTTACAGATGGGATAAATGGGTACAATGAAGGGCCAATAGCCCCTCCCTGTCTGTATTGAGGGGTGTGGGTCTCACCTTGGGTCTCTGCCTCAGGAGCTCTCGTCAATTGCAGG
ESTD-KRT10	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTTACCTTTTTGGCAATATTAAAGGAAGAAAATGCATTTTAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTGCTTTTTAAATAGTCTCTGCCCAGATACATCTCCCCTATATAAGTTATAACCAGTATTGATA
ESTD-KRT8	ACCCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATCGGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACGAACTTTCTAGAGTTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGAGGGCCAGAATGTTAAGTACAAAAGTGAGGCCCATAGGCTGCCTATCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
ESTD-LF79	GGGTGATTTTGAGGCTCAGTTAATATTTCAAAATTGTAACCGTAGCAAAACTGCATTGGTATTTAGAAAAATAAAAAATTTCCAATATGTAGTGCTGTGTTATACCTGCCCTCTGCCATGCAGCATCAGCAGCCTGTGGGAACCAGGAGGGCTTCCCTACCACCCAGA
ESTD-LMP2	TACACACTTTCCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGGAGTTGACCTTCCCAAAGCCACTACTATGATAAGCTATTGGTG
ESTD-LPL	TGTCAGTGTCCCTAGGGCACCTCACCACTCCCAGCTTCTTCAGCTCTGCCTGTCCTGCTGCTGCAAGGGTTTGCTTAATTCTCAATTCTCATCTTTAGCAGCTGTGGGGTTTTGTTGTTGTTCTTCTGTTTTGCTTAGTATCTGACTACTTTTAATTATAAAAAGAGATGTATCTAAACAAAATAGAGATTGTTATCAGAAGTTCACAACATTTATTAAAAAATTTTTCACCTG
ESTD-MCC	TTGTCAGGAGTGTGCTAGATGCTGCCCTCGCCTCCCCAGCTCTGTCCTGGATGCTGAGATGCTGATGCTGCCCTAGCCGAACTTCAGGACAACGTGCAG
ESTD-METH	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAAACAGCATGCATCCCGAATCTCAGGAAGTCTGTCTTCCAAGGGTTGGTCTAAGTGTGCTGATTACCCGGAATTTTCTGACGATCTTTCAACTGCTAGAGCATCTGGTTCCTGTTTTAGCATGG
ESTD-NF1	ATTATCCAGATGAATTTACAAAACTATACCAGATCCCACAGACTGATATGGCTGGT

Identifier	Sequence
ESTD-NFKB1	AACATGGACTTGTATATTTGTACAAAAAAAAAGTTTTATTTTCTAAAAAAAGAAAAAGAAGAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGAACTTTTGTAGGGGACGAGAAAGATCATTGAAATTCTGAG ATCAGCGCCCTCATTTGTCTTTGTGAACCTTCACCTTTGTGGGGTTTTGGGAGAAGGTTATCA AAAACTTCTTTAAACCTCAC
ESTD-NPPA	TGTCCCTAGGCCCAGCCCTGCTTGTCCCCCTGGCTGTTATCTTCAGTACTGCAAAGAGAACACAGAC AT
ESTD-NRAMP	GGAGGCAGGAGGTGGGGAGGGGGTCTGTCTGCTCCAGGTCCCACAGACCAGAGAGCGGCCTCAGTG TATCCCACCCCCAATGTGGGCGCTGGGGAGGATGAAGAGAGTTGATGCAGGT
ESTD-NRAS	GTGTTTTCTTAATCTTTTCCAGGAACACAGTGACCATATTCTTTTCTGCAGGCATATAGAATTTGGT GGGTTTTCTTTTATGTGTAGGGTGATATTGGATACTTTTTGTTTGTGATTATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTTAGATGCTTATTTAACCTTGGCAATAGCATTGC ATTCCCTGTGTTTTTAATAAAAT
ESTD-OTC	GTGACCTTCTCACTTTAAAAAACTTTACCGGAGAAGAAATTAAATATATGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAAGGAGGAGGTATGTAACA
ESTD-PAI1	GCCACCACCACCCCACCCCAGCACACCTCCAACCTCAGCCAGACAAGGTTGTTGACACAAGAGAGCCC TCAGGGGCACAGAGAGTCTGGACACGTGGGGAGTCAGCCGTGTATCATCGGAGGCGGGGGCAC ATGGCAGGGGATGAGGGAAAGACCAAAGAGTCCTCTGTTGGGCCCAAGTCCTAGACAGAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	CTCTTCAGGAACCACCAGTCTCTTCTTACCAAACACGACTTATTGCTGTCCGAGAGGTACAACCCGTAGA ACTTCTTCCTAACTGTAATTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTCATTAGCTCTGTGAGTGTTTCTTCTCACTTTCTGTGTTCTAGAAACGTTTTCTAG GACTGGCAGTTTAAGCTTTCACTTAGGCTTTCTGTATACCATGCC
ESTD-PBDA	CCTTCTCATGCCCAGATGGAAATTCCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGCTGGGAAGGGCAGGACTAATCCAAATCTCTCACCCGCAGCTGCTGCCATACAGACG GACAGTGTGGTGGCAACATTGAAAGCCTCGTACC
ESTD-PS-1	GGGGAGTAAAACTTGGATTGGGAGAGATTCATTTCTACAGTGTTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACAACCATAGCCTATTTCGTAGCCATATTAATTGGTTTGTGCCTTACATT ATTACTCCTTGCCATTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTTT CTACTTTGCCACAGATTATCTGTA
ESTD-PXMP1	ATGAAACATGGTTCTTTAATTTTATGATATGTTTGTTATAGCTATCTTAAAAGGGCTTCTTTTTTTA ATGCAGAAAGAGGGGAAAAAGAGAGCGAGTGTGGTGGACAAGGTGTTTTCTCAAGGCTCATACAGA TTCTGAAAATCATGGTCCCTAGAACATTTGTAAAGAGGTAAGTCTTATGAAATTATATCTT
ESTD-Per/RDS	ACCTACAGACGTCGCTGGATGGTGTGTCCAACCCCGAGAATCTGAGACGGGCGAGGCAGGCGGCTG CTGGAGAAGAGCGTGCCCGGAGACCTGGAAGGCCT

	Sequence
ESTD-RDS	CCCGAGGAATCTGAGAGCGAGAGCGAGAGGGCTGGCTGCTGGAGAGAAGAGCGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAAGCTGGGGCAAGCTGGGCAAGGGCAAGGCCGAGGGCGCAGACGCAGG CCAGGCCCCAGAGAGGCTGGCTGGGCCCTGGGCGGCCCTCCCCTCCCGAACACTGAGAAATAGTGCACT CCAAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD-RYR1	CTTCGTGACGGGGAGGTCACGTCCTCCCGCCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTGATGACCAGCGCAGACTTGTCTACTATGAGAGGGGAGCTGTGTGCACTCATGCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGAATCAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCCACT CCGAGTCCGGCCATGTCACTCACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-SPTB	TGAAACACCCTGGTGCCGGAGCCAGGTTGTGTTTCTCCTGGGAGCCTGAGGAGTTTGTTGTCTGTGTG CAGTCCCCCGGCCGGCCACCTGTCGTGGTTGAGCCTGGAGCATACACCTTCACCTCCTTGGCCCGGAGAAGAC ATTTACCCACCTGGCCATGTCCCTGCCCTGTTGTGCACACCCTCTGTGAAGACCCCAACCCCTGCCTCC CCCACCACCAGCCAGTTCCTAGCAAGGGCAGGGAC
ESTD-SSA1	TTCACTTTGTGGATTGTTCTTTTGCTGTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCCTGTGTCTTGTGTGGGATATTTGAAAGAGATCTTTGCCAGTCCCAATGTCCTAGAGAG TTTTCCCAATGTTTCTTGTGTAATAGTTTCATAGTTTGAGGCCTTAGATTTAAGTCTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	AAATGGTCAGGACCCTGATCCACAAGAAGTGGTACCATTTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACGTTGTTTACAACTTTTCTCCCAGTATGGATGGGGATTATGATGGGGGG ATTTCCTCTCACCTAGAACGTTTGTTTACAACTTTTCTCCCAGTATGGATGGGGATTATGATGGGGGG GAGAAGCAAATTTAAATAGGACCCATGAGACACATCA
ESTD-THRB	TGCGGGCCTTTCCTCCCGGCAGGGTAGACTTCTTACTTGGCTGTTGATTTCCAAGAGAAAGAGTCCAAG CACACGAAAACAGAAGTTGCAGATCCCATGAGGCCCAGTCTCAAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAAACAAGTCTGAGTGCCAGCGACTCAACGGTCCCCTGTAGATGGG
ESTD-TNFA	TTCCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGGAGGACGGGGTTCAGCCTGCAGGGTCCTACACACAAATCAGTCAGTG GCCCAGAAGACCCCCCTCAGAATCGGAGCAGGGAGCAGGGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCCAACTTTCCAAATCCCGGCCCCGGGGATGG
ESTD-TYR	TAGTGAAGTTTTCATCTCCTGTCAGCTTCTGATTTCTTGTTCCCACCGCAACAAGAAGAGTCTATGC CAAGGCAGAAAAGCTGGTGCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCAGATCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCATAAATATTGATGTCGTTAAACAT GGGTGTTGATCCATTTTCATTTGGCCATAGGTCCCTATGGGGGATGACA

ID	Sequence
ESTD-TYRP1	AGTAGTGGATGAAGCTAACCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAACGTCTGTGGTCTCAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATATAGATTGAGTATTAACTGTATTTTCTTTCACTTATTACCTTCTTTCT AATACAAGCATATGTTAGAATTAAAGTTCTAGGCATACTT
ESTD-VB12	TTCCCAAGGCCTCAATACAACATCAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGCCTGGGAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCAGTG ACTCTGAGATGTCACCAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	AGGTAGGAAAAGCAAAGAGTTGATTAGTGAAGGAGAGAATGACCTACCTTCCACACTGTCCTTTGG TCCCCTAGAGTCTG
ESTD-WT1	AAGACCTACGTGAATGTTCACATGTCGCTTAAAGCCTCCCTTCCTCTTACTCTCTGCCTGCAGGATGTG CGACGGTGTGCCTGGAGTAGCCCGACTCTTGTACGGTCGCATCTGAGACCCAGTGAGAAACGCCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD-s14544	TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTCGCTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTAACC TCT
EST717706	AGCACCACCTCTCACGTCAAGCCTCAGCACCAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGAGTTATTTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAAGAGAAAACCACTGACAGTACCAGCTGTGTTGGTGGAAGG AGTGCCCAGTCCCAGGGTGACACTGGACACAGAAGAGGCCATCCAAGG
EST524186	CAAATTACAGGGTCAACTGCTATGATGTGTTGGAGCCCAGTCACCCTTTGGTGCTACAAGATGTCG GGGAGTGGGCGGGGAGTTGGGCGAGTACGGGCGTGCAGGCATACAATACACTAAAGTGAAAACTGTGAGTGTGG
EST135863	CCCACTCTATTTGCCCAGCCCCAGGGACAGAGCTGATCCTTGAACTCTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGGCCAGGGCTGGCTTATCAGCCTCCCAGACCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCCTGCTGCCCCCG GTCACTC
EST519767	AGGCAGAAACTGGGCCCCCATGCGGGGGGACGTGGAAGGCCACTTGAGCTTCCTGGAGAAGGACCTGA GGGAGCAAGGTCAACTCAACTTCTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGAAAGAGACTCTCCCT CCCTGAGCTGGAGCTGAGCAACAGCAGCAGCAGCAGCAGCAGGTGCAGATGCTGGCC CCTTTGGAGAGCTGAGCTGCCCCTGGTGC

EST114586		CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTTCTCGAGTTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTCCACAGTGGT CCCATTAAAAACATTCTATGAGCCAGGAGAAGAGATTACGTATTCCTGCAAGCCGGGCTATGTGTCC CGAGGAGGGGATGAGAAAGTTTATCTGCCCTCACAGGACTGTGGCC
EST398528		CGGTCTTCCTTCCAGGTATTGTTGCAGAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAAAGGCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAAT ACAGCCCT
EST624480		ACCTGGTGTTGCTGCTGCTGTGGGTGAACCTGGTCCTTGGCATTGCCGGCCCCTCCTGGGCCCGTGG TCCTCCTGGTGCTGTGTGGGTAGTCCTGGAGTCAACGGTGCTCCTAGTGAAGCTGGTCGTGATGGCAACC CTGGGAACGATGGTCCCCAGGTCGCGCGATGGTCAACCCGGACACAAGGGAGGAGCGCGGTTACCCTGG CAATAT
EST360272		AGTGACTTGCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACACAGCATTGCATACATGGATGAGAGCACTGAAACCTGAAAAAGG CTGTCATTCTACAGGGCTCTCAATGATGTTGAACTTGTTGCTGAGGGCAACAGCAGTTCACTTACACT GTTCTTGTGAGATGGCTGCTCTAAAAAGACAAATGAATGGGGAAAGACAA
EST122740		CCCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGAAGTCAAGTCAGTTGGTTTACTCCTCATGACCAAATATTCTTCCCTCCTTAGGATGAGGTGA TAGTAAATGACCGATGGGGTCAGAACTGTTCCTGTCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGGCCACAGAGCTTGCCAGATC
EST76807		ATGCTAAGGGGGATCGGACATGAAAGGACCCTGTGAGCCGATTGTCCTATCTCCAGCGGCCCTGTCATC CAGCTCACTCACTCAATGGGGCCCAGTCAGGCCCAGCCACTGGGCTCCGGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGGACTTCTTG
EST444387		GCAGCCAGGAGCGCCGCTGCACCCGCTACCATGCCCCGCCATAGATGCGGGACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGCGGAGCGAGCAGCCTCAAGAGCGGAGCCGAGGTGGG
EST128393		TGCAAAACACAAAATCTTCTCCAGATATCTGGATTATCTAAATGAACACACGAGCTTACTCCAGAGATCAAGTCCAAGG CCTAACATCTATGTACTGGATTAATCTGAGTGATTAAATGAACAACACTGGTGAGTGATTACTTGAGTAAGGAAACTTGAATTGATTATTCAACTGG CCATTGGCTATCTCAACACTGGTATCTCAGTTACTTATGAATTATTATGATACTTAGCTTAG
EST544198		CTTCTGCCTAATTTGAATGAATGATATTGTGTGGGACCTGAGCACTTTTATGGCACAAATGATCACTA TTTCTTGACCCCTACTTACAATCCTGGGAGATGTATTTGGGTTTAGCGGTGGTCGATGTGTCTCTACTA TAGTCCAAGTGAA

EST ID	Sequence
EST10398 2	TGCCTGGGGTGGCAAGGCTGCAAACAAGGAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTCACATTGGGGCTTCCAACACGGAGAAG CATTGTTTTCTTCGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
EST36751 7	CCAAGTCGTTCAATTTTAGCTTTGCAGGTTTTAACTCGATTACTTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACTTAGTTTCTGATCTATGGTTCAAGTTAAACAG
EST40562	CACGTGGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAATCTGTCCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCATTAATAACAAATATTTACCTTTTGAAAAAATAAATG AAGGATTTGACCTGCTCTTCGCTGGAAAGAGTATCCGTACCGTCCTGACGTTTTGAAACAATACAGAT GCCTTCCCTTGTAGCAGTTTTCAGCCTCCTCTACCCTA
EST18288 3	GCTCTCTATACCCCTGTGGTCCTCCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCTGACGGGAGCCAGTGTGG ACAGCACCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	TTCCCGCCAGCCCCCATCCTTGGCACCTGGTCCCCCTCCAGGGGCCCACTCACCGCTCT CGCTCTCGGTAACATCCGGCCGGCGCCGTCCTTGAGCACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCCTTCCTCGTCGTCCGGGGCCCAGCCCCTGCAGAGAGAGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
EST58707 7	CAGTGTATCTGGAAAGCCTACAGGACACCACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAAGGCCAAATTCCGAGAAGATACACGAGACCGA ATGTATCAAAATGGACATTCAGCAGGAACTTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCTT
EST74167 6	AGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACTGGAGGAACAACTGACCCCGGTGGCGGAGG AGACGCGGGCGGCCGGCTGTCCAAGGAGCTGCAGGCGGCGGCCGACCATGGACGA CGTTGCGGGTGCGCGGCCTCGCCCTGGTGCAGTACGCGGCGGAGGTGCGGCAGGCACCGAGAGAGC TGCGGGTGCGGCCTCGCGCTCCCACCTGCGCGAAGCTGCGTAAGCGGCTCCTC
EST43211 8	CGCCCTGGTGCAGTAGCGGCGGCGGAGGTGCAGGCCATGCTCGGCGCAGAGCACCGAGGAGCTGCGGGGTGCG CCTCGGCCTCCCACCTGCGGCCAAGCTGCGGTAAGCGGCTCTCCCCGCGGATGACCTGCGAGAAGCGCC TGGCAGTGTACGCAGGGCGGCCGGCGGCCGCCATCGGCGCGCCGCGCGAGCGGCCCTG GGGCCCCTGGGTGGAACAGGGCCGGCCGCCGCCGCGGCCGGGCTC
EST36770 4	TGTAGCCAAAGTCACCTGCATCATTGGCTGCTGGCCAGGCTTGGCCAGTTTGGCCAGCTATAATCC ATCGAAATGTATTTTCATTGAGAACAACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCCTCCCGATAGGGCTGGCCTGACCAAAAATATACTGGGTTCCGTTCCTTTTCTGATCAT TCTTACAAGTTATACTCTTATTTGGAAGAAGGCCTTATG

EST	Sequence
EST260211	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTTGAGGTTGAGTGACATGTTCGAAACCTGT CCATAAAGTAATTTTGTGAAGAAGAAGGAGCAAGAGAACATTCCTCGCAGCACTTCACTACCAAATGA GCATTAGCTACTTTCAGAATTGAAGGAGAAAATGCATTATGTGACTGAACCGACTTTCTAAAGC TCTGAACAAAAGCTTTTCTTTCCTTTGCAACAAGACAAAGCAAAGCC
EST512120	ATCCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTTCTCTCTCCACAAGCCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTTGGAGCCTTGTGCTCCCACTCAATACAAAAGGCCCCCTCTCT ACATCT
EST201182	GTTCCGAATCCTCCTCCTGAAAGTGGCCGGGGTTAATCTGCTCATGACGCCTGCGGGTCTGTGGTCCAGCT GAGGTGAGGGCCTTGAAGCGGTGGGGTTTAGGGACGGCGGGGTTCTCTTGCGTGCATCCTAAGCTCT GAGAGCAAACCTCCCTTGAAGCTGGGGTTTAGGGACGGGTTTAGGGACCTCTGCGATCCTAAGCT CTGAGA
EST530186	ACAATCCAGGTCACACATTCCAGAAGAGGAGGGGTGGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST687875	CTTCCTATGGGATTTGACTTTATTTCTCCATTGTCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCAGCTCATGACAATTTGAAGCTGACAATTACACAAGAAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTCGAAACATTGAAGTTGTTTGAACTTGGTGTCACCTTTAATTACAACCTAG CAGACGGAACTGAACTCAGGGTAAGAAT
EST340882	GTGGGGGCAACAGTGGGAGGAGAAGGGGCCCAGGGTATAAAAGGGGCCCACAAGAGAGACCGGCTCAAGG ATCCCAAGGCCCAACTCCCCGAACCCACTCCAGGGGTCCTGTGGACAGCTCACCTCAGCTGCAATGGCTACA GGTAAG
EST373825	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCCCTCTTTCTTCTTCTTCCCCTTGGA CTTTGAGTCAAATTGGCCTGGACTTGAGTCCCTGAACCAGCAAAGAAAGAAGGACCCCAGAAAT CACAGGTGGGCACGTGCGTCTCACCGGCCATCTCCCTTCTCACGGGGTAAACT
EST740821	TCCAGGGGTGGCTGGACCCCAGCCCCAGCTCTGCAGCAGGGAGGACGTGGCTCGTGAAGCATG TGGGGGGTGAGCCCCAGGGGCCCCAAGGCAGGGCCCTGGCCTCAGCCTGCCCTCGTGCCTGCCTGTCAC CCAGATCACTGTCCTTCTTGCCCTGTGGATGCGGCGCCTTGGAATGCGCCTGCGCCCTGCCCCTC TGGGGACCTGACCCCAGCCCAGCCCAGCCTTTGTGAACCAACACCTGTGCG
EST453110	GCCCTCCTCTCTTCCCAATTCTGTCCCTATAGTTTTCCTCTATTAAGTGAACTACATGCATTCTTTAGT GGATAGATGCACAAACACAACACAGCCATTATGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAATCACCTCTTTCATTTCAATTTAACAGCCCTTATTCAATGGCCTTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTTGTTGAAT

EST65258 8	--	--	TGCCCCATCACGCGGCCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTCCACCCTGACTGACAGCCATGGCGGCCGGCCGGTGCTTCTGGGGGCTCGTCGTCGGGGGGG ACAGCTCCACTCTGACTGCCACAGTCTTTGCATGGACAGTCTTTGCATGGAGACTCAGTCTGATTAAA GTTAGGTGCGTGTTTCCTGCAAGTCAGGAGGAGCTTGAGGAGGGAGGCCTTGAGGTTGGTGAG
EST38216 3	--	--	ATGCAGGATGAAGGTGGACAGGGAGGAGGGGCCAACCTGTCATCCCAGGGCCTGCGAGATGTCGCTG GACTATGGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	--	--	ATACTAGTACAAGTGGTAATTTTTGTACATTACACTAAATTATTAGCATTGTTTTAGCATTACCTAA TTTTTTCCTGCTCCATGCAGACTGTTAGCTTTACCTAAATGCTTATTTAAAATGACAGTGGAAG TTTTTTTCCTGGAAGTGCAGTATTCCCAGAGTTTTGGTTTTGAACTAGCAATGCCTGTGAAAAA GAAACTGAATACCTAAGATTTCTGTCTTGGGGTTTTTGGTCATGCA
EST35879 9	--	--	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGCACACGTGTGCCACCGGCTGTACCCAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCCTGGAAGCAGCAGCGGGGCAGGAGAAGAGCTGCCTGGATGAA
EST68308 5	--	--	GGAAAGAGAATTTAAGAAGCTTGATTGGACAATTCTGGTTCTTGAGTGTGGAAGAGTTCATGTCTCT GCCTGAGTTACAACAGAATCCTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGAGACTTAAAGTAAGAAAGTAGTTATTTTTA
EST54045 6	--	--	GGAATATTAAAAATATTTTAAAATACCTCCATTTGCTTATCCTTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTGTTTCTTACAAAATCGGATGGGAAATCT GTTAAGTAAGTACTGTTTGGCCTTGGAATTGGATTTTTAATGTTGACTTTATCAT
EST52908 0	--	--	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCCTGGGAGATGGATGGTGGTCTGCAAGCCCTTTGG CAATGTGAGATTTGATG
EST19590 0	--	--	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAAAATGAC
EST76136 0	--	--	TGAAGCTTCTGCCCAGCTTGCATTGTTTCTAGGAGAACCCGCGTCATACCTTTATCTATAGCCTTCCCC TAGGTCTT
EST58607 0	--	--	CTCTGGGATGGGTTCACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAAGGAGCACAGCCACACATGGCGCGGGATGGCGCGGGGAGTTCTGGT TGCGGGCCACGGCGTGGCCCTGCCCTTGCCGGTTGAACGGTAGCCTTTGCGATGCCTAAACCTTTGTTTCT TGGGCCAAGGAGGGCGCGGGCTGCCATGCCTGAGATGTAGATGCGGCC

Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer
6=SNP Reverse Primer 7=Sequence

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EQUIVALENTS

   While this invention has been particularly shown and
described with references to preferred embodiments thereof,
it will be understood by those skilled in the art that
5   various changes in form and details may be made therein
without departing from the spirit and scope of the
invention as defined by the appended claims. Those skilled
in the art will recognize or be able to ascertain using no
more than routine experimentation, many equivalents to the
10   specific embodiments of the invention described
specifically herein. Such equivalents are intended to be
encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
    or a portion thereof which includes a polymorphic site,
    or the complement of the segment or portion thereof.

2. The nucleic acid segment of claim 1 that is DNA.

3. The nucleic acid segment of claim 1 that is RNA.

4. The segment of claim 1 that is less than 100 bases.

5. The segment of claim 1 that is less than 50 bases.

6. The segment of claim 1 that is less than 20 bases.

7. The segment of claim 1, wherein the polymorphic site is
    biallelic.

8. The segment of claim 1, wherein the polymorphic form
    occupying the polymorphic site is the reference base
    for the fragment listed in the Table, column 3.

9. The segment of claim 1, wherein the polymorphic form
    occupying the polymorphic site is an alternative form
    for the fragment listed in the Table, column 4.

10. An allele-specific oligonucleotide that hybridizes to a
    segment of a fragment shown in the Table, column 7 or
    its complement.

11. The allele-specific oligonucleotide of claim 10 that is
    a probe.

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12. The allele-specific oligonucleotide of claim 10, wherein a central position of the probe aligns with the polymorphic site of the fragment.

13. The allele-specific oligonucleotide of claim 10 that is a primer.

14. The allele-specific oligonucleotide of claim 13, wherein the 3' end of the primer aligns with the polymorphic site of the fragment.

15. The allele-specific oligonucleotide of Claim 10, which is selected from the group consisting of the nucleotide sequences of the Table, column 5.

16. The allele-specific oligonucleotide of Claim 10, which is selected from the group consisting of the nucleotide sequences of the Table, column 6.

17. An isolated nucleic acid comprising a sequence of the Table, column 7 or the complement thereof, wherein the polymorphic site within the sequence or complement is occupied by a base other than the reference base shown in the Table, column 3.

18. A method of analyzing a nucleic acid, comprising obtaining the nucleic acid from an individual; and determining a base occupying any one of the polymorphic sites shown in the Table.

19. The method of claim 18, wherein the determining comprises determining a set of bases occupying a set of the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is
    obtained from a plurality of individuals, and a base
    occupying one of the polymorphic positions is
    determined in each of the individuals, and the method
5   further comprising testing each individual for the
    presence of a disease phenotype, and correlating the
    presence of the disease phenotype with the base.